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OM protein - protein search, using SW model

Run on: September 16, 2005, 06:32:49 ; Search time 282.201 Seconds
(without alignments)
1074.481 Million cell updates/sec

Title: US-10-658-904-2

Perfect score: 4078
Sequence: 1 MEGDGTPTWALALRTFDAG.....SLKFGGHPATLIRSKT 784

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4078	100.0	784	7 ADE29193	Ad29193 Human nov
2	4078	100.0	784	6 ADL67198	AdL67198 Human 141
3	3980	97.6	784	6 ABP58154	Abp58154 Death as8
4	3980	97.6	784	7 ADE38377	Ad38377 Human pro
5	3980	97.6	784	7 ABW02412	Abw02412 Human pro
6	3977	97.5	784	5 ABBS3291	Abbs3291 Human pol
7	3977	97.5	784	6 ABP58150	Abp58150 Human pro
8	3976	97.5	784	6 ADL61229	Adl61229 Human pro
9	3959	97.1	784	4 AAB94037	Aab94037 Human pro
10	3946	96.8	832	4 AAU03539	Aau03539 Human pro
11	3946	96.8	832	5 ABP58155	Abp58155 Human pol
12	3835	94.0	759	6 ABP58155	Abp58155 Death as8
13	3803	93.3	750	6 ABP58156	Abp58156 Death as8
14	3661	89.8	725	6 ABP58157	Abp58157 Death as8
15	3628	89.0	786	6 AAY69163	Aay69163 Amino aci
16	3628	89.0	786	6 ABP58149	Abp58149 Mouse dea
17	3628	89.0	786	7 ABW02414	Abw02414 Mouse pro
18	3624	88.9	787	3 AAY76079	Aay76079 Murine pr
19	3624	88.9	787	4 AAB56018	Aab56018 Skin cell
20	3624	88.9	787	5 ABB72218	Abb72218 Murine pr
21	3620	88.8	786	7 ABW02422	Abw02422 Human PKK
22	3619	88.7	786	7 ABW02423	Abw02423 Human PKK
23	3615	88.7	786	7 ABW02424	Abw02424 Human PKK
24	3540	86.8	763	3 AAY79154	Aay79154 Mouse pro
25	2691	66.0	590	3 AAY76123	Aay76123 Murine RI

ALIGNMENTS

RESULT 1	
AD29193	
ID	AD29193 standard; protein; 784 AA.
AC	
XX	AD29193;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Human novel protein kinase 14171 amino acid sequence SegID2.
XX	
XX	kinase protein 14171; cell growth; cell division; gene therapy;
KM	cell differentiation; cellular metabolic pathway; cell metabolism;
KM	viral infection; hepatitis B; cellular growth related disorder;
KM	heart failure; hypertension; atrial fibrillation; dilated cardiomyopathy;
KM	idiopathic cardiomyopathy; angina; differentiative disorder;
KM	proliferative disorder; cancer; liver cancer; melanoma cancer;
KM	prostate cancer; cervical cancer; breast cancer; colon cancer; sarcoma;
KM	programmed cell death; Alzheimer's disease; Parkinson's disease;
KM	epilepsy; autoimmune disorder; systemic lupus erythematosus; human;
KM	enzyme.
XX	
OS	Homo sapiens.
XX	
PN	US6630335-B1.
XX	
PD	07-OCT-2003.
XX	
PF	12-FEB-2001; 2001US-00781882.
XX	
XX	11-FEB-2000; 2000US-0182096P.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Kapeller-Libermann R;
XX	
DR	WI1; 2003-810551/76.
XX	
DR	N-PSDB; AD29192; AD29194.
XX	
PT	New 14171 human protein kinase and nucleic acids encoding the protein,
PT	useful for treating viral infections, cellular growth related disorders,
PT	cancers, disorders related with programmed cell death, or autoimmune
PT	disorders.
XX	
PS	Claim 1; SEQ ID NO 2; 50pp; English.
XX	
CC	This invention relates to a novel isolated nucleic acid sequence and the
CC	novel kinase protein encoded by it. Protein kinases play critical roles
CC	in the regulation of biochemical and morphological changes associated

with cellular growth and division. The sequences of the invention may be useful for gene therapy. The protein kinase or the nucleic acid encoding the protein is useful for modulating cellular growth, differentiation and/or development, and for modulating cellular metabolic pathways, particularly for regulating one or more proteins involved in growth and metabolism. The invention may also be useful for development of therapeutics for the treatment of viral infections (for example hepatitis CC, cellular growth related disorders (for example heart failure, hypertension, atrial fibrillation, dilated and idiopathic cardiomyopathy or anginal), proliferative or differentiative disorders such as cancer (for example liver, melanoma, prostate, cervical, breast, colon or sarcoma), disorders related with programmed cell death (for example Alzheimer's disease, Parkinson's disease or epilepsy), or autoimmune disorders (for example systemic lupus erythematosus). The present sequence is the amino acid sequence of the novel human kinase protein 14171 of the invention.

Sequence 784 AA:

Query Match 100.0%; Score 4078; DB 7; Length 784;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
1 MEGDGGTWMALALRTFDAGEPTMEKVGSGGFGQVYKVRHVMKTMALAKCSPSLHYDD 60
1 MEGDGGTWMALALRTFDAGEPTMEKVGSGGFGQVYKVRHVMKTMALAKCSPSLHYDD 60
61 RERMELEBAKKMEKMAKFRYILPYVGIGREPVGLVMEYTGSLAEKLASPELPMDLFR 120
61 RERMELEBAKKMEKMAKFRYILPYVGIGREPVGLVMEYTGSLAEKLASPELPMDLFR 120
121 ITHETAVGMNPLHCAAPPLHLDLKPAHILDAHNVHISPGGLAKCMGSHSHDLSMDG 180
121 ITHETAVGMNPLHCAAPPLHLDLKPAHILDAHNVHISPGGLAKCMGSHSHDLSMDG 180
181 LFGTAVYVPERIRKESRLPTKHDVGFALIVMGVLTOCKPFADEKNIILHIMVAVVKGH 240
181 LFGTAVYVPERIRKESRLPTKHDVGFALIVMGVLTOCKPFADEKNIILHIMVAVVKGH 240
241 RPELPVPCRRAPRACSHLIRLMQRCWQGDPRVRPTFOBITSETEDLCCKPDDEVETAYHD 300
241 RPELPVPCRRAPRACSHLIRLMQRCWQGDPRVRPTFOBITSETEDLCCKPDDEVETAYHD 300
301 LDVKSPPPPRSEVVARLKASAPTFDNDYSISLISQLDGVGVQAVGPELSSESSES 360
301 LDVKSPPPPRSEVVARLKASAPTFDNDYSISLISQLDGVGVQAVGPELSSESSES 360
361 KLPSGSGKRLSGVSDSAFSSRGLSLSPFEREPSTDLGTTTRPEEEACGCHRVDTSS 420
361 KLPSGSGKRLSGVSDSAFSSRGLSLSPFEREPSTDLGTTTRPEEEACGCHRVDTSS 420
421 KLMKTLIQPDVDLALDSGASLHLAVEAGQEECAWMLNNANPNLSNRGSGTPLMAVE 480
421 KLMKTLIQPDVDLALDSGASLHLAVEAGQEECAWMLNNANPNLSNRGSGTPLMAVE 480
481 RRVKRVVELLARKTSVNAKXEDQMTALHFAQNGDESTRLLKKNASVNEVDPEGRTP 540
481 RRVKRVVELLARKTSVNAKXEDQMTALHFAQNGDESTRLLKKNASVNEVDPEGRTP 540
541 MNAVQOHQGENIVRILLRGVDSIQKDAWMLPLHYAAWQGHPLVKLLAKPGVSVNAQ 600
541 MNAVQOHQGENIVRILLRGVDSIQKDAWMLPLHYAAWQGHPLVKLLAKPGVSVNAQ 600
601 TLDSGTPLHLAAQRGHYVARILIDLCSDVNVCSLAQPLPLVAAETGHTSTARILLHRG 660
601 TLDSGTPLHLAAQRGHYVARILIDLCSDVNVCSLAQPLPLVAAETGHTSTARILLHRG 660
661 AKGEAVTSQGYTALHLAANGHLATYKLLVEEKADVLARGPILNORALHAAHGSEVYE 720
661 AKGEAVTSQGYTALHLAANGHLATYKLLVEEKADVLARGPILNORALHAAHGSEVYE 720
721 ELVSAVDVIDLFDREGSLALHLAAQGRHAQTVETILLRHGAHINLSLKFQGGHGPATLLR 780
721 ELVSAVDVIDLFDREGSLALHLAAQGRHAQTVETILLRHGAHINLSLKFQGGHGPATLLR 780
```

Db 721 ELVSAVDVIDLFDREGSLALHLAAQGRHAQTVETILLRHGAHINLSLKFQGGHGPATLLR 780

Qy 781 RSKT 784
|||
Db 781 RSKT 784

RESULT 2
ADL67198
ID ADL67198 standard; protein; 784 AA.
XX
XX ADL67198;
AC
XX 03-JUN-2004 (first entry)
DT
XX Human 14171 protein kinase.
DE
XX
XX Human; 14171 protein kinase; cancer; immunological disorder;
KW inflammation; heart failure; hypertension; atrial fibrillation;
KW viral disorder; apoptotic disorder; chromosome mapping; tissue typing;
KW predictive medicine; forensic biology; enzyme.
OS Homo sapiens.
XX
XX Key
FH Modified-site
FT 6. .11
FT /note= "N-myristoylation site"
FT 22. .279
FT /note= Protein kinase domain
FT 23. .26
FT /note= "Casein kinase II phosphorylation site"
FT 153. .168
FT /note= "N-myristoylation site"
FT 169. .174
FT /note= "N-myristoylation site"
FT 180. .185
FT /note= "N-myristoylation site"
FT 202. .205
FT /note= "Casein kinase II phosphorylation site"
FT 218. .220
FT /note= "Protein kinase C phosphorylation site"
FT 275. .278
FT /note= "Casein kinase II phosphorylation site"
FT 281. .284
FT /note= "Casein kinase II phosphorylation site"
FT 297. .300
FT /note= "Casein kinase II phosphorylation site"
FT 305. .308
FT /note= "Casein kinase II phosphorylation site"
FT 319. .322
FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
FT 331. .334
FT /note= "Casein kinase II phosphorylation site"
FT 337. .340
FT /note= "Casein kinase II phosphorylation site"
FT 342. .347
FT /note= "N-myristoylation site"
FT 356. .359
FT /note= "Casein kinase II phosphorylation site"
FT 365. .368
FT /note= "Glycosaminoglycan attachment site"
FT 367. .370
FT /note= "Amladation site"
FT 367. .369
FT /note= "Protein kinase C phosphorylation site"
FT 369. .372
FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
FT 375. .378
FT /note= "Casein kinase II phosphorylation site"
FT 382. .384
FT /note= "Protein kinase C phosphorylation site"

FT Modified-site 396..399
 /note="Casein kinase II phosphorylation site"
 FT Modified-site 402..404
 /note="Protein kinase C phosphorylation site"
 FT Modified-site 419..421
 /note="Protein kinase C phosphorylation site"
 FT Active-site 433..444
 /note="Bukaryotic and viral aspartyl protease active site"
 FT Domain 437..766
 /note="Ankyrin repeat domain"
 FT Modified-site 449..454
 /note="N-myristoylation site"
 FT Modified-site 465..468
 /note="Glycosylation site"
 FT Modified-site 467..469
 /note="Protein kinase C phosphorylation site"
 FT Modified-site 469..472
 /note="CAMP- and CGMP-dependent protein kinase phosphorylation site"
 FT Modified-site 493..496
 /note="CAMP- and CGMP-dependent protein kinase phosphorylation site"
 FT Modified-site 519..521
 /note="Protein kinase C phosphorylation site"
 FT Modified-site 527..530
 /note="Glycosylation site"
 FT Modified-site 529..532
 /note="Casein kinase II phosphorylation site"
 FT Modified-site 560..565
 /note="N-myristoylation site"
 FT Modified-site 594..599
 /note="N-myristoylation site"
 FT Modified-site 652..654
 /note="Protein kinase C phosphorylation site"
 FT Modified-site 685..687
 /note="Protein kinase C phosphorylation site"
 FT Modified-site 703..706
 /note="Glycosylation site"
 FT Modified-site 758..763
 /note="N-myristoylation site"
 FT Modified-site 765..767
 /note="Protein kinase C phosphorylation site"
 FT US2004048305-A1.
 PN 11-MAR-2004.
 PD 10-SEP-2003; 2003US-00658904.
 PP 11-FEB-2000; 2000US-0182096P.
 PR 12-FEB-2001; 2001US-00781882.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Kapeller-Liebermann R;
 PI WPI: 2004-226195/21.
 DR N-PSDB; ADL67197, ADL67199.
 PT New 14171 protein kinase and nucleic acid, useful for diagnosing or
 PT treating diseases with aberrant expression of the 14171 protein kinase,
 PT such as cancer, an immunological disorder, inflammation, heart failure
 PT and hypertension.
 XX Claim 5; SEQ ID NO 2; 62bp; English.
 PS
 XX The invention provides novel human 14171 protein kinase polypeptides and
 CC polynucleotides. The methods and compositions of the present invention
 CC are useful for the diagnosis and/or treatment of diseases or conditions
 CC associated with aberrant expression or activity of a 14171 protein kinase
 CC such as cancer, immunological disorder, inflammation, heart failure,
 CC hypertension, atrial fibrillation, viral disorder and apoptotic disorder.

CC The invention can also be used in chromosome mapping, tissue typing,
 CC predictive medicine, forensic biology and prognostic assays. The present
 CC sequence is human 14171 protein kinase.

SQ Sequence 784 AA;

Query Match 100.0%; Score 4078; DB 8; Length 784;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGDGTFWALALRTFDAGSEFTGMEKVGSGGEGQVTVKRVHMKMTALAKCSRLAYDD 60
 DB 1 MEGDGTFWALALRTFDAGSEFTGMEKVGSGGEGQVTVKRVHMKMTALAKCSRLAYDD 60
 QY 61 RERRELLERAKKMEAKRYTLPVYGCREFVGVIMEXMETGSEKTLASRLPMDLFR 120
 DB 61 RERRELLERAKKMEAKRYTLPVYGCREFVGVIMEXMETGSEKTLASRLPMDLFR 120
 QY 121 ITHETAVGMNPLHCAAPPLHLHLKPNAILDAHYHVKISDFGLAKCNGLSHSHDLSMDG 180
 DB 121 ITHETAVGMNPLHCAAPPLHLHLKPNAILDAHYHVKISDFGLAKCNGLSHSHDLSMDG 180
 QY 181 LFGTIAVLPPEERIRKSKRLPTKHDVYSFAIVIGVLTQKKPFADKNIILHIMVKVYKG 240
 DB 181 LFGTIAVLPPEERIRKSKRLPTKHDVYSFAIVIGVLTQKKPFADKNIILHIMVKVYKG 240
 QY 241 RPELPVCRAPPRACSHILRLMORCMQDPRVPRPQGITSETBTLCEKPDVEVETAMD 300
 DB 241 RPELPVCRAPPRACSHILRLMORCMQDPRVPRPQGITSETBTLCEKPDVEVETAMD 300
 QY 301 LDVSPPEPRSRVVPARLKRAAPTFDNDYLSLRLSOLDGVSQAQVGEPELSRSSSES 360
 DB 301 LDVSPPEPRSRVVPARLKRAAPTFDNDYLSLRLSOLDGVSQAQVGEPELSRSSSES 360
 QY 361 KLPSSSGSKRLSGVSVDSAFSSRGLSLSPEREPSTDLGTRRPEEBACGCHRVDT 420
 DB 361 KLPSSSGSKRLSGVSVDSAFSSRGLSLSPEREPSTDLGTRRPEEBACGCHRVDT 420
 QY 421 KLMKTLQPDVDLALDSASLHLAVEGGERCAWLLNNANPMLSRRGSTPLHMAVE 480
 DB 421 KLMKTLQPDVDLALDSASLHLAVEGGERCAWLLNNANPMLSRRGSTPLHMAVE 480
 QY 481 RRVGVVVELLARKISVNAKEDQWTLHPAQNDESSSTRLLLEKNASVNEVDEGRT 540
 DB 481 RRVGVVVELLARKISVNAKEDQWTLHPAQNDESSSTRLLLEKNASVNEVDEGRT 540
 QY 541 MHVACQHQENIVRILRRGVDSLOGKDAMLPLHYAAMOGHLPIVKLLAKQPGVSVNAQ 600
 DB 541 MHVACQHQENIVRILRRGVDSLOGKDAMLPLHYAAMOGHLPIVKLLAKQPGVSVNAQ 600
 QY 601 TLDRTPHLAAQRGHYVARILIDLCSDVNVCSLLAOTPLHVAEFTGHTSTARLLLRG 660
 DB 601 TLDRTPHLAAQRGHYVARILIDLCSDVNVCSLLAOTPLHVAEFTGHTSTARLLLRG 660
 QY 661 AKGEAVTSQGTALHAAANGHLATVKLLVEKAVLARGPINOATLHAAANGSEVYE 720
 DB 661 AKGEAVTSQGTALHAAANGHLATVKLLVEKAVLARGPINOATLHAAANGSEVYE 720
 QY 721 ELVSAVDVLDLFDQGLSALHLAAQGRHAQVETLLRHGHINILQSLKFGGSHGPATTLR 780
 DB 721 ELVSAVDVLDLFDQGLSALHLAAQGRHAQVETLLRHGHINILQSLKFGGSHGPATTLR 780
 QY 781 RSKT 784
 DB 781 RSKT 784

RESULT 3
 ABP58154
 ID ABP58154 standard; protein; 784 AA.
 XX
 AC ABP58154;
 XX

DT 18-MAR-2003 (first entry)
XX Death associated kinase containing ankyrin repeats (DAKAR) variant.
XX
XX Death associated kinase containing ankyrin repeats; DAKAR; human;
XX protein kinase; enzyme; psoriasis; squamous cell carcinoma; melanoma;
XX antiapoptotic; cytoskeletal.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 22..302
FT /note= "catalytic or kinase domain"
FT Region 142..148
FT /note= "serine/threonine catalytic loop motif"
FT Region 160..162
FT /note= "serine/threonine catalytic loop motif"
FT Cleavage-site 433..437
FT /note= "caspase cleavage site"
FT Region 469..482
FT /note= "putative nuclear localisation site"
XX
XX WO200298894-A1.
XX
XX 12-DEC-2002.
XX
XX 04-JUN-2002; 2002WO-US018039.
XX
XX 04-JUN-2001; 2001US-0295959P.
XX PR 29-NOV-2001; 2001US-0334362P.
XX
XX (IMMUNEX CORP.
XX
XX Bird TA, Holland PM, Peschon JJ, Virca GD;
XX
XX WPI; 2003-148648/14.
XX
XX New isolated human death associated kinase containing ankyrin repeats
XX polypeptide and polynucleotide, useful for treating psoriasis, melanoma
XX or squamous cell carcinoma.
XX
XX Example 1; Page; 154pp; English.
XX
XX The present sequence is the protein sequence of a naturally occurring
XX variant of human death associated kinase containing ankyrin repeats
XX (DAKAR, see ABP4150). The variant has a valine for methionine
XX substitution at amino acid 666. DAKAR is a novel member of the
XX serine/threonine protein kinase family. DAKAR is a mediator of apoptosis
XX and putative modulator of cellular differentiation, proliferation, cell
XX cycle and/or senescence. Human DAKAR includes a catalytic domain has
XX similarity to the receptor interaction protein (RIP) family of apoptosis-
XX inducing kinases, and contains 9 ankyrin repeats in its C-terminal
XX regulatory domain. It also includes a number of putative protein kinase C
XX phosphorylation sites. The invention provides DAKAR nucleic acids and
XX polypeptides, as well as recombinant vectors, transfected host cells and
XX methods of producing DAKAR polypeptides. The polypeptides are used in a
XX claimed method of identifying candidate compounds that modulate DAKAR
XX activity. DAKAR agonists can be used to treat psoriasis, melanoma and
XX squamous cell carcinoma (claimed). Note: The present sequence is not
XX shown in the specification but is derived from the human DAKAR sequence
XX given in the Sequence Listing (see ABP58150)
XX
SQ Sequence 784 AA;
Query Match 97.6%; Score 3980; DB 6; Length 784;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 1 MEGDGTTPALALLTPDAGFTGWEKVGSGFGQVYKRRHNTKMTLAIKSPSLHVD 60
DB 1 MEGDGTTPALALLTPDAGFTGWEKVGSGFGQVYKRRHNTKMTLAIKSPSLHVD 60
QY 61 RRMWELBEAKKEMAFRYILPYVGI CREPVGVLWMEVMTGSLKLLASBPDPMDLRF 120

DB 61 RRMWELBEAKKEMAFRYILPYVGI CREPVGVLWMEVMTGSLKLLASBPDPMDLRF 120
QY 121 ITHETAVGNMFLHOMAPPLHLHDLKPNITLLDAHYHKIDFGLAKKNGSHSDLSMDG 180
DB 121 ITHETAVGNMFLHOMAPPLHLHDLKPNITLLDAHYHKIDFGLAKKNGSHSDLSMDG 180
QY 181 LFGTIAVLPERRIERKSLPDTKHDVYSFAIVIGVLTOKKPFADENKIIHIMKVKKH 240
DB 181 LFGTIAVLPERRIERKSLPDTKHDVYSFAIVIGVLTOKKPFADENKIIHIMKVKKH 240
QY 241 RPELPPVCARPRACSHLIRLMORCWQGDPRVRPFOETSETEDLCEDDVEKETAMD 300
DB 241 RPELPPVCARPRACSHLIRLMORCWQGDPRVRPFOETSETEDLCEDDVEKETAMD 300
QY 301 LDVKSPPSPSEVVPALUKRASAPTFPNDSLSLTLQDLSGVQAVGPELSRSSSES 360
DB 301 LDVKSPPSPSEVVPALUKRASAPTFPNDSLSLTLQDLSGVQAVGPELSRSSSES 360
QY 361 KLPSGSGKRLSGVSVDSAFSSRSGLSLSPERPSTSDGTTTRPREBACGHRVDT 420
DB 361 KLPSGSGKRLSGVSVDSAFSSRSGLSLSPERPSTSDGTTTRPREBACGHRVDT 420
QY 421 KLAKTIQPOVDLALDSGASHLHVAEAGECAKWLILNNANPNLSNRRGSTPLMAVE 480
DB 421 KLAKTIQPOVDLALDSGASHLHVAEAGECAKWLILNNANPNLSNRRGSTPLMAVE 480
QY 481 RRVGVVELLARKISVNAQDEDMTALHPAQNQDSSSTRLLERKASVNEVDFEGRT 540
DB 481 RRVGVVELLARKISVNAQDEDMTALHPAQNQDSSSTRLLERKASVNEVDFEGRT 540
QY 541 MHVACQGOENIVAILRGGVDSLQGDAMLPHTVYAMQCHLPYVLLAKQPGVSVNAQ 600
DB 541 MHVACQGOENIVAILRGGVDSLQGDAMLPHTVYAMQCHLPYVLLAKQPGVSVNAQ 600
QY 601 TLDRTPHLHAQRGHYRVARILLDQSDVNVCSLAQTPHLVAETGHTSTABLLHRG 660
DB 601 TLDRTPHLHAQRGHYRVARILLDQSDVNVCSLAQTPHLVAETGHTSTABLLHRG 660
QY 661 AGKRAVTSQGTALHLAARNGHLATVGLVBEKDVYLRGNTALHLAAAHGSEVVE 720
DB 661 AGKRAVTSQGTALHLAARNGHLATVGLVBEKDVYLRGNTALHLAAAHGSEVVE 720
QY 721 ELVSADVLDLDFEGQSLALHLAQRHAQVETLLRHGAHINTLSLFGQSGHAPATLLR 780
DB 721 ELVSADVLDLDFEGQSLALHLAQRHAQVETLLRHGAHINTLSLFGQSGHAPATLLR 780
QY 781 RSKT 784
DB 781 RSKT 784
RESULT 4
AD38377
ID AD38377 standard; protein; 784 AA.
XX
XX AD38377;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human protein 14171 amino acid sequence.
XX
XX tumorigenic disorder; angiogenic disorder; aberrant gene expression;
XX aberrant protein activity; cytoskeletal; antidiabetic;
XX ophthalmological; cancer; breast cancer; colon cancer; lung cancer;
XX prostatic cancer; Grave's disease; diabetic retinopathy; protein 14171.
OS Homo sapiens.
XX
XX WO2003065006-A2.
XX
XX 07-AUG-2003.
XX

PF 30-JAN-2003; 2003WO-US0025588.
 XX 31-JAN-2002; 2002US-0353600P.
 PR 15-MAR-2002; 2002US-0364517P.
 PR 09-APR-2002; 2002US-0371075P.
 PR 10-APR-2002; 2002US-0371507P.
 PR 16-APR-2002; 2002US-0372984P.
 PR 19-APR-2002; 2002US-0374194P.
 PR 24-MAY-2002; 2002US-0382995P.
 PR 31-MAY-2002; 2002US-0385023P.
 PR 14-JUN-2002; 2002US-0388853P.
 PR 17-JUN-2002; 2002US-0389395P.
 PR 25-JUN-2002; 2002US-0391324P.
 PR 15-JUL-2002; 2002US-0395944P.
 PR 22-JUL-2002; 2002US-0397726P.
 PR 13-AUG-2002; 2002US-0403046P.
 PR 22-AUG-2002; 2002US-0405155P.
 PR 27-AUG-2002; 2002US-0406361P.
 PR 25-OCT-2002; 2002US-0421195P.
 PR 12-NOV-2002; 2002US-0425456P.
 PR 19-NOV-2002; 2002US-0427626P.
 PR 10-DEC-2002; 2002US-0432122P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Hunter JJ, Macbeth KJ, Tsai F, Lesoon A, Lightcap ES;
 PI Williamson MW, Rudolph-Owen LA;
 XX N-PSDB; AD538376.
 DR MPI: 2003-646176/61.
 XX
 PT Treating subject having tumorigenic disorder or angiogenic disorder
 PT caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic
 PT acid, by administering a modulator.
 XX
 XX Disclosure; SEQ ID NO 38; 454pp; English.
 PS
 XX
 CC This invention relates to a novel method of treating a human subject
 CC having a tumorigenic disorder or angiogenic disorder, caused by aberrant
 CC gene expression or activity of an isolated protein, by administering a
 CC modulator. The modulator may have cytostatic, antihydroid, antidiabetic
 CC or ophthalmologic activity. The method is useful for treating a subject
 CC having a tumorigenic or angiogenic disorder, in particular for treating
 CC cancer (for example breast cancer, colon cancer, lung cancer or prostatic
 CC cancer) and, for example, Grave's disease and diabetic retinopathy. The
 CC present sequence is the amino acid sequence of the novel isolated human
 CC protein 14171 of the invention.
 CC
 XX
 XX Sequence 784 AA;
 SQ
 Query Match 97.6%; Score 3980; DB 7; Length 784;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 301 LDVKSPEPESEVYPAULKASAPTFPNNDYSLSELSQLDSGVSQAVEGPEELSRSSSES 360
 DB 301 LDVKSPEPESEVYPAULKASAPTFPNNDYSLSELSQLDSGVSQAVEGPEELSRSSSES 360
 QY 361 KLPSGSGKRLSGVSVDSAPSSRGSLSLSPEREPSTSDIGTTRPPEEACGCHRVDTLS 420
 DB 361 KLPSGSGKRLSGVSVDSAPSSRGSLSLSPEREPSTSDIGTTRPPEEACGCHRVDTLS 420
 QY 421 KLKMLLPQVDVLDLDSGASLHLAVBAGQBECAKMLLNANPNLSRRGSTPLHMAVE 480
 DB 421 KLKMLLPQVDVLDLDSGASLHLAVBAGQBECAKMLLNANPNLSRRGSTPLHMAVE 480
 QY 481 RRVGVVELLARKTSVNAKQEDQMTALHPAONGDESSRTLLEKNASVNEVPEGRTP 540
 DB 481 RRVGVVELLARKTSVNAKQEDQMTALHPAONGDESSRTLLEKNASVNEVPEGRTP 540
 QY 541 MEVACQHQENIVHLLRQGVDSLQSKDAMIPLHYAMQGHLPYKLLAQPGVSVNAQ 600
 DB 541 MEVACQHQENIVHLLRQGVDSLQSKDAMIPLHYAMQGHLPYKLLAQPGVSVNAQ 600
 QY 601 TLDEGTPHLAAQGRHVRVARIILDLCSDVAVCSILAQTPLHVAEFGHTSTARLLHRG 660
 DB 601 TLDEGTPHLAAQGRHVRVARIILDLCSDVAVCSILAQTPLHVAEFGHTSTARLLHRG 660
 QY 661 AGKEAVTSDGYTALHLAARNGHIAVTYKLVREKQDVYLRGPANOTALHMAAHGSEVYE 720
 DB 661 AGKEAVTSDGYTALHLAARNGHIAVTYKLVREKQDVYLRGPANOTALHMAAHGSEVYE 720
 QY 721 ELVSAVDVLDLFDQGLSALHLAAGRHQVETLLRHGAHINTLSLKEQGGHGPATLLR 780
 DB 721 ELVSAVDVLDLFDQGLSALHLAAGRHQVETLLRHGAHINTLSLKEQGGHGPATLLR 780
 QY 781 RSKT 784
 DB 781 RSKT 784
 RESULT 5
 ABW02412
 ID ABW02412 standard; protein; 784 AA.
 XX
 AC ABW02412;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human protein kinase C-associated kinase (PKC) protein.
 XX
 KW Human; cellular signalling; protein kinase C-associated kinase; PK; DIK;
 KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; enzyme.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 173..177
 FT /note= "Activation loop motif"
 PN US2003199462-A1.
 XX
 PD 23-OCT-2003.
 XX
 PR 23-APR-2002; 2002US-00128174.
 XX
 PR 23-APR-2002; 2002US-00128174.
 XX
 PA (NUNEZ/) NUNEZ G.
 PA (INOH/) INOHARA N.
 PA (MUTO/) MUTO A.
 PI Nunez G, Inohara N, Muto A;
 XX
 DR MPI: 2003-852808/79.
 DR N-PSDB; AAD64329.

XX New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKC induced NF-KB activation for treating hyperglycemia.
XX Claim 20; SEQ ID NO 12; Opp; English.
XX The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKC induced NF-kappaB activation for treating hyperglycemia.
CC The invention is also used in gene therapy. The present sequence is human
CC PKC protein
XX
XX Sequence 784 AA;
SQ
Query Match 97.6%; Score 3980; DB 7; Length 784;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY 1 MEGDGTWALALRTFDAGEFTGMEKYGSGGFGVYVRHVHMKTWLAIKCPSLHADD 60
DB 1 MEGDGTWALALRTFDAGEFTGMEKYGSGGFGVYVRHVHMKTWLAIKCPSLHADD 60
QY 61 RERBELLEAKKMEAKFRYIIPVYGICREPIVGLMEYETGSLKLAASEPLPMDLFR 120
DB 61 RERBELLEAKKMEAKFRYIIPVYGICREPIVGLMEYETGSLKLAASEPLPMDLFR 120
QY 121 IIEHNAVGMNPLHCAAPPLHLHDLPANILDAHYHVTSDGLAKCNGLSHSHDLSMDG 180
DB 121 IIEHNAVGMNPLHCAAPPLHLHDLPANILDAHYHVTSDGLAKCNGLSHSHDLSMDG 180
QY 181 LFGTAYLPERRIRKESRLFTDKDVSFAIYIVGVLTKCKPFADEKNILHIMVYVKGH 240
DB 181 LFGTAYLPERRIRKESRLFTDKDVSFAIYIVGVLTKCKPFADEKNILHIMVYVKGH 240
QY 241 RPELPVVCARPARACSHLIRLMQRCWQDPRVRPFQETSTSTBDLCEKPDDEVKETAHD 300
DB 241 RPELPVVCARPARACSHLIRLMQRCWQDPRVRPFQETSTSTBDLCEKPDDEVKETAHD 300
QY 241 RPELPVVCARPARACSHLIRLMQRCWQDPRVRPFQETSTSTBDLCEKPDDEVKETAHD 300
DB 241 RPELPVVCARPARACSHLIRLMQRCWQDPRVRPFQETSTSTBDLCEKPDDEVKETAHD 300
QY 301 LDVKSPPPEPRSEVVARLKRAAPTEPDNDYLSSELLSOLDGVSQAVGPEELSSSES 360
DB 301 LDVKSPPPEPRSEVVARLKRAAPTEPDNDYLSSELLSOLDGVSQAVGPEELSSSES 360
QY 361 KLPSSGSGKRLSGVSDSAFSSRSGLSISFEREPSTDLGTTTRPEEBEACGCHRVDT 420
DB 361 KLPSSGSGKRLSGVSDSAFSSRSGLSISFEREPSTDLGTTTRPEEBEACGCHRVDT 420
QY 421 KLMKLIQDQVDLADSGASLIHLAVEAGQEECAWMLLNANPMLSNRSGSTPLHMAVE 480
DB 421 KLMKLIQDQVDLADSGASLIHLAVEAGQEECAWMLLNANPMLSNRSGSTPLHMAVE 480
QY 481 RRVGVVELLEARKISVNAKDEDMWTALHFAQNGDESSRTLLKKNASVNEVDEGRTP 540
DB 481 RRVGVVELLEARKISVNAKDEDMWTALHFAQNGDESSRTLLKKNASVNEVDEGRTP 540
QY 541 RRVGVVELLEARKISVNAKDEDMWTALHFAQNGDESSRTLLKKNASVNEVDEGRTP 540
DB 541 RRVGVVELLEARKISVNAKDEDMWTALHFAQNGDESSRTLLKKNASVNEVDEGRTP 540
QY 541 MHVACQHQGENTVRLILRRGVDSLQGDWMLPLHYAAMQGHLPVKLLAQPGVSVNAQ 600
DB 541 MHVACQHQGENTVRLILRRGVDSLQGDWMLPLHYAAMQGHLPVKLLAQPGVSVNAQ 600
QY 601 TLIDGTPPLHAAQORGHYVARILLIDLCSDVNVCSLLAQTPPLHVAEFGHTSTARILLHRG 660
DB 601 TLIDGTPPLHAAQORGHYVARILLIDLCSDVNVCSLLAQTPPLHVAEFGHTSTARILLHRG 660
QY 661 AGKEAVTSQGYTALHAARNGHLATVKKLVEEKAVILARGPLNQTALHAAAHGSEVE 720
DB 661 AGKEAVTSQGYTALHAARNGHLATVKKLVEEKAVILARGPLNQTALHAAAHGSEVE 720
QY 721 ELVSAADVIDLFDQEGISALHLLAAQGRHQAQVETTLRHGHNIMLSLKTQGGHGPAAATLLR 780
DB 721 ELVSAADVIDLFDQEGISALHLLAAQGRHQAQVETTLRHGHNIMLSLKTQGGHGPAAATLLR 780

QY 781 RSKT 784
DB 781 RSKT 784
RESULT 6
ID ABB53291
ABB53291 standard; protein; 784 AA.
AC ABB53291;
XX 12-FEB-2002 (first entry)
XX Human polypeptide #31.
DE Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
KW neuroleptic; tranquilizer; antiarrhythmic; cardiant; antiaesthetic;
KW antiinflammatory; antilipemic; hepatotropic; vitamin; antidiabetic;
KW nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
KW cardiovascular disease; respiratory disease; liver disease;
KW renal disease; skeletal muscle disease; gastrointestinal disease;
KW placental disease; testicular cancer; male fertility; pancreatic disease.
XX Homo sapiens.
XX WO200181363-A1.
XX 01-NOV-2001.
XX 26-APR-2001; 2001WO-US013360.
XX 27-APR-2000; 2000US-0199963P.
XX 11-MAY-2000; 2000US-0203336P.
XX 25-MAY-2000; 2000US-0207087P.
XX 26-MAY-2000; 2000US-0207546P.
XX (SMIT) SMITHKLINE BEECHAM CORP.
XX (SMIT) SMITHKLINE BEECHAM PLC.
XX Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS,
PI Lai Y, Xie Q;
XX WPI; 2002-041392/05.
XX N-ESDB; ABA90356.
XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
PT and treating diseases associated the polypeptide, e.g. Alzheimer's
PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
XX Claim 1; Page 101-103; 116pp; English.
XX The invention relates to an isolated polypeptide comprising a 277, 480,
XX 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
XX 844, 782, 652, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
XX 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
XX given in the specification. The polypeptides, modulators of the
XX polypeptides and antibodies against the polypeptides are useful for
XX treating diseases such as neurological and psychiatric diseases including
XX Alzheimer's, paraneuronal nuclear palsy, Huntington's disease, myotonic
XX dystrophy, anorexia and depression; cardiovascular diseases including
XX congestive heart failure, Hodgkin's disease and myocardial infarction;
XX respiratory diseases including asthma, chronic obstructive pulmonary
XX disease, cystic fibrosis and adult respiratory distress syndrome; liver
XX diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
XX hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
XX renal disease including renal failure, acute tubular necrosis and
XX glomerulonephritis; skeletal muscle diseases including Burenburg's
XX disease, hypoglycaemia and obesity; gastrointestinal diseases including
XX myotonia congenita and intestinal obstruction; lymph diseases including
XX lymphoglectasia; diseases of placenta including choriochorionoma; diseases
XX of testes including testicular cancer, male reproductive diseases
XX including low testosterone and male infertility; and disease of pancreas

including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The present sequence is a polypeptide of the invention

Sequence 784 AA;

Query Match 97.5%; Score 3977; DB 5; Length 784;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

```

QY 1 MEGDGTPTMALALRTFDAGEFTGWEKVGSGFGQVYKRVHVMKWTALIKCPSLIHYDD 60
DB 1 MEGDGTPTMALALRTFDAGEFTGWEKVGSGFGQVYKRVHVMKWTALIKCPSLIHYDD 60
QY 61 RRMELLEBAKKEMAKFRYYILPVYGCIREPVGLVMEYMETGSLKTLASBPDPDLRR 120
DB 61 RRMELLEBAKKEMAKFRYYILPVYGCIREPVGLVMEYMETGSLKTLASBPDPDLRR 120
QY 121 ITHETAVGNPLHCAPPLHLHLKXPANILLAHYVKISDFGLAKCNGLSHSHLSMDG 180
DB 121 ITHETAVGNPLHCAPPLHLHLKXPANILLAHYVKISDFGLAKCNGLSHSHLSMDG 180
QY 181 LFGTIAVLPERRIRKSRILFTKHDVYSPAIYIWGLVTKKPEPADEKNILHIMVKKVKG 240
DB 181 LFGTIAVLPERRIRKSRILFTKHDVYSPAIYIWGLVTKKPEPADEKNILHIMVKKVKG 240
QY 241 REELPVPCARAPRACSHLIRLMQRCQGDPRVPTFOITSTETEDICEKPDDEKETAHD 300
DB 241 REELPVPCARAPRACSHLIRLMQRCQGDPRVPTFOITSTETEDICEKPDDEKETAHD 300
QY 301 LUVKSPPEERSEVRPARLRASAPTFDNDYSLSELISQDSGQVQVEGPEELSRSSSS 360
DB 301 LUVKSPPEERSEVRPARLRASAPTFDNDYSLSELISQDSGQVQVEGPEELSRSSSS 360
QY 361 KLPSGSGKRLSGVSSVDASFSSRGSLSLSPEREPTSDLGTTREBEACGCHRRDTS 420
DB 361 KLPSGSGKRLSGVSSVDASFSSRGSLSLSPEREPTSDLGTTREBEACGCHRRDTS 420
QY 421 KLMKTIQPODDVLDLDSGASLHLAVAGQEBEACAKMLNNANPNISNRGSTPLHMAVE 480
DB 421 KLMKTIQPODDVLDLDSGASLHLAVAGQEBEACAKMLNNANPNISNRGSTPLHMAVE 480
QY 481 RRRRGVVELLARKISVNAKDEDMQWALHPAONGESSRLLLEKNAVNEVDFEGRTP 540
DB 481 RRRRGVVELLARKISVNAKDEDMQWALHPAONGESSRLLLEKNAVNEVDFEGRTP 540
QY 541 MHVACQHGQENIVRIILRGVDVSLQKXAMPLPHYAAQGHPLPYKLLAKQPGVSVNAQ 600
DB 541 MHVACQHGQENIVRIILRGVDVSLQKXAMPLPHYAAQGHPLPYKLLAKQPGVSVNAQ 600
QY 601 TLDRTPPLHMAQRGHYVARIIIDICSDVNVCSLIAQTPPLHVAETGHTSTARLLHNG 660
DB 601 TLDRTPPLHMAQRGHYVARIIIDICSDVNVCSLIAQTPPLHVAETGHTSTARLLHNG 660
QY 661 AGKEATNSGTYTHLAARNGHLATYKLVBEKADVLAQPLNQTALHIAAHGSEVVE 720
DB 661 AGKEATNSGTYTHLAARNGHLATYKLVBEKADVLAQPLNQTALHIAAHGSEVVE 720
QY 721 ELVSADVIDLFDQGSALHLAAQGRHAQVETLHNGAHINQSLKFGQGHAPATLLR 780
DB 721 ELVSADVIDLFDQGSALHLAAQGRHAQVETLHNGAHINQSLKFGQGHAPATLLR 780
QY 781 RSKT 784
DB 781 RSKT 784

```

RESULT 7
ABP58150 standard; protein; 784 AA.

DT 18-MAR-2003 (first entry)

XX Human death associated kinase containing ankyrin repeats (DAKAR).
XX Death associated kinase containing ankyrin repeats; DAKAR; human;
XX protein kinase; enzyme; peptidase; squamous cell carcinoma; melanoma;
XX antiproliferative; cytotoxic.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Domain 22..302
XX /note= "catalytic or kinase domain"
XX Region 142..148
XX /note= "serine/threonine catalytic loop motif"
XX Region 160..162
XX /note= "serine/threonine catalytic loop motif"
XX Cleavage-site 433..437
XX /note= "casease cleavage site"
XX Region 469..482
XX /note= "putative nuclear localisation site"

WO200298894-A1.

12-DEC-2002.

04-JUN-2002; 2002WO-US018039.

04-JUN-2001; 2001US-0295959P.

29-NOV-2001; 2001US-0334362P.

(IMMUNEX CORP.

Bird TA, Holland PM, Peschon JT, Virca GD;

WPI; 2003-148648/14.

N-PsDB; ABZ24424.

PT New isolated human death associated kinase containing ankyrin repeats

PT polypeptide and polynucleotide, useful for treating psoriasis, melanoma

PT or squamous cell carcinoma.

PS Claim 1; Page 148-151; 154pp; English.

The present sequence is the protein sequence of human death associated kinase containing ankyrin repeats (DAKAR), a novel member of the serine/threonine protein kinase family. DAKAR is a mediator of apoptosis and putative modulator of cellular differentiation, proliferation, cell cycle and/or senescence. Human DAKAR includes a catalytic domain has similarity to the receptor interaction protein (RIP) family of apoptosis-inducing kinases, and contains 9 ankyrin repeats in its C-terminal regulatory domain. It also includes a number of putative protein kinase C phosphorylation sites. The invention provides DAKAR nucleic acids and polypeptides, as well as recombinant vectors, transfected host cells and methods of producing DAKAR polypeptides. The polypeptides are used in a claimed method of identifying candidate compounds that modulate DAKAR activity. DAKAR agonists can be used to treat psoriasis, melanoma and squamous cell carcinoma (claimed). Naturally-occurring variants of DAKAR (see ABP58154-57) have been identified

Sequence 784 AA;

Query Match 97.5%; Score 3977; DB 6; Length 784;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

```

QY 1 MEGDGTPTMALALRTFDAGEFTGWEKVGSGFGQVYKRVHVMKWTALIKCPSLIHYDD 60
DB 1 MEGDGTPTMALALRTFDAGEFTGWEKVGSGFGQVYKRVHVMKWTALIKCPSLIHYDD 60
QY 61 RRMELLEBAKKEMAKFRYYILPVYGCIREPVGLVMEYMETGSLKTLASBPDPDLRR 120
DB 61 RRMELLEBAKKEMAKFRYYILPVYGCIREPVGLVMEYMETGSLKTLASBPDPDLRR 120

```

QY	121	IIHETAVGMNPIHCAAPPLIHLIDLKPAKNTLLDAHHYKISDFELACNGISHSDDLSMDG	180
Db	121	IIHETAVGMNPIHCAAPPLIHLIDLKPAKNTLLDAHHYKISDFELACNGISHSDDLSMDG	180
QY	181	LEGTATLPPERIREKSRLEFDTHQDVYSFAIVMGVLTQKKPAPADEKNILIHVKKVKGH	240
Db	181	LEGTATLPPERIREKSRLEFDTHQDVYSFAIVMGVLTQKKPAPADEKNILIHVKKVKGH	240
QY	241	REELPVCARPRACSHLIRLMQRCMQGDPVRVPTFOEITSETEDICEKPDVEKETAHD	300
Db	241	REELPVCARPRACSHLIRLMQRCMQGDPVRVPTFOEITSETEDICEKPDVEKETAHD	300
QY	301	LDVKSPPPERSEVVPARKLRKASAPPTDNDYSLSELLSOLDSGVSOAVEGPEELSRSSSES	360
Db	301	LDVKSPPPERSEVVPARKLRKASAPPTDNDYSLSELLSOLDSGVSOAVEGPEELSRSSSES	360
QY	361	KLPSGGSGRRLSGVSDSAFSSRGSLSLSPFERPESTSDLTGRRPEEBEACGHRVDTG	420
Db	361	KLPSGGSGRRLSGVSDSAFSSRGSLSLSPFERPESTSDLTGRRPEEBEACGHRVDTG	420
QY	421	KLMLTIQPDVDLALDSGASLLHLAEAGQEECAKMLLNNANPNLSNRGSTPLHMAVE	480
Db	421	KLMLTIQPDVDLALDSGASLLHLAEAGQEECAKMLLNNANPNLSNRGSTPLHMAVE	480
QY	481	RRVRGVVELLARKISVNAKDEQDQWTAHPAQNQDESSSTRILLEKNAVNEVDPEGRTP	540
Db	481	RRVRGVVELLARKISVNAKDEQDQWTAHPAQNQDESSSTRILLEKNAVNEVDPEGRTP	540
QY	541	MHVACQHQGENIVRILIRRGVNVSLQGXQAMPLHVAAMQGHPIYKTLAKQGVSVNAQ	600
Db	541	MHVACQHQGENIVRILIRRGVNVSLQGXQAMPLHVAAMQGHPIYKTLAKQGVSVNAQ	600
QY	601	TLDRGPTLHAAQGHYVARILIDLCSDPVNCSLIAQPTLHVAAYETGHTSTARLLIHRG	660
Db	601	TLDRGPTLHAAQGHYVARILIDLCSDPVNCSLIAQPTLHVAAYETGHTSTARLLIHRG	660
QY	661	AGEKAVTSDGYTALHLAARNGHILATYKLLVEEKADYVLRGPNLQOTALHLAAHGSHVVE	720
Db	661	AGEKAVTSDGYTALHLAARNGHILATYKLLVEEKADYVLRGPNLQOTALHLAAHGSHVVE	720
QY	721	ELVSAADVIDLPEQGLSALHLAAQGRHAQTVETLLRHGAHINLSLKEFGGHPAATLIR	780
Db	721	ELVSAADVIDLPEQGLSALHLAAQGRHAQTVETLLRHGAHINLSLKEFGGHPAATLIR	780
QY	781	RSKT 784	
Db	781	RSKT 784	
RESULT 8			
ADL61229			
ID	ADL61229	standard; protein; 784 AA.	
AC	ADL61229;		
DT	03-JUN-2004	(first entry)	
DE	Human protein tyrosine kinase biomarker ankyrin repeat domain 3 protein.		
XX			
XX			
KW	predictor set; protein tyrosine kinase; cytostatic; antiangiogenic; vasotropic; vulnerary; pharmacogenomic; drug sensitivity; breast cancer; hypervascular disease; angiogenesis; wound healing scar; human; biomarker; ankyrin repeat domain 3.		
XX			
OS	Homo sapiens.		
PN	WO2004020583-A2.		
XX			
PD	11-MAR-2004.		
XX			
PF	26-AUG-2003; 2003WO-US026491.		
XX			
PR	27-AUG-2002; 2002US-0406385P.		

Query Match	Best Local Similarity	97.5%	Score 3976;	DB 8;	Length 784;
Matches 769;	Conservative	4;	Mismatches 11;	Indels 0;	Gaps 0
1	MEGDGDTWALALATFTPDAGEFTGWEKVGSGGQVYKVRHVMKTMALIKCSPSLHVD	60			
1	MEGDGDTWALALATFTPDAGEFTGWEKVGSGGQVYKVRHVMKTMALIKCSPSLHVD	60			
61	RRMELLEEAKKMEAKFRYIIPVYGTICREPVGLVMEYMETGSLKSLASEPLPMDLR	120			
61	RRMELLEEAKKMEAKFRYIIPVYGTICREPVGLVMEYMETGSLKSLASEPLPMDLR	120			
61	RRMELLEEAKKMEAKFRYIIPVYGTICREPVGLVMEYMETGSLKSLASEPLPMDLR	120			
121	IIHETAVGMNPLHCMAAPPLHLIDLPANTILDAHNVKISDGLAKCNGLSHSHDLSMG	180			
121	IIHETAVGMNPLHCMAAPPLHLIDLPANTILDAHNVKISDGLAKCNGLSHSHDLSMG	180			
121	IIHETAVGMNPLHCMAAPPLHLIDLPANTILDAHNVKISDGLAKCNGLSHSHDLSMG	180			
181	LEGTAYLPPERIRKSRFLDTKHVVSFAIYMGVLTQKFFADEKNILHIMVYVKGH	240			
181	LEGTAYLPPERIRKSRFLDTKHVVSFAIYMGVLTQKFFADEKNILHIMVYVKGH	240			
241	REELPPVCRARERACSHLIRLMQRCMGQDPVRRVPTFOBITSTEDLCERPDDEVKETAHD	300			
241	REELPPVCRARERACSHLIRLMQRCMGQDPVRRVPTFOBITSTEDLCERPDDEVKETAHD	300			
241	REELPPVCRARERACSHLIRLMQRCMGQDPVRRVPTFOBITSTEDLCERPDDEVKETAHD	300			
301	LDVKSPPPRRSVAVARLKRASAPFPNDYSLSEILLSQDLSGVQAVEPEELSRSSSS	360			
301	LDVKSPPPRRSVAVARLKRASAPFPNDYSLSEILLSQDLSGVQAVEPEELSRSSSS	360			
301	LDVKSPPPRRSVAVARLKRASAPFPNDYSLSEILLSQDLSGVQAVEPEELSRSSSS	360			
361	KLPSGSGSGRLSGVSVDSAFSSRSLSLSPFRBPSTPLGTRRPEEACGCHRVDT	420			
361	KLPSGSGSGRLSGVSVDSAFSSRSLSLSPFRBPSTPLGTRRPEEACGCHRVDT	420			
361	KLPSGSGSGRLSGVSVDSAFSSRSLSLSPFRBPSTPLGTRRPEEACGCHRVDT	420			
421	KLMKLIQPDVDLADSGASLIHLAVEAGQEBEACMLLNANPNLSNRGSTPLHAYE	480			
421	KLMKLIQPDVDLADSGASLIHLAVEAGQEBEACMLLNANPNLSNRGSTPLHAYE	480			
421	KLMKLIQPDVDLADSGASLIHLAVEAGQEBEACMLLNANPNLSNRGSTPLHAYE	480			
481	RRVRGVVELLARKTSVNAKDEDTALHFAAONGDESTRILLEKNASVNEVDFGRTP	540			
481	RRVRGVVELLARKTSVNAKDEDTALHFAAONGDESTRILLEKNASVNEVDFGRTP	540			
481	RRVRGVVELLARKTSVNAKDEDTALHFAAONGDESTRILLEKNASVNEVDFGRTP	540			
541	MEVAQOHQENIVRILIRRGVVSLOQKQAMPLHYAAQGHPLTYKLAKQPGVSVNAQ	600			
541	MEVAQOHQENIVRILIRRGVVSLOQKQAMPLHYAAQGHPLTYKLAKQPGVSVNAQ	600			
541	MEVAQOHQENIVRILIRRGVVSLOQKQAMPLHYAAQGHPLTYKLAKQPGVSVNAQ	600			

QY 601 TLDSRTPLHLAQRGHYVARILLIDCSDVNVCSLAQTPLHVAETGHTSTARLLHRG 660
DB 601 TLDSRTPLHLAQRGHYVARILLIDCSDVNVCSLAQTPLHVAETGHTSTARLLHRG 660
QY 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEEKADVLARGPLNQTALHLAAAHGSEYVE 720
DB 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEEKADVLARGPLNQTALHLAAAHGSEYVE 720
QY 721 ELVSADVIDLPEDEGLSALHLAQRHQAQTVETLLRHGHINVLQSLKQGGHGPATTLR 780
DB 721 ELVSADVIDLPEDEGLSALHLAQRHQAQTVETLLRHGHINVLQSLKQGGHGPATTLR 780
QY 781 RSKT 784
DB 781 RSKT 784

RESULT 9
AAB94037
ID AAB94037 standard; protein; 784 AA.
XX AAB94037;
AC
XX
DT 26-JUN-2001 (first entry)
XX
XX Human protein sequence SEQ ID NO:14189.
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
XX 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Iehi S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
PS Claim 8; SEQ ID NO 14189; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13632 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 784 AA:
Query Match 97.1%; Score 3959; DB 4; Length 784;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 767; Conservative 3; Mismatches 14; Indels 0; Gaps 0;
QY 1 MEGDGGTWMALALRTPDAGFTGMEKVGSGGFGQVYKRVHVKMTALIKCSPLHYND 60
DB 1 MEGDGGTWMALALRTPDAGFTGMEKVGSGGFGQVYKRVHVKMTALIKCSPLHYND 60
QY 61 RERMELEBAKMEMAKFRYILPYGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
DB 61 RERMELEBAKMEMAKFRYILPYGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
QY 121 ITHETAVGMNPLHCAAPPLHLDKPANILLDAHYYKISDFGLACKGSLSHSDDLMDG 180
DB 121 ITHETAVGMNPLHCAAPPLHLDKPANILLDAHYYKISDFGLACKGSLSHSDDLMDG 180
QY 181 LFGTAYLPERIRKESLPTDKHDVYSFAIVIVGVLTKQKPPADEKNILHMYKVKGH 240
DB 181 LFGTAYLPERIRKESLPTDKHDVYSFAIVIVGVLTKQKPPADEKNILHMYKVKGH 240
QY 241 RPELPVCRAPRACSHLIRIMORCMQDPPRPTFOETSETEDLCEKPDDEVETAMD 300
DB 241 RPELPVCRAPRACSHLIRIMORCMQDPPRPTFOETSETEDLCEKPDDEVETAMD 300
QY 301 LDVSPPEPSEVVPARLKRAAPTFDNDYSLSLSQLDSGVQAVGPEELSRSSSES 360
DB 301 LDVSPPEPSEVVPARLKRAAPTFDNDYSLSLSQLDSGVQAVGPEELSRSSSES 360
QY 361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSEPERBSTDLGTRRPEEACGCHRVRTS 420
DB 361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSEPERBSTDLGTRRPEEACGCHRVRTS 420
QY 421 KLPSGSGKRLSGVSVDSAFSSRGSLSLSEPERBSTDLGTRRPEEACGCHRVRTS 420
DB 421 KLPSGSGKRLSGVSVDSAFSSRGSLSLSEPERBSTDLGTRRPEEACGCHRVRTS 420
QY 421 KLMLTLPQVDVLDLDSGASLLHLAVEAGOECAKMLLNANPNLSNRSGSTPLHMAVE 480
DB 421 KLMLTLPQVDVLDLDSGASLLHLAVEAGOECAKMLLNANPNLSNRSGSTPLHMAVE 480
QY 481 RRVRGVVELLARKISVNAKXEDQWTLHPAQNGBDESTRLLLEKNASVNEVDPEGLTP 540
DB 481 RRVRGVVELLARKISVNAKXEDQWTLHPAQNGBDESTRLLLEKNASVNEVDPEGLTP 540
QY 541 MNAVCOHQENIVRILLRGVDVSLQKQDANLPLHYAAWQGHPLVTKLAAQPGVSVNAQ 600
DB 541 MNAVCOHQENIVRILLRGVDVSLQKQDANLPLHYAAWQGHPLVTKLAAQPGVSVNAQ 600
QY 601 TLDSRTPLHLAQRGHYVARILLIDCSDVNVCSLAQTPLHVAETGHTSTARLLHRG 660
DB 601 TLDSRTPLHLAQRGHYVARILLIDCSDVNVCSLAQTPLHVAETGHTSTARLLHRG 660
QY 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEEKADVLARGPLNQTALHLAAAHGSEYVE 720
DB 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEEKADVLARGPLNQTALHLAAAHGSEYVE 720
QY 721 ELVSADVIDLPEDEGLSALHLAQRHQAQTVETLLRHGHINVLQSLKQGGHGPATTLR 780
DB 721 ELVSADVIDLPEDEGLSALHLAQRHQAQTVETLLRHGHINVLQSLKQGGHGPATTLR 780
QY 781 RSKT 784
DB 781 RSKT 784

RESULT 10
AAU03539
ID AAU03539 standard; protein; 832 AA.

XX AAU03539;
 AC 12-SEP-2001 (first entry)
 XX 12-SEP-2001 (first entry)
 XX Human protein kinase #39.
 DE Human protein kinase #39.
 XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder.
 XX Homo sapiens.
 XX W0200138503-A2.
 XX 31-MAY-2001.
 XX 22-NOV-2000; 2000WO-US032085.
 XX 24-NOV-1999; 99US-0167482P.
 XX (SUGEN-) SUGEN INC.
 XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX WPI; 2001-343950/36.
 DR N-PSDB; AAS06739.
 XX Nucleic acid encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX Claim 7; Fig 2; 433pp; English.
 XX AA03501-AAU03557 represent novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancer (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC polypeptides may be used as antigens in the production of antibodies
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity
 CC
 CC Sequence 832 AA;
 SQ
 Query Match 96.8%; Score 3946; DB 4; Length 832;
 Best Local Similarity 92.5%; Pred. No. 0;
 Matches 770; Conservative 3; Mismatches 11; Indels 48; Gaps 1;
 QY 1 MEGDGGTTPALALATPTPAGSEPTGMEKYGSGGFGOVYKRVHMYKMTLAIKSPSLAYDD 60
 DB 1 MEGDGGTTPALALATPTPAGSEPTGMEKYGSGGFGOVYKRVHMYKMTLAIKSPSLAYDD 60
 QY 61 RERMELEBAKMEKAKFRYILPVYGI CRBPVGLVMEYMETSTLEKLASEPLPMDLRF 120
 DB 61 RERMELEBAKMEKAKFRYILPVYGI CRBPVGLVMEYMETSTLEKLASEPLPMDLRF 120
 QY 121 ITHETAVGNNFLHCAAPPLILHDLKPANILDLDAHVHKISDGLACKNGLSHSLSDMG 180
 DB 121 ITHETAVGNNFLHCAAPPLILHDLKPANILDLDAHVHKISDGLACKNGLSHSLSDMG 180
 QY 181 LEFTIAYLDPERIRKRSRLFDTKHDVYSFAIVYWGVLTKQKPFADKNIILHIMVAVVGH 240

DB 181 LEFTIAYLDPERIRKRSRLFDTKHDVYSFAIVYWGVLTKQKPFADKNIILHIMVAVVGH 240
 QY 241 RPELPRVCGARRPACGHLIRLMQRCWQSPRRPPT----- 276
 DB 241 RPELPRVCGARRPACGHLIRLMQRCWQSPRRPPT----- 276
 QY 277 -----QRTSETEDLCRKPDEVEKETAHDLVKSPPPPRSE 312
 DB 301 RSPGEGFRLSEVIYIKVTCPLSPQBITTSETBELCKRPDEVEKETAHDLVKSPPPPRSE 360
 QY 313 VVPARLKRAAPTFDNDYSISELISQLDSGVSAVEGPEELSRSSSESKLPSSGSGKRUS 372
 DB 361 VVPARLKRAAPTFDNDYSISELISQLDSGVSAVEGPEELSRSSSESKLPSSGSGKRUS 420
 QY 373 GVSSVDSAPSSRGSLSLSPEREPSTDLGTRRPEEACGCHRVRTSKLMLKLOPODV 432
 DB 421 GVSSVDSAPSSRGSLSLSPEREPSTDLGTRRPEEACGCHRVRTSKLMLKLOPODV 480
 QY 433 IALDSGASLHLAVEAGQEECAKMLLNANPNLSNRGSGTPHMAVERRVGVVELLA 492
 DB 481 IALDSGASLHLAVEAGQEECAKMLLNANPNLSNRGSGTPHMAVERRVGVVELLA 540
 QY 493 RKISVNAKDEDQWTALHFAAQNGDESSTRLLLEKNASVNEVDEGRTPMHVAQCOGQENT 552
 DB 541 RKISVNAKDEDQWTALHFAAQNGDESSTRLLLEKNASVNEVDEGRTPMHVAQCOGQENT 600
 QY 553 VRILIRGVDSVLSQGDAMPLPHYAMQGHLPVYKLLAQPGVSVNAQTLDGRTPLHLAA 612
 DB 601 VRILIRGVDSVLSQGDAMPLPHYAMQGHLPVYKLLAQPGVSVNAQTLDGRTPLHLAA 660
 QY 613 QRGHYVARILIDLCSDVNVCSLLAQTPLHVALETGHTSTARLLHRGAKKAVTSDGYT 672
 DB 661 QRGHYVARILIDLCSDVNVCSLLAQTPLHVALETGHTSTARLLHRGAKKAVTSDGYT 720
 QY 673 ALHLAARNGHLATVKLLVEEKADVLARGPINQTAHLHLAAHGSSEVEELVSAVDIDLFD 732
 DB 721 ALHLAARNGHLATVKLLVEEKADVLARGPINQTAHLHLAAHGSSEVEELVSAVDIDLFD 780
 QY 733 EGGISALHLAAOGRHQAQTVETLLRHGHNTLQSLKPGCGHGPAAATLLRBSKT 784
 DB 781 EGGISALHLAAOGRHQAQTVETLLRHGHNTLQSLKPGCGHGPAAATLLRBSKT 832
 RESULT 11
 ID ABB69806 standard; protein; 832 AA.
 XX ABB69806;
 DE 20-JAN-2003 (first entry)
 XX Human polypeptide SEQ ID NO 1853.
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
 KW antiarthritic.
 OS Homo sapiens.
 XX W0200270539-A2.
 XX 12-SEP-2002.
 XX 05-MAR-2002; 2002WO-US005095.
 XX 05-MAR-2001; 2001US-00799451.
 XX

PA (HYSE-) HYSQ INC.
XX
XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Dimanac RT;
XX
DR MPI; 2002-759812/82.
DR N-PSDB; ABZ12023.
XX
XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
XX
XX Claim 9; SEQ ID NO 1853; 1012pp + Sequence listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ1119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_poc_sequences
XX
XX SEQ Sequence 832 AA;

Query Match 96.8%; Score 3946; DB 5; Length 832;

Best Local Similarity 92.5%; Pred. No. 0;
Matches 770; Conservative 3; Mismatches 11; Indels 48; Gaps 1;

QY 1 MEGDGGTPTMALALRTFDAGEPTGWEKVGSGFGQYKRVHVMKTLAIKCSPLAHVD 60
DB 1 MEGDGGTPTMALALRTFDAGEPTGWEKVGSGFGQYKRVHVMKTLAIKCSPLAHVD 60
QY 61 REMMELLEBAKKNEMAKFRYITLVYGI CREPVGLVMEYMETSGLEKILASBPPLRLRR 120
DB 61 REMMELLEBAKKNEMAKFRYITLVYGI CREPVGLVMEYMETSGLEKILASBPPLRLRR 120
QY 121 IIRHTVGMNFTLGMAPLILHLDLKPAKITLDAHYVKISDFGLAKCNGLSHSHDLSMDG 180
DB 121 IIRHTVGMNFTLGMAPLILHLDLKPAKITLDAHYVKISDFGLAKCNGLSHSHDLSMDG 180
QY 181 LFGTIAVLPERIRKSRRLFDTRGDVYSFAIVIGWLTOKKPPADEKNILHIMVKVKGH 240
DB 181 LFGTIAVLPERIRKSRRLFDTRGDVYSFAIVIGWLTOKKPPADEKNILHIMVKVKGH 240
QY 241 RPELPRVCARRPACSHLIRLMORCMQGDPRVPTF----- 276
DB 241 RPELPRVCARRPACSHLIRLMORCMQGDPRVPTF----- 276
QY 277 -----OITSETDLCEKPDDEVKETAHLDLVKSPPEPRSE 312
DB 277 -----OITSETDLCEKPDDEVKETAHLDLVKSPPEPRSE 312
QY 301 RSTGEGRLESEVITIRVTCPLSSPQETSTETEDLCEKPDDEVKETAHLDLVKSPPEPRSE 360
DB 301 RSTGEGRLESEVITIRVTCPLSSPQETSTETEDLCEKPDDEVKETAHLDLVKSPPEPRSE 360
QY 313 VVPARLKRAAPPTFDNDYLSSELLSGLDVGSAVABGPEELSRSSSESKLPSGSGGRSL 372
DB 313 VVPARLKRAAPPTFDNDYLSSELLSGLDVGSAVABGPEELSRSSSESKLPSGSGGRSL 372
QY 361 VVPARLKRAAPPTFDNDYLSSELLSGLDVGSAVABGPEELSRSSSESKLPSGSGGRSL 420
DB 361 VVPARLKRAAPPTFDNDYLSSELLSGLDVGSAVABGPEELSRSSSESKLPSGSGGRSL 420
QY 373 GVSASVDSAFSSRSGLSLSPFRPSTSLGTTTRPPEBAOCCHAVRTSKMLKLOQDDV 432
DB 373 GVSASVDSAFSSRSGLSLSPFRPSTSLGTTTRPPEBAOCCHAVRTSKMLKLOQDDV 432
QY 421 GVSASVDSAFSSRSGLSLSPFRPSTSLGTTTDQKKCLVDIAVYSGTSLKMLKLOQDDV 480
DB 421 GVSASVDSAFSSRSGLSLSPFRPSTSLGTTTDQKKCLVDIAVYSGTSLKMLKLOQDDV 480
QY 433 LALDSGASLHLAVEAGQEBEACAKMLLNANPNLSNRSGSTPLHMAVERRVGVVELLLA 492
DB 433 LALDSGASLHLAVEAGQEBEACAKMLLNANPNLSNRSGSTPLHMAVERRVGVVELLLA 492

DB 481 LALDSGASLHLAVEAGQEBEACAKMLLNANPNLSNRSGSTPLHMAVERRVGVVELLLA 540
QY 493 RRTSYNACDEQWTLALHPAQNQDESSSTRLLLEKRAASVNEVDPEERTPMHVAQCHQENI 552
DB 541 RRTSYNACDEQWTLALHPAQNQDESSSTRLLLEKRAASVNEVDPEERTPMHVAQCHQENI 600
QY 553 VRIILRRGVDSLOGKDAMLPLHYAAMQGHPIYVLAKQPCVSNAQTLDSRTPLHLAA 612
DB 601 VRIILRRGVDSLOGKDAMLPLHYAAMQGHPIYVLAKQPCVSNAQTLDSRTPLHLAA 660
QY 613 QRGHYRVARILIDCSNVNVCSLAQTPPLHVAEFTGHTSTARLLHRGAKCAVTSQGYT 672
DB 661 QRGHYRVARILIDCSNVNVCSLAQTPPLHVAEFTGHTSTARLLHRGAKCAVTSQGYT 720
QY 673 ALHLAARNGHLATVYGLVBEKRDVTLARGPINOTALHLAAAHGSHSVSEIVSADYIDLFD 732
DB 721 ALHLAARNGHLATVYGLVBEKRDVTLARGPINOTALHLAAAHGSHSVSEIVSADYIDLFD 780
QY 733 ECGLSALHLAAGRAQVETLLRHGAHINLQSLKFGGSGHPATILRRSKT 784
DB 781 ECGLSALHLAAGRAQVETLLRHGAHINLQSLKFGGSGHPATILRRSKT 832
RESULT 12
ID ABP58155 standard; protein; 759 AA.
XX ABP58155;
AC
XX ABP58155;
AC
XX 18-MAR-2003 (first entry)
DT
XX
DE Death associated kinase containing ankyrin repeats (DAKAR) variant.
XX
XX Death associated kinase containing ankyrin repeats; DAKAR; human;
KW protein kinase; enzyme; psoriasis; squamous cell carcinoma; melanoma;
XX antipsoriatic; cytoskeletal.
XX
XX Homo sapiens.
OS
XX
XX WO200298894-A1.
PN
XX
XX 12-DEC-2002.
PD
XX
XX 04-JUN-2002; 2002WO-US018039.
PF
XX
XX 04-JUN-2001; 2001US-0295959P.
PR
XX
XX 29-NOV-2001; 2001US-0334362P.
PR
XX
XX (IMMV) IMMUNE CORP.
PA
XX
XX Bird TA, Holland PM, Peschon JJ, Virca GD;
PI
XX
XX MPI; 2003-148648/14.
DR
XX
XX
PT New isolated human death associated kinase containing ankyrin repeats
PT polypeptide and polynucleotide, useful for treating psoriasis, melanoma
PT or squamous cell carcinoma.
XX
XX
XX Example 1; Page: 154pp; English.
XX
XX The present sequence is the protein sequence of a naturally occurring
CC variant of human death associated kinase containing ankyrin repeats
CC (DAKAR). The variant comprises amino acids 26-784 of the DAKAR sequence
CC given in ABP58155. DAKAR is a novel member of the serine/threonine
CC protein kinase family. It is a mediator of apoptosis and putative
CC modulator of cellular differentiation, proliferation, cell cycle and/or
CC senescence. The invention provides DAKAR nucleic acids and polypeptides,
CC as well as recombinant vectors, transfected host cells and methods of
CC producing DAKAR polypeptides. The polypeptides are used in a claimed
CC method of identifying candidate compounds that modulate DAKAR activity.
CC DAKAR agonists can be used to treat psoriasis, melanoma and squamous cell
CC carcinoma (claimed). Note: The present sequence is not shown in the
CC specification but is derived from the human DAKAR sequence given in the

CC	Sequence Listing (see ABP58150)
XX	Sequence 759 AA;
XX	Query Match 94.0%; Score 3835; DB 6; Length 759;
XX	Best Local Similarity 98.0%; Pred. No. 0;
XX	Matches 744; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY	26 EKVGSGGQGVYKVRHVHMKWTMLAIKSPSLHVDREEMELLEAKKEMAKFRYLIPY 85
DB	1 EKVGSGGQGVYKVRHVHMKWTMLAIKSPSLHVDREEMELLEAKKEMAKFRYLIPY 60
QY	86 GICRPPVGLVMEYMTGSLSEKLLASEPLPMDLRPIIHETAVGMFLHMAPELLHLDLK 145
DB	61 GICRPPVGLVMEYMTGSLSEKLLASEPLPMDLRPIIHETAVGMFLHMAPELLHLDLK 120
QY	146 PANILLDAHVKISDFGLAKNGLSHSHDLSMDGLFGTIAVLPPERIREKSRLEPDTKHD 205
DB	121 PANILLDAHVKISDFGLAKNGLSHSHDLSMDGLFGTIAVLPPERIREKSRLEPDTKHD 180
QY	206 VYSFAIVWGVLTQKKPFADEKNIHIMVKYVKGHPRLPVYCARAPACSHLRLMQR 265
DB	181 VYSFAIVWGVLTQKKPFADEKNIHIMVKYVKGHPRLPVYCARAPACSHLRLMQR 240
QY	266 WQGDPRVAPTFQETSETEDLCEKPDDEYKETAHDLVYKSPPEPSEVVPARLKASAPT 325
DB	241 WQGDPRVAPTFQETSETEDLCEKPDDEYKETAHDLVYKSPPEPSEVVPARLKASAPT 300
QY	326 PDNDYSLSBELLSQLDGVSQAAYEGPEELSRSSSESKLPSGSGSKLGGVSVDSAFSSRG 385
DB	301 PDNDYSLSBELLSQLDGVSQAAYEGPEELSRSSSESKLPSGSGSKLGGVSVDSAFSSRG 360
QY	386 SLSTSFEREPEPSTSDIGTTRRPEBEACGCHRVADTYSKMLKLIQPOVDLALDSGASLHLA 445
DB	361 SLSTSFEREPEPSTSDIGTTRRPEBEACGCHRVADTYSKMLKLIQPOVDLALDSGASLHLA 420
QY	446 VEAQGEBCAKMLLNANPNLSNRGSGTPIHMAVRRVGVVELLARKISVNADEPDQW 505
DB	421 VEAQGEBCAKMLLNANPNLSNRGSGTPIHMAVRRVGVVELLARKISVNADEPDQW 480
QY	506 TALAFAAONGDESSSTRLLLEKNASVNEVDPEGRTPMAYACQHQENIVRIILRGVDVSL 565
DB	481 TALAFAAONGDESSSTRLLLEKNASVNEVDPEGRTPMAYACQHQENIVRIILRGVDVSL 540
QY	566 QCKDAMLPYHAYAAWGCHLPYVGLAKQPGVSVNAQTLDGRTPYHLAAQRGHYRVARIID 625
DB	541 QCKDAMLPYHAYAAWGCHLPYVGLAKQPGVSVNAQTLDGRTPYHLAAQRGHYRVARIID 600
QY	626 LCSDEVNCSLLAQTPYHAAETGHTSTARLLHARGAGKAVTSDDGYTALHLAARGHLAT 685
DB	601 LCSDEVNCSLLAQTPYHAAETGHTSTARLLHARGAGKAVTSDDGYTALHLAARGHLAT 660
QY	686 VKGLVEEKADVLARGPLNQTALHLAAAGHSEVEELVSADVIDLFDGQGLSALHLAAQG 745
DB	661 VKGLVEEKADVLARGPLNQTALHLAAAGHSEVEELVSADVIDLFDGQGLSALHLAAQG 720
QY	746 RHAQTVETLLRHGAHINLSLKEPQGGHGPAAATLLRRSKT 784
DB	721 RHAQTVETLLRHGAHINLSLKEPQGGHGPAAATLLRRSKT 759

KW	antiapoptotic; cytostatic.
XX	
OS	Homo sapiens.
XX	
PN	WO200298894-A1.
XX	
XX	12-DEC-2002.
PD	
XX	
PF	04-JUN-2002; 2002WO-US018039.
XX	
PR	04-JUN-2001; 2001US-0295959P.
XX	
PR	29-NOV-2001; 2001US-0334362P.
XX	
PA	(IMMUNEX CORP.
XX	
PI	Bird TA, Holland PM, Peschon JJ, Virca GD,
XX	
DR	WPI; 2003-148648/14.
XX	
PT	New isolated human death associated kinase containing ankyrin repeats
XX	polypeptide and polynucleotide, useful for treating psoriasis, melanoma
XX	or squamous cell carcinoma.
PS	Example 1; Page; 154pp; English.
XX	
CC	The present sequence is the protein sequence of a naturally occurring
CC	variant of human death associated kinase containing ankyrin repeats
CC	(DAKAR). The variant comprises amino acids 1-750 of the DAKAR sequence
CC	given in ABP58150. DAKAR is a novel member of the serine/threonine
CC	protein kinase family. It is a mediator of apoptosis and putative
CC	modulator of cellular differentiation, proliferation, cell cycle and/or
CC	senescence. The invention provides DAKAR nucleic acids and polypeptides,
CC	as well as recombinant vectors, transfected host cells and methods of
CC	producing DAKAR polypeptides. The polypeptides are used in a claimed
CC	method of identifying candidate compounds that modulate DAKAR activity.
CC	DAKAR agonists can be used to treat psoriasis, melanoma and squamous cell
CC	carcinoma (claimed). Note: The present sequence is not shown in the
CC	specification but is derived from the human DAKAR sequence given in the
CC	Sequence Listing (see ABP58150)
XX	
XX	Sequence 750 AA;
XX	
XX	Query Match 93.3%; Score 3803; DB 6; Length 750;
XX	Best Local Similarity 98.0%; Pred. No. 0;
XX	Matches 735; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY	1 MEGDGGTPMALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHMKWTMLAIKSPSLHVD 60
DB	1 MEGDGGTPMALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHMKWTMLAIKSPSLHVD 60
QY	61 RERRELLLEAKKEMAKFRYLIPYVGI CREVVGIVMEYMTGSLSEKLLASEPLPMDLRFR 120
DB	61 RERRELLLEAKKEMAKFRYLIPYVGI CREVVGIVMEYMTGSLSEKLLASEPLPMDLRFR 120
QY	121 IHHETAAGMFLHMAFPPLHLDLKPANILLDAHVKISDFGLAKNGLSHSHDLSMDG 180
DB	121 IHHETAAGMFLHMAFPPLHLDLKPANILLDAHVKISDFGLAKNGLSHSHDLSMDG 180
QY	181 LFGTIAVLPERRIREKSRLEPDKHDVYSFAIVWGVLTQKKPFADEKNIHIMVKYVKG 240
DB	181 LFGTIAVLPERRIREKSRLEPDKHDVYSFAIVWGVLTQKKPFADEKNIHIMVKYVKG 240
QY	241 RPELPVYCARAPACSHLRLMQRCKWQGDPRVAPTFQETSETEDLCEKPDDEYKETAH 300
DB	241 RPELPVYCARAPACSHLRLMQRCKWQGDPRVAPTFQETSETEDLCEKPDDEYKETAH 300
QY	301 LDVKSPEPSEVVPARLKASAPTNDYSLSBELLSQLDGVSQAAYEGPEELSRSSSES 360
DB	301 LDVKSPEPSEVVPARLKASAPTNDYSLSBELLSQLDGVSQAAYEGPEELSRSSSES 360
QY	361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSEFERPEPSTSDIGTTRRPEBEACGCHRVDT 420
DB	361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSEFERPEPSTSDIGTTRRPEBEACGCHRVDT 420

QY 421 KLMKILQPOVDVLDLADSGASLHLAVERAGOEBCAKWLLNNANPNLSNRGSTPLHMAVE 480
 DB 421 KLMKILQPOVDVLDLADSGASLHLAVERAGOEBCAKWLLNNANPNLSNRGSTPLHMAVE 480
 QY 481 RRVGVVLLILARKTSVNAKDEDMTALHPAANGDESTRLLLEKNASVNEVDEGRTP 540
 DB 481 RRVGVVLLILARKTSVNAKDEDMTALHPAANGDESTRLLLEKNASVNEVDEGRTP 540
 QY 541 MHVACQHQENIVRILIRGVDSVLSQKQDAMLPLHYAAMQGHLPYKLLAKQPGVSVAQ 600
 DB 541 MHVACQHQENIVRILIRGVDSVLSQKQDAMLPLHYAAMQGHLPYKLLAKQPGVSVAQ 600
 QY 601 TLDSGTPLHLAARQGHYVARILIDLCSDVNVCSLLAQTPLHVAEFTGHTSTARLLHRG 660
 DB 601 TLDSGTPLHLAARQGHYVARILIDLCSDVNVCSLLAQTPLHVAEFTGHTSTARLLHRG 660
 QY 661 AGKEAVTSDGTATLHLAARNGHLATVYKLLVEEKADVLARGPLNQTALHLAAHGHSEVVE 720
 DB 661 AGKEAVTSDGTATLHLAARNGHLATVYKLLVEEKADVLARGPLNQTALHLAAHGHSEVVE 720
 QY 721 ELVSADVIDLFDQGLSALHLAAQGRHAQT 750
 DB 721 ELVSADVIDLFDQGLSALHLAAQGRHAQT 750

RESULT 14
 ABP58157
 ID ABP58157 standard; protein; 725 AA.
 AC ABP58157;
 DT 18-MAR-2003 (first entry)
 XX
 DE Death associated kinase containing ankyrin repeats (DAKAR) variant.
 XX
 KW Death associated kinase containing ankyrin repeats; DAKAR; human;
 KW protein kinase; enzyme; psoriasis; squamous cell carcinoma; melanoma;
 KW antipsoarctic; cyostatic.
 OS Homo sapiens.
 PN WO200298894-A1.
 PD 12-DEC-2002.
 XX
 PF 04-JUN-2002; 2002WO-US018039.
 XX
 PR 04-JUN-2001; 2001US-0295959P.
 PR 29-NOV-2001; 2001US-0334362P.
 XX
 PA (IMMV) IMMUNEX CORP.
 PI Bird TA, Holland PM, Peschon JJ, Virca GD;
 DR WPI; 2003-148648/14.
 XX
 PT New isolated human death associated kinase containing ankyrin repeats
 PT polypeptide and polynucleotide, useful for treating psoriasis, melanoma
 PT or squamous cell carcinoma.
 XX
 PS Example 1; Page; 154pp; English.
 XX
 CC The present sequence is the protein sequence of a naturally occurring
 CC variant of human death associated kinase containing ankyrin repeats
 CC (DAKAR). The variant comprises amino acids 26-750 of the DAKAR sequence
 CC given in ABP58150. DAKAR is a novel member of the serine/threonine
 CC protein kinase family. It is a mediator of apoptosis and putative
 CC modulator of cellular differentiation, proliferation, cell cycle and/or
 CC senescence. The invention provides DAKAR nucleic acids and methods of
 CC as well as recombinant vectors, transfected host cells and methods of
 CC producing DAKAR polypeptides. The polypeptides are used in a claimed
 CC method of identifying candidate compounds that modulate DAKAR activity.

CC DAKAR agonists can be used to treat psoriasis, melanoma and squamous cell
 CC carcinoma (claimed). Note: The present sequence is not shown in the
 CC specification but is derived from the human DAKAR sequence given in the
 CC Sequence Listing (see ABP58150)
 CC
 XX
 SQ Sequence 725 AA;
 Query Match 89.8%; Score 3661; DB 6; Length 725;
 Bees Local Similarity 97.9%; Pred. No. 2.3e-316;
 Matches 710; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
 QY 26 EKVSQGFQYQYKVRHVMKWTALAIKCSPSLHVDREMBLEBAKQEMAKFRYILPVY 85
 DB 1 EKVSQGFQYQYKVRHVMKWTALAIKCSPSLHVDREMBLEBAKQEMAKFRYILPVY 60
 QY 86 GICEPVGVLVMEYMETSGLEKLAISELPMDLRRIIHEAVGNFPHCAPPLHLIDK 145
 DB 61 GICEPVGVLVMEYMETSGLEKLAISELPMDLRRIIHEAVGNFPHCAPPLHLIDK 120
 QY 146 PANTILDAHNVKISDGLAKCNGLSHSHLSMDGLGTATLPPERIREKSLFDTKHD 205
 DB 121 PANTILDAHNVKISDGLAKCNGLSHSHLSMDGLGTATLPPERIREKSLFDTKHD 180
 QY 206 VYSFALVIMGYLTQKKPFADEKNILIMVYKVGHRPELPVCARAPRACSHLIRLMQRC 265
 DB 181 VYSFALVIMGYLTQKKPFADEKNILIMVYKVGHRPELPVCARAPRACSHLIRLMQRC 240
 QY 266 WQGDPRVAFPTFOEITSETEDICEKPDDEVKETAHLDVKSPPERSSEVPARLRASAPT 325
 DB 241 WQGDPRVAFPTFOEITSETEDICEKPDDEVKETAHLDVKSPPERSSEVPARLRASAPT 300
 QY 326 FDNDSYSELSSQLDSGVSAVEGPEELSRSSSESKLPSGSGKRLSGVSSVDSAFSSRG 385
 DB 301 FDNDSYSELSSQLDSGVSAVEGPEELSRSSSESKLPSGSGKRLSGVSSVDSAFSSRG 360
 QY 386 SLISFEPERESTDLSGTRRPEEBAACGHRVDRYSKLMKILQPOVDVLDLADSGASLHLA 445
 DB 361 SLISFEPERESTDLSGTRRPEEBAACGHRVDRYSKLMKILQPOVDVLDLADSGASLHLA 420
 QY 446 VEAGOEBCAKWLLNNANPNLSNRGSTPLHMAVERVGVVLLILARKTSVNAKDEDM 505
 DB 421 VEAGOEBCAKWLLNNANPNLSNRGSTPLHMAVERVGVVLLILARKTSVNAKDEDM 480
 QY 506 TALHPAANGDESTRLLLEKNASVNEVDEGRTPMHAACQHQENIVRILIRGVDSVLS 565
 DB 481 TALHPAANGDESTRLLLEKNASVNEVDEGRTPMHAACQHQENIVRILIRGVDSVLS 540
 QY 566 QGKQAMLPPLHYAAMQGHLPYKLLAKQPGVSVAQTLDSGTPLHLAARQGHYVARILID 625
 DB 541 QGKQAMLPPLHYAAMQGHLPYKLLAKQPGVSVAQTLDSGTPLHLAARQGHYVARILID 600
 QY 626 LCSDVNVCSLLAQTPLHVAEFTGHTSTARLLHHRGAKAVTSDGTATLHLAARNGHLAT 685
 DB 601 LCSDVNVCSLLAQTPLHVAEFTGHTSTARLLHHRGAKAVTSDGTATLHLAARNGHLAT 660
 QY 686 VKLVEEKADVLARGPLNQTALHLAAHGHSEVVEELVSADVIDLFDQGLSALHLAAG 745
 DB 661 VKLVEEKADVLARGPLNQTALHLAAHGHSEVVEELVSADVIDLFDQGLSALHLAAG 720
 QY 746 RHAQT 750
 DB 721 RHAQT 725

RESULT 15
 AAY69163
 ID AAY69163 standard; protein; 786 AA.
 AC AAY69163;
 DT 30-MAY-2000 (first entry)
 XX
 DE Amino acid sequence of a death associated kinase with ankyrin repeats.

XX Death associated kinase protein containing ankyrin repeats; DAKAR;
 KW kinase; quality assurance agent; shelf life; marker.
 XX Mus sp.
 OS
 XX
 FH
 FT Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met encoded by GTG"
 FT Domain 17..297
 FT Region /note= "N-terminal kinase domain"
 FT /note= "768
 FT /note= "this region contains a series of nine tandem
 FT ankyrin repeats"
 FT
 FN WO200008177-A2.
 PD 17-FEB-2000.
 PD
 PE 04-AUG-1999; 99WO-US017576.
 PE
 PR 04-AUG-1998; 98US-0095269P.
 PR 11-SEP-1998; 98US-0099973P.
 PR 09-FEB-1999; 99US-0119353P.
 PR
 PA (IMMUNEX CORP.
 PI Bird TA, Virca GD;
 DR WPI; 2000-195582/17.
 DR N-PSDB; AA261161.
 XX
 PT Novel death associated kinase containing ankyrin repeats (DAKAR) used as
 PT molecular weight marker and as controls for peptide fragmentation.
 PS
 PS Claim 13; Page 10; 71pp; English.
 CC The present sequence represents a murine death associated kinase protein,
 CC containing ankyrin repeats, designated DAKAR. The DAKAR polynucleotides
 CC can be used to express the polypeptides, and as probes to identify
 CC nucleic acids encoding proteins having kinase activity. DAKAR
 CC polypeptides and fragmented polypeptides are used for purifying proteins,
 CC e.g. to measure protein activity; as quality assurance agents to monitor
 CC shelf life and stability of binding partner proteins; as research agents,
 CC e.g. in assays to determine protein kinase activity, to identify novel
 CC molecules involved in signal transduction pathways, and to identify
 CC therapeutic compounds which may interfere with apoptosis; as molecular
 CC weight and isoelectric focusing markers; as controls for peptide
 CC fragmentation; identification of unknown proteins, e.g. by comparison
 CC with proteins in databases; and for preparation of antibodies. The
 CC antibodies can be used in assays to detect the presence of the protein,
 CC and to purify the protein by immunoaffinity chromatography. The
 CC antibodies can also be used to block binding of the DAKAR polypeptides to
 CC their binding partners. Compounds that inhibit or enhance the kinase
 CC activity of DAKAR can be used to treat diseases characterized by
 CC overproduction or upregulated production or underproduction or
 CC downregulated production of DAKAR
 CC
 SQ Sequence 786 AA;
 Query Match 89.0%; Score 3628; DB 3; Length 786;
 Best Local Similarity 88.9%; Pred. No. 2,2e-313;
 Matches 699; Conservative 34; Mismatches 51; Indels 2; Gaps 1;
 QY 1 MEGDGTWVALALRTFDAGEFTGWEKXVSGGFGVYKVRHVMTWLAIKCPSLHYVD 60
 DB 1 MEGEGRGKRALGLTRPDAGEPAGWEKXVSGGFGVYKVRHVMTWLAIKCPSLHYVD 60
 QY 61 RRRMELLEBAKXOMAKFRYIIPYVGICREPIVGLWEYMETGSLKTLASEPLPMDLRR 120
 DB 61 RRRMELLEBAKXOMAKFRYIIPYVGICREPIVGLWEYMETGSLKTLASEPLPMDLRR 120
 QY 121 ITHETAVGNFPLHCAPPLIHLDLKPANILLDAHYHVKISDFGLAKCNGLSHSHDLSMDG 180

DB 121 ITHETAVGNFPLHCAPPLIHLDLKPANILLDAHYHVKISDFGLAKCNGLSHSHDLSMDG 180
 QY 181 LFGTIALTPPERIREKRLPDTKIDVYSFAIVMGVLTOKKPRADENILHIMKYVKGH 240
 DB 181 LFGTIALTPPERIREKRLPDTKIDVYSFAIVMGVLTOKKPRADENILHIMKYVKGH 240
 QY 241 RPELPVCRARPRACSHLIRLMQRCWQGDPRVRPTFOEITSETEDLCPEPDEVKETAHD 300
 DB 241 RPELPVCRARPRACSHLIRLMQRCWQGDPRVRPTFOEITSETEDLCPEPDEVKETAHD 300
 QY 301 LDVKSPEPRSEVVP--ARLKRAAPTFDNDYSISELLSQDLSGVSAVGEPELSRSS 358
 DB 301 PGEKSSLESSEAPPESSRLKRAAPPFNDNCISIELLSQDLSGISTLEGPEELSRSS 360
 QY 359 ESKLPSSSGSKRLSGVSVDSAPSSRSLSISPREESTDGLGTRPBEACGCHVRD 418
 DB 361 ECKLPSSSSGKRLSGVSVDSAPSSRSLSISPREESTDGLGTRDIOKKKLDVALISGD 420
 QY 419 TSKLMKTILOPODVLDALDSGASILLHLAVEAGQEECAKMLLNANPNLSNRSGSTPLHMA 478
 DB 421 TSKLMKTILOPODVLDALDSGASILLHLAVEAGQEECAKMLLNANPNLSNRSGSTPLHMA 480
 QY 479 VERRRGVVELLARKISVNAKEDQWTALHPAAQNGDESTRLLLEKNASVNEVDEGR 538
 DB 481 VERRRGVVELLARKISVNAKEDQWTALHPAAQNGDESTRLLLEKNASVNEVDEGR 540
 QY 539 TPMHVAQCHQENIVRILLRGVDSIQGKDAMIPLHYAAMOGHLPTVKLLAQPGVSVN 598
 DB 541 TPMHVAQCHQENIVRILLRGVDSIQGKDAMIPLHYAAMOGHLPTVKLLAQPGVSVN 600
 QY 599 AQTLDGRTPHLAAQRGHYVARILIDCSDVNCSLLAOTPLHVAETGHTSTARLLH 658
 DB 601 AQTLDGRTPHLAAQRGHYVARILIDCSDVNCSLLAOTPLHVAETGHTSTARLLH 660
 QY 659 RGAGKEAVTSDGYTALHLAARNGHLATVKLLVEEKADVILARGPLNQALHLAAAGHSEV 718
 DB 661 RGAGKEAVTSDGYTALHLAARNGHLATVKLLVEEKADVILARGPLNQALHLAAAGHSEV 720
 QY 719 VEEIVSADVIDLPEQGLSALHLAAGRHQVTYTLRHGAHINTLSLQKQGCGHPAATL 778
 DB 721 VEEIVSADVIDLPEQGLSALHLAAGRHQVTYTLRHGAHINTLSLQKQGCGGSAATL 780
 QY 779 LRRSKT 784
 DB 781 LRRSKT 786

Search completed: September 17, 2005, 02:39:01
 Job time : 314.201 secs

Db 241 GGCAGATTGCTACATCTGCTGTGTATGGCATCTGCGCGAACCCTGTGCGCTGAT 300
Qy 301 CATGAGATACATGAGAGAGGGCTCCCTGGAAAAAGCTGCTGGGTTTGGAGCCATTGGCCATG 360
Db 301 CATGAGATACATGAGAGAGGGCTCCCTGGAAAAAGCTGCTGGGTTTGGAGCCATTGGCCATG 360
Qy 361 GGAATCCGGTTCCGAATCATTCACGAGACGGCGGTGGGCATGAACTTCTGCACTGCAAT 420
Db 361 GGAATCCGGTTCCGAATCATTCACGAGACGGCGGTGGGCATGAACTTCTGCACTGCAAT 420
Qy 421 GGCCTCCGCACTCTCTGCACTTGAAGCTTGAAGCCGCGAATCATCTGCTGAATGCCACTA 480
Db 421 GGCCTCCGCACTCTCTGCACTTGAAGCTTGAAGCCGCGAATCATCTGCTGAATGCCACTA 480
Qy 481 CCACTTCAAGATTTTGTGTTTGTCTGGCCAAAGTGCACCGGGCTGTGCCACTGCCATGA 540
Db 481 CCACTTCAAGATTTTGTGTTTGTCTGGCCAAAGTGCACCGGGCTGTGCCACTGCCATGA 540
Qy 541 CCTCAGCATGATGAGCTGTGTTGGCACAATGCTACCTCCCTCCAGAGCGCATGAGGA 600
Db 541 CCTCAGCATGATGAGCTGTGTTGGCACAATGCTACCTCCCTCCAGAGCGCATGAGGA 600
Qy 601 GAAAGAGCGGCTCTTTCGACACCAAGCAGATGTATACAGCTTTGGGATGTCATCTGAGG 660
Db 601 GAAAGAGCGGCTCTTTCGACACCAAGCAGATGTATACAGCTTTGGGATGTCATCTGAGG 660
Qy 661 CGTGTCAACAGAAAGCCGTTTGGATGAGAGAAACATCCGTCATCATATGTATA 720
Db 661 CGTGTCAACAGAAAGCCGTTTGGATGAGAGAAACATCCGTCATCATATGTATA 720
Qy 721 GGTGTGAAAGGCGCACCGCCCGAGCTGCGCCGCTGTGACAGAGCCGCGCGCGCTG 780
Db 721 GGTGTGAAAGGCGCACCGCCCGAGCTGCGCCGCTGTGACAGAGCCGCGCGCGCTG 780
Qy 781 CAGCCACTGATACGCTTCATGACAGCGGTGCTGCGAGGGGATTCGCGAGTTAGGCCAC 840
Db 781 CAGCCACTGATACGCTTCATGACAGCGGTGCTGCGAGGGGATTCGCGAGTTAGGCCAC 840
Qy 841 CTTCGAAGAAATTAATTTCTGAAACCGAGGACCTGTGTGTAAGAAAGCTGTATGACGAATGA 900
Db 841 CTTCGAAGAAATTAATTTCTGAAACCGAGGACCTGTGTGTAAGAAAGCTGTATGACGAATGA 900
Qy 901 AGAAACTGCTCATGATCTGAGACGTGAAAAAGCCCCCGAGCCACAGAGCGAGTGTGCC 960
Db 901 AGAAACTGCTCATGATCTGAGACGTGAAAAAGCCCCCGAGCCACAGAGCGAGTGTGCC 960
Qy 961 TCGAGGCTCAAGCGGGCTCTGCCCCCACTTGCATTAACGACTACAGCTCTCCGAGCT 1020
Db 961 TCGAGGCTCAAGCGGGCTCTGCCCCCACTTGCATTAACGACTACAGCTCTCCGAGCT 1020
Qy 1021 TCTCTCAGAGCTGAGCTGAGGTTTCCAGGCTGTGAGGGCCCGAGAGGCTCAGCG 1080
Db 1021 TCTCTCAGAGCTGAGCTGAGGTTTCCAGGCTGTGAGGGCCCGAGAGGCTCAGCG 1080
Qy 1081 CAGCTCTCTGAGTCAAGCTGCAATGTCGGGAGTGGAAAGAGGCTCTGCGGGGTGTCT 1140
Db 1081 CAGCTCTCTGAGTCAAGCTGCAATGTCGGGAGTGGAAAGAGGCTCTGCGGGGTGTCT 1140
Qy 1141 CTGGTGAATCTCGGCTTCTCTTCCAGAGATCATCTGTGCTGTCTTTGAGCGGAAACC 1200
Db 1141 CTGGTGAATCTCGGCTTCTCTTCCAGAGATCATCTGTGCTGTCTTTGAGCGGAAACC 1200
Qy 1201 TTCAACAGCGGATCTGGGATCAACAAGACGTCAAGAAAGAGGCTTGGAGTGCATCG 1260
Db 1201 TTCAACAGCGGATCTGGGATCAACAAGACGTCAAGAAAGAGGCTTGGAGTGCATCG 1260
Qy 1261 TGTCCGGGACACCAAGAAATGATGAATCTTGAAGCGCGCAGAGCTGAGACTTGGCACT 1320
Db 1261 TGTCCGGGACACCAAGAAATGATGAATCTTGAAGCGCGCAGAGCTGAGACTTGGCACT 1320
Qy 1321 GGAAGCGGCTGCAAGCTGCTGACCTGCGGTGAGAGCGCGGCAAGAGAGTGGCCAA 1380
Db 1321 GGAAGCGGCTGCAAGCTGCTGACCTGCGGTGAGAGCGCGGCAAGAGAGTGGCCAA 1380

Qy 1381 GTGGCTGTGCTCAACAATGCAACCCCAACTGAGGACCGTAGGGGCTCACCCGTT 1440
Db 1381 GTGGCTGTGCTCAACAATGCAACCCCAACTGAGGACCGTAGGGGCTCACCCGTT 1440
Qy 1441 GCAATGAGCGGTGAGAGAGGGGTGTGCTGAGAGCTCTGCTGCGACGGAAGAT 1500
Db 1441 GCAATGAGCGGTGAGAGAGGGGTGTGCTGAGAGCTCTGCTGCGACGGAAGAT 1500
Qy 1501 CAGTGTCAAGCCCAAGATGAGACAGTGTGACAGCCCTCCACTTTGACGCGCAAGACG 1560
Db 1501 CAGTGTCAAGCCCAAGATGAGACAGTGTGACAGCCCTCCACTTTGACGCGCAAGACG 1560
Qy 1561 GGATGAGCTGTGACACAGGCTGTGTGAGAAAGAGGCTCTGCTGACAGAGTGAATT 1620
Db 1561 GGATGAGCTGTGACACAGGCTGTGTGAGAAAGAGGCTCTGCTGACAGAGTGAATT 1620
Qy 1621 TGAAGGCGGACCGCCCATGCACTGTGAGCTGCGACACCGGCAAGAGAAATCTGTGCGAT 1680
Db 1621 TGAAGGCGGACCGCCCATGCACTGTGAGCTGCGACACCGGCAAGAGAAATCTGTGCGAT 1680
Qy 1681 CTTGCTGCGCGAGAGCGGTGACCTGACCTGACAGGACGAAGATGCTGTGCTGCACTGCA 1740
Db 1681 CTTGCTGCGCGAGAGCGGTGACCTGACCTGACAGGACGAAGATGCTGTGCTGCACTGCA 1740
Qy 1741 CTAAGCTGCTGTGAGAGGCGCACCTGCGCATCTGTCAAGCTGTGCGACAGAGCGGAGGT 1800
Db 1741 CTAAGCTGCTGTGAGAGGCGCACCTGCGCATCTGTCAAGCTGTGCGACAGAGCGGAGGT 1800
Qy 1801 GAGTGTGAACCGCCCAAGACGCTGATGAGAGAGACCCCATTTGACCTGTGCGCGACAGCGCG 1860
Db 1801 GAGTGTGAACCGCCCAAGACGCTGATGAGAGAGACCCCATTTGACCTGTGCGCGACAGCGCG 1860
Qy 1861 GCACTACCGGCTGCGCGCGCATCTTCATGACCTGTGCTCCGACCTCAACCTGTGCAAGCT 1920
Db 1861 GCACTACCGGCTGCGCGCGCATCTTCATGACCTGTGCTCCGACCTCAACCTGTGCAAGCT 1920
Qy 1921 GCTGAGCAAGACCCCTGACGCTGAGCGGCGAGAGACGAGGACACAGAGCATGCGAGGCT 1980
Db 1921 GCTGAGCAAGACCCCTGACGCTGAGCGGCGAGAGACGAGGACACAGAGCATGCGAGGCT 1980
Qy 1981 GCTCTGTGATGAGGAGCGCTGAGAGAGGCGGTGACTTCAGACGAGCTACACGCTCTGCA 2040
Db 1981 GCTCTGTGATGAGGAGCGCTGAGAGAGGCGGTGACTTCAGACGAGCTACACGCTCTGCA 2040
Qy 2041 CTTGCTGCTGCGGACAGGACCTGTGCACTGTGCAAGCTGTTGTGAGAGAGAGCGCGA 2100
Db 2041 CTTGCTGCTGCGGACAGGACCTGTGCACTGTGCAAGCTGTTGTGAGAGAGAGCGCGA 2100
Qy 2101 TGTGCTGAGCGGAGGACCCCTGAAACAGAGCGGCTGCACTGTGCTGCGCGCCAGGCA 2160
Db 2101 TGTGCTGAGCGGAGGACCCCTGAAACAGAGCGGCTGCACTGTGCTGCGCGCCAGGCA 2160
Qy 2161 CTGAGAGGTGAGAGAGATTGTACAGCGCCGATGTCAATTGACTGTTCAGAGCAAGG 2220
Db 2161 CTGAGAGGTGAGAGAGATTGTACAGCGCCGATGTCAATTGACTGTTCAGAGCAAGG 2220
Qy 2221 GCTCAGCGCGGTGACCTGTGCGCGGACAGGCGCGGACAGACAGCGGTGAGACTGTGCT 2280
Db 2221 GCTCAGCGCGGTGACCTGTGCGCGGACAGGCGCGGACAGACAGCGGTGAGACTGTGCT 2280
Qy 2281 CAGGATGAGGCGCCACATCAACTGACAGAGCTCAAGTTCAGAGGCGGCGCATGCGCCGC 2340
Db 2281 CAGGATGAGGCGCCACATCAACTGACAGAGCTCAAGTTCAGAGGCGGCGCATGCGCCGC 2340
Qy 2341 CGCCACTCTCTGCGGAGAGCAAGACCTTGTGCTGCGGAGACCGGGGTCTCAC 2400
Db 2341 CGCCACTCTCTGCGGAGAGCAAGACCTTGTGCTGCGGAGACCGGGGTCTCAC 2400
Qy 2401 GTGGGCTCTTGTCTGTCTGTGTCTGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
Db 2401 GTGGGCTCTTGTCTGTCTGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460

OY	2461	TGTTGGCTTA	CTTAAT	TGTTAT	CCAAAG	CAAGAT	CAAT	GGTCCAT	CAAGAGGCGG	2522													
Db	2461	CGTTGGCTTA	CTTAAT	GTTTAA	CCAAAG	CAAGAT	CAAT	GGTCCAT	CAAGAGGCGG	2520													
OY	2521	TGCTGCTGA	CCGGAAGT	GCCTCC	TCAGGCTGA	AGCTGCT	CAAGTGC	CAATGCCGCT	CA	2580													
Db	2521	TGCTGCTGA	CCGGAAGT	GCCTCC	TCAGGCTGA	AGCTGCT	CAAGTGC	CAATGCCGCT	CA	2580													
OY	2581	TCATCGAT	CTTAGG	CACTGCT	GTCTGA	AGGACCGT	GGTCA	GAATCAT	TTTCTGTGTCT	2640													
Db	2581	TCATCGAT	CTTAGG	CACTGCT	GTCTGA	AGGACCGT	GGTCA	GAATCAT	TTTCTGTGTCT	2640													
OY	2641	CTTAATGGGT	GCCTGA	GGCTGCT	CTCAAG	GAATGA	AGCCCA	GGCGGTGA	AGATCCAC	2700													
Db	2641	CTTAATGGGT	GCCTGA	GGCTGCT	CTCAAG	GAATGA	AGCCCA	GGCGGTGA	AGATCCAC	2700													
OY	2701	TCTCTCC	TGAAGG	CCAGCACT	CTGGGGT	GTCTGA	AGCTCA	CCAGTCT	TGAAGGAGTGCAG	2760													
Db	2701	TCTCTCC	TGAAGG	CCAGCACT	CTGGGGT	GTCTGA	AGCTCA	CCAGTCT	TGAAGGAGTGCAG	2760													
OY	2761	GGGAAACT	GTGT	TTTTAT	CTTCA	TACA	TGACGGT	GGCAGAGAGG	CCCTGTCTTAAAGTT	2820													
Db	2761	GGGAAACT	GTGT	TTTTAT	CTTCA	TACA	TGACGGT	GGCAGAGAGG	CCCTGTCTTAAAGTT	2820													
OY	2821	TCATGGAAT	TGTTTAT	TAAAAAT	CTTAA	AGATGA	TAACTCTT	ATACGCTGT	GTCTGA	2880													
Db	2821	TCATGGAAT	TGTTTAT	TAAAAAT	CTTAA	AGATGA	TAACTCTT	ATACGCTGT	GTCTGA	2880													
OY	2881	AACCTGT	TAAAAAT	TGTTTAT	CAAT	CAAT	TGAT	GTCTAGTCT	CTAATATATGGCTAAGT	2940													
Db	2881	AACCTGT	TAAAAAT	TGTTTAT	CAAT	CAAT	TGAT	GTCTAGTCT	CTAATATATGGCTAAGT	2940													
OY	2941	GGGGT	TGCTT	TGAAAA	CAAT	GT	TTTTAT	TGCAACAGGA	CGAATGTGACGCACTTT	3000													
Db	2941	GGGGT	TGCTT	TGAAAA	CAAT	GT	TTTTAT	TGCAACAGGA	CGAATGTGACGCACTTT	3000													
OY	3001	GGGGGCG	GTAT	TGTGT	GGCAGCT	CTTAA	CAAT	TCCAGT	CTATTA	CTTGGGTGAATCCTTG	3060												
Db	3001	GGGGGCG	GTAT	TGTGT	GGCAGCT	CTTAA	CAAT	TCCAGT	CTATTA	CTTGGGTGAATCCTTG	3060												
OY	3061	TGGAACA	CAACA	CACAG	GGCCACA	TAGAT	GTAC	TGCTG	CCGTGTTCT	GGTCCCTAA	3120												
Db	3061	TGGAACA	CAACA	CACAG	GGCCACA	TAGAT	GTAC	TGCTG	CCGTGTTCT	GGTCCCTAA	3120												
OY	3121	GATGTTT	TGGCA	ACT	CTA	AGCCACA	GGCCT	TAA	AGTCA	TTPAAAAAT	TTCTCCCTTGT	3180											
Db	3121	GATGTTT	TGGCA	ACT	CTA	AGCCACA	GGCCT	TAA	AGTCA	TTPAAAAAT	TTCTCCCTTGT	3180											
OY	3181	ACCTCAG	TGCT	TGGGGA	CT	GAGGCGAG	CCCCCT	CAG	TGCTG	AGATGTGA	CCAGTCTTGGG	3240											
Db	3181	ACCTCAG	TGCT	TGGGGA	CT	GAGGCGAG	CCCCCT	CAG	TGCTG	AGATGTGA	CCAGTCTTGGG	3240											
OY	3241	GAAAGG	GTG	CAGGA	AAAGCT	GTGTTT	TAT	TCTCCA	CGAGAT	TGAAGAT	TAATAATAC	3300											
Db	3241	GAAAGG	GTG	CAGGA	AAAGCT	GTGTTT	TAT	TCTCCA	CGAGAT	TGAAGAT	TAATAATAC	3300											
OY	3301	ATAGAT	TATTA	CT	TAGA	CAT	TAGACAT	TAATTA	CT	TAGAT	ATGCACTG	CACTGCACCT	3360										
Db	3301	ATAGAT	TATTA	CT	TAGA	CAT	TAATTA	CT	TAGAT	ATGCACTG	CACTGCACCT	3360											
OY	3361	TCCCA	AGCT	CTCA	TTTTTT	TGT	TAGAT	ATTTGG	AGAT	TAGAT	TGTTTGGGGAT	TGGGGG	3420										
Db	3361	TCCCA	AGCT	CTCA	TTTTTT	TGT	TAGAT	ATTTGG	AGAT	TAGAT	TGTTTGGGGAT	TGGGGG	3420										
OY	3421	GAGT	TTTTCT	TGA	CCGT	T	TGA	AGT	GGCCCT	CGCA	CTCAG	CAAGCT	TGAAGG	GTGGCC	3480								
Db	3421	GAGT	TTTTCT	TGA	CCGT	T	TGA	AGT	GGCCCT	CGCA	CTCAG	CAAGCT	TGAAGG	GTGGCC	3480								
OY	3481	CCAGG	CGCGT	TT	TGGAT	T	TAA	AAAGT	GTGG	CCAT	CT	GA	CTT	CA	CTGT	CA	3540						
Db	3481	CCAGG	CGCGT	TT	TGGAT	T	TAA	AAAGT	GTGG	CCAT	CT	GA	CTT	CA	CTGT	CA	3540						
OY	3541	TGTGT	CCAT	TAG	GGT	CC	TT	TGA	AT	CT	GT	TAT	TAA	TA	AGTT	GT	TG	TG	CA	GA	CG	GA	3600

Db	3541	TGTCCTCCATAGGGTGCCTTCTGAAATACCTGTATTGTGAATAAGATTGGTTCAGAAACCTGA	3600
OY	3601	CCCTGCGCTGCMAACATCTACCCGTGCGCTGGTATATATGATAGATAGATTTGATTTAATGTACCA	3660
Db	3601	CCCTGCGCTGCMAACATCTACCCGTGCGCTGGTATATATGATAGATAGATTTGATTTAATGTACCA	3660
OY	3661	TGTATGTTAATNGTAATCTGTGGGACAGAGATACCTTTTTCATGACGAGAAATATCCAACTG	3720
Db	3661	TGTATGTTAATNGTAATCTGTGGGACAGAGATACCTTTTTCATGACGAGAAATATCCAACTG	3720
OY	3721	TTGAAACTGCGTATGTTTATATATATGCTCATATGCTCTTACTGTTGTGTGACCTGCGTG	3780
Db	3721	TTGAAACTGCGTATGTTTATATATGCTCATATGCTCTTACTGTTGTGTGACCTGCGTG	3780
OY	3781	AGGACCAAGAACTTCCATTGATGTCAATTAAGCAAGTACTTGCCCACTTTTGTGANC	3840
Db	3781	AGGACCAAGAACTTCCATTGATGTCAATTAAGCAAGTACTTGCCCACTTTTGTGANC	3840
OY	3841	TGAAAAAAGG	3860
Db	3841	TGAAAAAAGG	3860
RESULT 2			
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DEFINITION	Homo sapiens ANKRD3 mRNA for dual-specificity Ser/Thr/Tyr kinase, complete cds.		
ACCESSION	AB047783		
VERSION	AB047783.1	GI:14245728	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukacynska, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (sites)		
AUTHORS	Shimizu,N., Kudoh,J. and Shibuya,K.		
TITLE	Homo sapiens mRNA for ANKRD3, complete cds		
JOURNAL	Published Only in Database (2001)		
REFERENCE	2 (bases 1 to 3882)		
AUTHORS	Shimizu,N., Kudoh,J. and Shibuya,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-ANG-2000) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizu@med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)		
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Qy	487	CAAGATTTCTGATTTGGCTGGCCAGATGCAACGGGCTGTCCCATCTGCACTGCACTG	546	
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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 AUTHORS Bhr,C., Rohwer,A., Stempka,L., Rincke,G., Marko,F. and Geschwendt,M.
 TITLE dlk, a novel protein kinase that interacts with protein kinase
 JOURNAL Delta. Cloning, characterization, and gene analysis
 MEDLINE J. Biol. Chem. 275 (46), 36350-36357 (2000)
 PUBMED 10948194
 REFERENCE 2 (bases 1 to 3879)
 AUTHORS Geschwendt, M.
 TITLE Direct Submission

JOURNAL

Submitted (18-MAY-2000) Geschwendt M., Biochemistry of
Tissue-specific Regulation, German Cancer Research Center, Im
Neuenheimer Feld 280, D-69151 Heidelberg, GERMANY

FEATURES

source

Location/Qualifiers

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ORIGIN

Query Match

Best Local Similarity 98.6%; Score 3804.2; DB 9; Length 3879;

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ACCESSION BD157754.1 GI:27863512
VERSION BD157754.1
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 3876)
Ota.T., Isogai.T., Nishikawa.T., Hayashi.K., Salto.K., Yamamoto.J.,
Ishii.S., Sugiyama.T., Makamatsu.A., Nagai.K. and Otsuki.T.
Primer for synthesizing full-length cDNA and use thereof.
Patent: JP 2002191363-A 12597 09-JUL-2002;
HELIX RESEARCH INSTITUTE

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PI SHITO, YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI MAKAMATSU,
PI JUNICHI YAMAGI, TETSUJI OTSUKI
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10,
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Primer for synthesizing full-length cDNA and use thereof FH Key
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FT CDS (66)..(2417).
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ORIGIN
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 3813; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003
TITLE	Ota,T., Iogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003
JOURNAL	Ishii,S., Sugiyama,T., Wakematsu,A., Nagai,K. and Otsuki,T.	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003
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/translation="MEGCGCPMALILRTPDAGPFGMEKVGSGFGGVYKVVHVM	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
KTWLAIRKSPSLHDDRERMELEBAKKMEAKRRYLLPYVGICREPEVGLMEFMETG	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
SLEKLALASEPLRWDLRPIHETVAGNLFHCQMLPPLHLIDLRANLILDAHVKVLS	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
DFGLKALCSGLSHSDRLSMDGILFETAVLPERRIREKSLSDTKDVSFAVIGVLT	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
OKKPEADEKNILHIVKVGKRPRLPVCAPRAPACSLIRLQRCQGDPRVRFPEE	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
OEITSEEDTCEKPDDEVETKRAHLDIVKSPPESEVYPARLKAAPTPNDVLSSE	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
ILSDSDSGVSAVGRRELSRSSSESKLPSGSGKRLDVGVSUNASRSGLSPFE	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
REPISDGLTTDVQKKLVDAIVSDDTSKLKILQPDVDLALSGASLHLAYAGQ	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
BECAWMLLNANPVLNRRGSTPLAHAVERRVGVVERLLARKIIVNAKDEDTWAL	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
HFPAQNGDESDTRLLEKNASVNEVDFGLPDMVAQCHQGEIVRLIRKGVNSIL	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
GKDALPLHVAWQCHLPIVKLAKQPEVSVNAQTLDRSTPLHAAGRHVARVIL	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
DLGSAVNVCSLLAOTPLHVAATGHTSTARLLIRHGKKAIVSDGYTALHARNGH	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
LATKLVIAEKKDVIARPLNQTALHAAAGHSVVEELVSAVYIDLFPDQGLSALH	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
LIAQGRHAQIVETLLRHGAHNLQSLKRFQGGHPATLLRRSKT"	AX879283.1	3876 bp DNA Linear PAT 17-DEC-2003	3924
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Query Match	98.1%;	Pred. 3787.4;	DB 6; Length 3876;
Best Local Similarity	99.8%;	Pred. No. 0;	
Matches 3813; Conservative	0;	Mismatches	6; Indels 2; Gaps 2;
Qy	7	GTCGCGCGCATGAGAGGCGACAGCGGAGACCCCATGAGGACCTTGCGCTGTCGCGACCTT	66
Db	56	GACGCGCGGAGTGAAGGCGGACGCGGGACCCCATGAGGACCTTGCGCTGTCGCGACCTT	115
Qy	67	GCAAGCGGCGCATGACGAGCTGGGAGAGAGGTGGGCTTCGGCGGCTTGGGCAAGGTGA	126

Db	116	CGACGCGGCGCACTTCAOGBGCTGGGAGAAAGTGGGCTCGGCGCGCTTTCGGGCAAGGTGTA	175
Qy	127	CAAGTGGCGCATGTGTCATGGAAGACCTGGCTGGCATCAAGTGTCTCGCCACCTTGC	186
Db	176	CAAGTGGCGCATGTGTCATGGAAGACCTGGGCTGGCATCAAGTGTCTCGCCACCTTGC	235
Qy	187	CGTGCAGACAGGGGAGGGAGCTTTGGGAAGGACCAAGAAAGATGTGAGATGGGCCAA	246
Db	236	CGTGCAGACAGGGGAGGGAGCTTTGGGAAGGACCAAGAAAGATGTGAGATGGGCCAA	295
Qy	247	GTTTCGCTACATCCGTGCTGTGTATGTGCATCTGCGGAAACCTGTCCGCGCTGTCA	306
Db	296	GTTTCGCTACATCCGTGCTGTGTATGTGCATCTGCGGAAACCTGTCCGCGCTGTCA	355
Qy	307	GTACATGAGAGCGGGCTCTCCGTGAAAGCTGTGGCTTCCGAGCATTTGCCATGGATCT	366
Db	356	GTACATGAGAGCGGGCTCTCCGTGAAAGCTGTGGCTTCCGAGCATTTGCCATGGATCT	415
Qy	367	CCGGTTCGAAATCATTCACGAGACGGGGGTGGGAGTAACTTTCCTGACATGCAAGGCC	426
Db	416	CCGGTTCGAAATCATTCACGAGACGGGGGTGGGAGTAACTTTCCTGACATGCAAGGCC	475
Qy	427	GCACATCTCGTGAACCTTGGACCTCAAGCCCGGCAACATCTGTGTGATGCCACTACAGT	486
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Qy	487	CAAGATTTCTGATTTTGGTCTGGCCAAAGTGCACGGGCTGTCCCACTGCATGACCTTCA	546
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Qy	607	CCGGCTCTTCGACACCAAGACCAATGTATACGCTTTTGCATCGTCACTTGGGCGTGTCT	666
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Qy	667	CACAAGAAAGACCGTTTGCAGATGGAAGAACATCTGCACATCATGTGAAGTGT	726
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Qy	847	AGAAATTACTTCTGAAACCGAGAGACTGTGTGTGAAGAACCTGATGACGAAAGTGAAGAAAC	906
Db	896	AGAAATTACTTCTGAAACCGAGAGACTGTGTGTGAAGAACCTGATGACGAAAGTGAAGAAAC	955
Qy	907	TGCTCATGATTTGACCTGGAAGAACCCCCCGGAGACCCAGAGGCGAGGTGTGTCTTGGAG	966
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Qy	967	GCTCAAGGGGCGCTGTGCCCCCACCCTTGATTAAGACGACCTTCCGAGCTTCTCTC	1026
Db	1016	GCTCAAGGGGCGCTGTGCCCCCACCCTTGATTAAGACGACCTTCCGAGCTTCTCTC	1075
Qy	1027	ACAGCTGGACTCTGAGATTTCCACAGGCTGTGAGGGCCCCGAGAGAGCTCAACCCAGCTC	1086
Db	1076	ACAGCTGGACTCTGAGATTTCCACAGGCTGTGAGGGCCCCGAGAGAGCTCAACCCAGCTC	1135
Qy	1087	CTTGAAGTCCAGCTGCCATGTCTCGGCAGTGGGAAGAGCTTCTCGGGGGGTGTCTCTGGT	1146
Db	1136	CTTGAAGTCCAGCTGCCATGTCTCGGCAGTGGGAAGAGCTTCTCGGGGGGTGTCTCTGGT	1195
Qy	1147	GGACTCCGCGCTTCTTCCAGAGGATCATCTGTGCTGTCTTTTGAAGCGGGAACCTTCAAC	1206
Db	1196	GGACTCCGCGCTTCTTCCAGAGGATCATCTGTGCTGTCTTTTGAAGCGGGAACCTTCAAC	1255

OY	1207	TAGGATCTGGGTATCCACAAACGTCGAGAAAGAAAGCTTTGGAGTGCATGTCGCC -	1265
Db	1256	CAGCGATCTGGGTATCCAC - AGACGTCGAGAAAGAAAGCTTTGGATGCCATGTCGCC	1314
OY	1266	GGGACACCAAGCAAACTGATGAAAGATCTCGACAGCCGCGAGACGTGGACTTGGACA	1325
Db	1315	GGGACACCAAGCAAACTGATGAAAGATCTCGACAGCCGCGAGACGTGGACTTGGACA	1374
OY	1326	GCGGTGCCAGCCTGTGTGACCTGGCGGTGGAGGCGCGGCAAGAGATTTGGCCAGTGGC	1385
Db	1375	GCGGTGCCAGCCTGTGTGACCTGGCGGTGGAGGCGCGGCAAGAGATTTGGCCAGTGGC	1434
OY	1386	TGCTGCTCAACAAATGCCAAACCCCAACCTGAGCAACCGTAAAGGGGTCCACCCGTTGGACA	1445
Db	1435	TGCTGCTCAACAAATGCCAAACCCCAACCTGAGCAACCGTAAAGGGGTCCACCCGTTGGACA	1494
OY	1446	TGGCCGTGAGAGAGAGGGTGGCGGGGTGTCGTGAGACTTCCTGTGGCAACGAAAGATCACTG	1505
Db	1495	TGGCCGTGAGAGAGAGGGTGGCGGGGTGTCGTGAGAGCCTGTGTGGCAACGAAAGATCACTG	1554
OY	1506	TCAACGCCCAAGATGAGAGACCAAGTGGACAGGCCCTCACTTTGGAGGCCAAGACGGGGATG	1565
Db	1555	TCAACGCCCAAGATGAGAGACCAAGTGGACAGGCCCTCACTTTGGAGGCCAAGACGGGGATG	1614
OY	1566	AGTCATGACACACGCGCTGCTGTTGGAGAAAGACGCGTCGCTCAACGAGGTGGACTTTGAGG	1625
Db	1615	AGTCATGACACACGCGCTGCTGTTGGAGAAAGACGCGTCGCTCAACGAGGTGGACTTTGAGG	1674
OY	1626	GCCGGAGCCCAATGACCTGTGGCCTGGCCAGCACACGGGCAAGAGATATATGTGTGCACTCTGC	1685
Db	1675	GCTTGAACCCCAATGACCTGTGGCCTGGCCAGCACACGGGCAAGAGATATATGTGTGCACTCTGC	1734
OY	1686	TGGCGCGAGGGGTGGACGTGAGCCCTGACGGGCAAGAGATGCTGGCTGGCACTGACCTAGC	1745
Db	1735	TGGCGCGAGGGGTGGACGTGAGCCCTGACGGGCAAGAGATGCTGGCTGGCACTGACCTAGC	1794
OY	1746	CTGCTTGGCAGGGGCCACCTGGCCATCTGTCAAGCTGTGGCCCAAGACGCCGGGGTGAAGTG	1805
Db	1795	CTGCTTGGCAGGGGCCACCTGGCCATCTGTCAAGCTGTGGCCCAAGACGCCGGGGTGAAGTG	1854
OY	1806	TGAATGCCCAAGACGTGTGATGAGGAGAGAGCCCAATTGACCTTGGCCGCGACAGGCGGGGACT	1865
Db	1855	TGAATGCCCAAGACGTGTGATGAGGAGAGAGCCCAATTGACCTTGGCCGCGACAGGCGGGGACT	1914
OY	1866	ACCGGCTGGGCGCGCATCTCTCAATCGACCTGTGTCTCGACGTCAACGTCCTGCAACGCTGTGG	1925
Db	1915	ACCGGCTGGGCGCGCATCTCTCAATCGACCTGTGTCTCGACGTCAACGTCCTGCAACGCTGTGG	1974
OY	1926	CAACAACACCCCTTGACACTGTGCGCGGAGACGGGGCAACAACAACCTGCGCAGGCTGTCC	1985
Db	1975	CAACAACACCCCTTGACACTGTGCGCGGAGACGGGGCAACAACAACCTGCGCAGGCTGTCC	2034
OY	1986	TGCAATCGGGGGCGCTGGCAAGAGAGGCGAGACCTCAAGCAGGCTCAACGCTCTGCAACTGG	2045
Db	2035	TGCAATCGGGGGCGCTGGCAAGAGAGGCGGTGACCTCAAGCAGGCTCAACGCTCTGCAACTGG	2094
OY	2046	CTGACCGCAACGAGACACTGTGCGCACTGTCAAGCTTGTCTGAGAGAGAGGCGCATGTGC	2105
Db	2095	CTGACCGCAACGAGACACTGTGCGCACTGTCAAGCTTGTCTGAGAGAGAGGCGCATGTGC	2154
OY	2106	TGGCCCGGGGACCCCTTGAAACCAAGAGGCGTGCACCTGGCTGCGGCCCAACGGGCAACTCGG	2165
Db	2155	TGGCCCGGGGACCCCTTGAAACCAAGAGGCGGTGCACTTGACTGCGGCCCAACGGGCAACTCGG	2214
OY	2166	AGGTGGTGAAGAGTGTGATCAGCGCGATGTCAATTCATTGACCTGTTTCGACGACGAGGGGCTCA	2225
Db	2215	AGGTGGTGAAGAGTGTGATCAGCGCGATGTCAATTCATTGACCTGTTTCGACGACGAGGGGCTCA	2274
OY	2226	GGCGCGCTGACCTGGCGCGCCACAGGCGCGGACGCAACAACGTTGAGACTTCTGCTCAAGC	2285
Db	2275	GGCGCGCTGACCTGGCGCGCCACAGGCGCGGACGCAACAACGTTGAGACTTCTGCTCAAGC	2334

QY	2286	ATGGGACCAATCAACTGAGAGCTCAAGTTCCAGGGGCGGCANATGGGCCCGCGCCA	2345
Db	2335	ATGGGGCCCAATCAACTGAGAGCTCAAGTTCCAGGGGCGGCANATGGGCCCGCGCCA	2394
QY	2346	CACCTCGGGCGAAGCAAGACCTAGAGCTGGCTGCTGCGAGACCGGGGGTCCACGTGGG	2405
Db	2395	CACCTCGGGCGAAGCAAGACCTAGAGCTGGCTGCTGCGAGACCGGGGGTCCACGTGGG	2454
QY	2406	GCTCTGTGCTGTGCTGTGTCTCGTGGGAGTGAACGATCTGTGGGGGCCCGTTG	2465
Db	2455	GCTCTGTGCTGTGCTGTGTCTCGTGGGAGTGAACGATCTGTGGGGGCCCGTTG	2514
QY	2466	TGGCTTAACCTTAAGTTAACCAACAGAGGTGACATGTGTCCANTCAAGAGCGGCTGCTG	2525
Db	2515	TGGCTTAACCTTAAGTTAACCAACAGAGGTGACATGTGTCCANTCAAGAGCGGCTGCTG	2574
QY	2526	CTGACCCGAGAGTCCCCCTCCAGAGTGAAGCTGGCTCAGGTGCAATATGCCGCTCATATC	2585
Db	2575	CTGACCCGAGAGTCCCCCTCCAGAGTGAAGCTGGCTCAGGTGCAATATGCCGCTCATATC	2634
QY	2586	GATCTAGGCACTGTGTCTGAGAGGACCGTGGTCAGAATCATTTGCTGTGCTCTAA	2645
Db	2635	GATCTAGGCACTGTGTCTGAGAGGACCGTGGTCAGAATCATTTGCTGTGCTCTAA	2694
QY	2646	TGGGTGCTGAGGCTGTGTCTCACTGATGAAGCCCCAGGGGTGGAGACATCCACTCTCT	2705
Db	2695	TGGGTGCTGAGGCTGTGTCTCACTGATGAAGCCCCAGGGGTGGAGACATCCACTCTCT	2754
QY	2706	CCTGAGGGAGACCACTTGGGTGTGTGGAGTCAACAGTCTGTAGGGAGGTGCGAGGGAA	2765
Db	2755	CCTGAGGGAGACCACTTGGGTGTGTGGAGTCAACAGTCTGTAGGGAGGTGCGAGGGAA	2814
QY	2766	ACTGAGTTTTTATCTTCAATCATGACGATGGGAGAGAGGCTGTCTTAAAGTTTCAAT	2825
Db	2815	ACTGAGTTTTTATCTTCAATCATGACGATGGGAGAGAGGCTGTCTTAAAGTTTCAAT	2874
QY	2826	GGAATTTGTTTTATAAATATCTTAAAGATGAATACCTTATCAAGTGTGTCTTAAACT	2885
Db	2875	GGAATTTGTTTTATAAATATCTTAAAGATGAATACCTTATCAAGTGTGTCTTAAACT	2934
QY	2886	GTTAAAAATGTTCAATTAATGGATGATGCTGATCTTAAAGATGGGCTAAATAGGGGGT	2945
Db	2935	GTTAAAAATGTTCAATTAATGGATGATGCTGATCTTAAAGATGGGCTAAATAGGGGGT	2994
QY	2946	TGGCTTTGAAAACAATGTTTTATGCAACAGAAAGAAATGATGTATGACGACAGCTTTGCGGG	3005
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QY	3066	AACCAACAACAGTGTCCCAATGTGATCTAGCTGCCGTTCCGTTTCGCTTGGCTAAGAGT	3125
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QY	3126	TTTGGCAACTCAGAGCCACAGGGCTTAAGATCATTAATAAATTTCCCTTGTGTAACTC	3185
Db	3175	TTTGGCAACTCAGAGCCACAGGGCTTAAGATCATTAATAAATTTCCCTTGTGTAACTC	3234
QY	3186	AGTGTCTGGGACTGAGGGGAGGCCCTCAGGTGCTGTGAGTGCACCAAGTCTTGGGAGAA	3245
Db	3235	AGTGTCTGGGACTGAGGGGAGGCCCTCAGGTGCTGTGAGTGCACCAAGTCTTGGGAGAA	3294
QY	3246	GGTGCAGAGAAAGCTGTGTTTTTTATCTTCCACAGCAGTATGAAGATTAATTAATTAAT	3305
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QY	3306	ATTAACTTACATAGACATGATTAATCTTAGGTAGATGCACTGCTCACTGCACCCCTTCCA	3365
Db	3355	ATTAACTTACATAGACATGATTAATCTTAGGTAGATGCACTGCTCACTGCACCCCTTCCA	3414
QY	3366	GCTCTCATTTTGTAGGTGATTTGGGATAGGAGATGTTTTGGGGTATGGGGGAGAGTG	3425

Db	3415	GCTTCATTTTGTAGGTAATTGGATTTGGATAGGATAGTGTTTTGGGGGTATGGGGGAAGTG	3474
Oy	3426	TTTTCGACCTTGCTTTCGACGACGTGCCTCCGACCCTCAGACAGTTTGGGGTGTGGCCCCAGG	3485
Db	3475	TTTTCGACCTTGCTTTCGACGACGTGCCTCCGACCCTCAGACAGTTTGGGGTGTGGCCCCAGG	3534
Oy	3486	GCGGTTCTTGGATGTAAAAAGATGTGCCATCTAGACCTGTGAACCTCACTGTCACTGTGT	3545
Db	3535	GCGGTTCTTGGATGTAAAAAGATGTGCCATCTAGACCTGTGAACCTCACTGTCACTGTGT	3594
Oy	3546	CCCATAGGAGTGCCTTCGATAACTGTATTATAGATTAAAGTTTGTGGCAGAAAGTAGACCTTG	3605
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Oy	3606	CGTGGCAAACATGTACCGTGGCCCTGTATATAGTATAGAGTTGATATTAATGTAACCATGTAT	3665
Db	3655	CGTGGCAAACATGTACCGTGGCCCTGTATATAGTATAGAGTTGATATTAATGTAACCATGTAT	3714
Oy	3666	GTTAATGTGAATCTGTGGCGACGATACCTTTTCATGCGACGAGAANAATCCAGCTGTGAA	3725
Db	3715	GTTAATGTGAATCTGTGGCGACGATACCTTTTCATGCGACGAGAANAATCCAGCTGTGAA	3774
Oy	3726	ACTGGCTATGTTTAAATPAGCCCTCAATGGCCCTTACCTGTTGTGTGACCTGGGTAGGGA	3785
Db	3775	ACTGGCTATGTTTAAATPAGCCCTCAATGGCCCTTACCTGTTGTGTGACCTGGGTAGGGA	3833
Oy	3786	CAGAAGTTCCATTGTGATGTCATATTAAGCAAAAGTACTTGGC	3826
Db	3835	CAGAAGTTCCATTGTGATGTCATATTAAGCAAAAGTACTTGGC	3875
RESULT 6			
AKO27424			
LOCUS	AKO27424	3876 bp mRNA linear PRI 30-JAN-2004	
DEFINITION	Homo sapiens CDNA FLJ14518 flc, clone NT2RPM1000850, weakly similar to ANKRRIN R.		
ACCESSION	AKO27424		
VERSION	AKO27424.1	GI:14042089	
KEYWORDS	nlgo caplins; fls (full insect sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
REFERENCE			
AUTHORS	1 Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,K., Sudoh,K., Hosobri,T., Kaku,Y., Kodaira,H., Kondoh,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuma,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishida,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hirooka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yoshida,M., Houchuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komati,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yunki,H., Oshima,A., Saeki,N., Aotsuka,S., Yoshihara,Y., Matsunaga,H., Ichihara,T., Shiohara,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kakumaki,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hiro,M., Omori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,K., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shiga,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Shugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Ohmura-K., Nagase,T., Nomura,N., Kikuchi,H., Maehno,Y., Yamaeshita,R.,		

TITLE	JOURNAL	PUBMED	REFERENCES	AUTHORS
Nakai, K., Yada, T., Nakamura, Y., Ohata, O., Isogai, T. and Sugano, S.	human cDNAs	Complete sequencing and characterization of 21,243 full-length		
14702039				
2				
Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,				
Mishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,				
Wagatsuma, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H.,				
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,				
Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,				
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,				
Nakamura, Y., Nagahai, K., Maeho, Y., Nimomiya, K. and Iwayanagi, T.				
NEDO human cDNA sequencing project				
Unpublished				
3 (bases 1 to 3876)				
Isogai, T. and Otsuki, T.				
Direct Submission				
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,				
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan				
(E-mail:genomic@hri.co.jp; Tel:81-438-52-3975, Fax:81-438-52-3986)				
NEDO human cDNA sequencing project supported by Ministry of				
Economy, Trade and Industry of Japan; cDNA full insert sequencing;				
Research Association for Biotechnology; cDNA library construction;				
5', 3' and one pass sequencing and clone selection; Helix				
Research Institute (supported by Japan Key Technology Center etc.)				
and Department of Virology, Institute of Medical Science,				
University of Tokyo.				
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Db	176	CAAGGTGGCCATGTCACCTGGAAGACTGGCTGCATCAAGTCTGCCACCTGCA	235
Oy	187	CGTCACGACAGGGAGCGCATGAGCTTTTGAAGAACCAGAAAGATGAGATGGCCAA	246
Db	236	CGTCACGACAGGGAGCGCATGAGCTTTTGAAGAAGCCAGAAAGATGAGATGGCCAA	295
Oy	247	GTTCGCTACATCTCGCTGTGTATGAGCATCTGCCGAGAACCTGTCCGCTGGTCAATGA	306
Db	296	GTTCGCTACATCTCGCTGTGTATGAGCATCTGCCGAGAACCTGTCCGCTGGTCAATGA	355
Oy	307	GTAATGAGAGACGGGCTCCCTGGAAAAGCTGTGGCTTCGAGACCATTTGCCATGGGATCT	366
Db	356	GTAATGAGAGACGGGCTCCCTGGAAAAGCTGTGGCTTCGAGACCATTTGGCATGGGATCT	415
Oy	367	CCGGTTCGGATCAATCCAGAGAGGGGGTGGGCAATGAATTTCCGTGCACTGCATGGACCC	426
Db	416	CCGGTTCGGATCAATCCAGAGAGGGGGTGGGCAATGAATTTCCGTGCACTGCATGGACCC	475
Oy	427	GCCAATCCCTGCACTGGAACCTCAAGCCGCGACATCTCTGTGATGACCACTACAGT	486
Db	476	GCCAATCCCTGCACTGGAACCTCAAGCCGCGACATCTCTGTGATGACCACTACAGT	535
Oy	487	CAAGATTTCTGATTTTGGTCTGGCCAGTGCACGGGCTGTCCACTGCAATGACTTGA	546
Db	536	CAAGATTTCTGATTTTGGTCTGGCCAGTGCACGGGCTGTCCACTGCAATGACTTGA	595
Oy	547	CATGATAGGCGCTTTTGGCAATGCGCCTACCTCCCTCAGAGGCGCATCAAGGAGAAAG	606
Db	596	CATGATAGGCGCTTTTGGCAATGCGCCTACCTCCCTCAGAGGCGCATCAAGGAGAAAG	655
Oy	607	CCGGCTCTTCGACACCAAGACAGATGTATACAGCTTTGCGATCGTCACTGGGGGCTGCT	666
Db	656	CCGGCTCTTCGACACCAAGACAGATGTATACAGCTTTGCGATCGTCACTGGGGGCTGCT	715
Oy	667	CAACAAGAAAGCCGTTTGCAATGAGAAACATCTGCACATATGTGTGAAGTGTGT	726
Db	716	CAACAAGAAAGCCGTTTGCAATGAGAAACATCTGCACATATGTGTGAAGTGTGT	775
Oy	727	GAAGGGCCACCGCCCGCGAGCTGCGCCCGGTGTGAGAGCGGGCGCGCGCTGACAGCA	786
Db	776	GAAGGGCCACCGCCCGCGAGCTGCGCCCGGTGTGAGAGCGGGCGCGCGCTGACAGCA	835
Oy	787	CCTGATACGCTCATGACAGCGGTGCTGGCAGGGGAGTCGCGAGTTTAAAGCCACCTTCCA	846
Db	836	CCTGATACGCTCATGACAGCGGTGCTGGCAGGGGAGTCGCGAGTTTAAAGCCACCTTCCA	895
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Db	896	AGAAATTAATTTCTGAAAACGAGAGACCTGTGTGAAAAGCTGATGACGAATGAAAAGAAC	955
Oy	907	TGCTCATGATCTGGAAGCTGTAAGACCCCGGAGCCAGAGACGAGGTGTGTGCTGGCAG	966
Db	956	TGCTCATGATCTGGAAGCTGTAAGACCCCGGAGCCAGAGACGAGGTGTGTGCTGGCAG	1015
Oy	967	GCTCAAGCGGGGCTGTGCGCCCACTTGATGATGACGCTCTCCGAGCTTCTCTC	1026
Db	1016	GCTCAAGCGGGGCTGTGCGCCCACTTGATGATGACGCTCTCCGAGCTTCTCTC	1075
Oy	1027	ACAGCTGGAATCTGGAATTTCCAGGCTGTGAGAGGGCCCGAGAGCTCAGCCGAGCTC	1086
Db	1076	ACAGCTGGAATCTGGAATTTCCAGGCTGTGAGAGGGCCCGAGAGCTCAGCCGAGCTC	1135
Oy	1087	CTCTGAGTCCAGAGCTGCCATGTCCGGCAGTGGGAAGAGGCTCTGGGGGTGTCTCCGCT	1144
Db	1136	CTCTGAGTCCAGAGCTGCCATGTCCGGCAGTGGGAAGAGGCTCTGGGGGTGTCTCCGCT	1199
Oy	1147	GGACTCCGGCTTCTCTTCCAGAGAGATCATGTCCGCTGTCTTGTGAGCGGGAACCTTCAAC	1200
Db	1196	GGACTCCGGCTTCTCTTCCAGAGAGATCATGTCCGCTGTCTTGTGAGCGGGAACCTTCAAC	1255
Oy	1207	CAGCGATCTGGGTACCAAGAGCTCCAGAAAGAAAGCTTGTGATGTCATCGTGTCC-	1265

Db	1256	CAGCGATCTGGGTATCAAC-AGAAGTCAGAGAAAGAAAGCTTTGTGATGTCATCGTGTCCG	1314
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Db	1315	GGGACACCAAGCAAACTGATGAAGATCTCTGCAGCCCTGCAGAGAGTGTGACCTTGCACATGGACA	1374
QY	1336	GCGGTGCGAAGCTGTGCACTCTGGCGGTGGAGGCGCGGGCAAGAGAGTGGCCAAATGTGC	1385
Db	1375	GCGGTGCGAAGCTGTGCACTCTGGCGGTGGAGGCGCGGGCAAGAGAGTGGCCAAATGTGC	1434
QY	1386	TGCTGTCAAAATGSCCAACCCCAACCTGAGCAACCGTAAAGGAGCTTCAACCCCTTGGACA	1445
Db	1435	TGCTGTCAAAATGSCCAACCCCAACCTGAGCAACCGTAAAGGAGCTTCAACCCCTTGGACA	1494
QY	1446	TGGCGGTGAGAGAGAGGTGCGGGGTATCTGTAGACTCTGTGCAACGAGAAATCAGTG	1505
Db	1495	TGGCGGTGAGAGAGAGGTGCGGGGTATCTGTAGAGCCCTGTGCAACGAGAAATCAGTG	1554
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QY	1626	GCCGAGCCGCCATGACAGTGGCCCTGCCAGCAACGAGGCAAGAGAAATATCTGTGCATCTTGC	1685
Db	1675	GCTTAGGCCCATGACAGTGGCCCTGCCAGCAACGAGGCAAGAGAAATATCTGTGCATCTTGC	1734
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QY	1746	CTGCCTGACAGGAGCCACCTGCCCAATCTGCAAGCTGTGACCAAGAGCCGCGGCTGAGTG	1805
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Db	1915	ACCGGTGGCCCGCATCTCTCATCCAGCTGTGTCTGCAGATCAAGTCTGTGACGCTGTGCTGG	1974
QY	1926	CACAAACAACCCCTGTGACGTGGCCGCGGAGAGAGGGGCAACAGAGCACTGCAAGGCTGTCC	1985
Db	1975	CACAAACAACCCCTGTGACGTGGCCGCGGAGAGAGGGGCAACAGAGCACTGCAAGGCTGTCC	2033
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Db	2215	AGGTGTGAGAGAGTGTGTGACAGCGCCGATGTCTATTGACCTGTTCGACAGCAAGGGGCTCA	2274
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Db	2275	GGCGGCTGCACTGTGCCCGCCAGGGGCGGCACAGCAACAGGTGAGACTGTGTCTAAGG	2333
QY	2286	ATGGGGGCCCAATCAACCTGTGACAGGCTCAAGTTTCAAGGGGGGCAATGGCCCGCGGCA	2345
Db	2335	ATGGGGGCCCAATCAACCTGTGACAGGCTCTCAAGTTTCAAGGGGGGCAATGGCCCGCGGCA	2394

Oy	2346	AACTCTCGGGCGAAGCAAGACCTAAGCTGCTGCTGGGAGAACCGGGGGCTCAAGTGGG	2405
Db	2395	CACCTCTCGGGCGAAGCAAGACCTAAGCTGCTGCTGGGAGAACCGGGGGCTCAAGTGGG	2454
Oy	2406	GCTCTGTCTCTGTCTGTCTGTCTGTGGGATGGAAGATCTCTGTGGGGCCCGTTG	2465
Db	2455	GCTCTGTCTCTGTCTGTCTGTCTGTGGGATGGAAGATCTCTGTGGGGCCCGTTG	2514
Oy	2466	TGGCTTAACTTAAATGTTAACCAAGCAGGTGACATGTGTCCATCCAGAGCGGCTGTG	2525
Db	2515	TGGCTTAACTTAAATGTTAACCAAGCAGGTGACATGTGTCCATCCAGAGCGGCTGTG	2574
Oy	2526	CTGACCGGAGTGTCCCCCTCCAGGTGAAGCTGGCTCAGGTGACATGACCCGCTCATCATC	2585
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Oy	2586	GATCTAAGGCACCTGTGTCTGAAGGAGCCGTGGGTCAGAATCATTTCTGTGTCTTAA	2645
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Db	3595	CCCATAGGGTCCCTTCTGAAATACCTGTATTAGAAATAGTTTGTTCAGAACTGACCTTG	3654
QY	3606	CGTGCAAACATGTACCGTGGCCGTGTATAGATAGATGATATATATGACATGAT	3665
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QY	3666	GTTATATGTGAATCTGTGGGACAGAAATACCTTCCATGCGAAGAAATATCCAACTGTTGAA	3725
Db	3715	GTTATATGTGAATCTGTGGGACAGAAATACCTTCCATGCGAAGAAATATCCAACTGTTGAA	3774
QY	3726	ACTGGCTATGTTTAAATATATGCTCATGTTGCTTTACTGTGTGTGGAATGCGTGAAGGA	3785
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LOCUS	BC035755	3867 bp	mRNA	linear	PRI 25-JUN-2004
DEFINITION	BC035755	3867 bp	mRNA	linear	PRI 25-JUN-2004
ACCESSION	BC035755				
VERSION	BC035755.1				
KEYWORDS	GI:23242902				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 3867)				
REFERENCE	Strausberg, R., Feingold, E.A., Grouse, L.H., Derge, J.G., Alausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Alekschul, S.F., Zeeberg, B., Bluetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stjepanovic, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uebelin, T.B., Toshikuni, S., Carminci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wille, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huyl, S.W., Vallal, D.C., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahney, J., Helton, E., Kerteman, M., Madan, A., Rodriguez, S., Bonfield, A., Whiting, M., Madan, A., Young, A.C., Shenchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Gimwood, J., Schmutz, J., Myers, R.M., Butlerfield, V.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 3867)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (31-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov				
COMMENT	Contact: MGC help desk				

Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhers, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dierich, N.L., Grante, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W.,
Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Series: IRMA Plate: 79 Row: 0 Column: 16
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 10190675.
Location/Qualifiers

FEATURES

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/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 97.8%; Score 3774.8; DB 9; Length 3867;
Best Local Similarity 99.5%; Freq. No. 0;
Matches 3827; Conservative 0; Mismatches 13; Indels 5; Gaps 4;

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1 CGATGAGGGCGAGCGCGGAGCCCATGAGGCTCTGCGCTGCGACCTTTCAGACGCG 60
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JOURNAL Published Only in Database (2000)
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TITLE	The DNA sequence of human chromosome 21		
JOURNAL	Nature 405 (6784), 311-319 (2000)		
PMID	20289799		
POBMD	10830953		
REFERENCE	2 (bases 1 to 219256)		
AUTHORS	Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Patterson,D., Reichwald,K., Kudoh,J., Shibusaki,K., Kawasaki,K., Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyma,S., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordtief,K., Hornischer,K., Barand,P., Scharfe,M., Schoen,O., Desario,A., Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S., Hemig,S., Resselmann,L., Dgand,E., Wehrmeyer,S., Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Leinrich,H., Reinhardt,R. and Yaspo,M.L. Direct Submission Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below) On May 30, 2000 this sequence version replaced gi:7717391. The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan, e.mail: hattori@gsc.riken.go.jp * URL: http://hgp.gsc.riken.go.jp/ and * Institute of Molecular Biotechnology, Genome Analysis, * Beutenbergstrasse 11, D-07745 Jena, Germany, e.mail: gscj-submit@genome.imb-jena.de * URL: http://genome.imb-jena.de/ and * Keio University School of Medicine, Molecular Biology, * Tokyo 160-8582, Japan, e.mail: nshimizu@mb.med.keio.ac.jp * URL: http://www.dmb.med.keio.ac.jp/ and		
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AL163288: Submitted (10-Apr-2000).
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 ACCESSION BS000130 BA000046
 VERSION BS000130.1 GI:37537397
 KEYWORDS HTG.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
 REFERENCE
 AUTHORS 1
 TITLE The International Chimpanzee Chromosome 22 Consortium.
 JOURNAL DNA sequence and comparative analysis of chimpanzee chromosome 22
 REFERENCE Nature 429, 382-388 (2004)
 AUTHORS 2 (bases 1 to 201997)
 Hattori,M., Toyoda,A., Watanabe,H., Taylor,T.D., Kuroki,Y.,
 Fujiyama,A. and Sakaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (12-MAY-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
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 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 *The Chimpanzee Chromosome 22 Sequencing Consortium consists of:
 *Chinese National Human Genome Center at Shanghai, Shanghai, China;
 *GRI, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
 of Molecular Biotechnology, Jena, Germany; *KIRB Genome Research
 Center, Daejeon, Korea;
 *Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
 *National Institute of Genetics, Mishima, Japan;
 *National Yang Ming University Genome Research Center, Taipei,
 Taiwan;
 *RIKEN Genomic Sciences Center, Yokohama, Japan.
 COMMENT
 ----- Genomic Sciences Center
 Center: RIKEN Genomic Sciences Center
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gsc.riken.go.jp
 ----- Project Information
 Center Project name: The Chimpanzee Chromosome 22 Sequencing Project
 Center clone name: CH251-010A09
 ----- Summary Statistics
 Sequencing vector: pUC18, pUC13, pTZ19R; 100% of reads Chemistry:
 Dye-terminator Big Dye and ET; 100% of reads Assembly program:
 Phrap; version 0.990329
 Consensus quality: 201,997 bases at least Q40

Consensus quality: 0 bases at least Q30
 Consensus quality: 0 bases at least Q20

 This sequence was finished as follows unless otherwise noted: all
 regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >= 30);
 an attempt was made to resolve all sequencing problems, such as
 compressions and repeats; all regions were covered by at one
 plasmid
 subclone or more than one M13 subclone;
 and the assembly was confirmed by restriction digest.

 Source information:
 The RPCR-43 chimpanzee BAC library was prepared from DNA isolated
 from the blood of a single male chimpanzee using published
 protocols (Osogawa,K. et al. Genomics 52:1-8). The DNA from the
 chimpanzee ('Clint') was obtained from the Yerkes Primate Center in
 Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu,
 Kazutoyo Osogawa, Evan Richler & Pieter J de Jong. The library
 characteristics are described at
 http://www.chori.org/bacpac/mchimp43.htm.
 The clone may be obtained from Pieter J. de Jong and coworkers
 (http://www.chori.org/bacpac).
 VECTOR: pBACe3.6
 The CHORI-251 chimpanzee BAC library was prepared from DNA isolated
 from the blood of a single male chimpanzee using published
 protocols (Osogawa,K. et al. Genomics 52:1-8). The DNA from the
 chimpanzee ('Clint') was obtained from the Yerkes Primate Center in
 Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu,
 Kazutoyo Osogawa, Evan Richler & Pieter J de Jong. The library
 characteristics are described at
 http://www.chori.org/bacpac/chimpanzee251.htm.
 The clone may be obtained from Pieter J. de Jong and coworkers
 (http://www.chori.org/bacpac).
 VECTOR: pTABAC2.1
 The PTB1 chimpanzee BAC library was prepared from DNA isolated from
 cultured cells established from the blood of a single male
 chimpanzee.
 Clones may be obtained from Aaao Fujiyama and co-workers
 (http://www.gsc.riken.go.jp).
 VECTOR: pKS145
 The PTF22 chimpanzee Fosmid library was prepared from DNA isolated
 from cultured cells established from the blood of a single male
 chimpanzee.
 Clones may be obtained from Aaao Fujiyama and co-workers
 (http://www.gsc.riken.go.jp).
 VECTOR: pKS143

 Sequence Quality Assessment:
 This entry has been annotated with sequence
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than 1 error in
 10,000 bp.

 Neighboring clones:
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RESULT 11
AR406004
LOCUS AR406004 2355 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6630335.
ACCESSION AR406004
VERSION AR406004.1 GI:40155104
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 2355)
AUTHORS Kapeller-Liebermann, R.
TITLE 14171 protein kinase, a novel human protein kinase and uses thereof
JOURNAL Patent: US 6630335-A 3 07-OCT-2003;
FEATURES
Location/Qualifiers
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ORIGIN

Query Match 61.0%; Score 2355; DB 6; Length 2355;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GAGTTCAAGGCTGTGGAGAAAGTGGCTCGGGCGGCTTTCGGGCAAGTGTTCAGAGTGGCG 120
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QY 197 AGGAGAGGCAATGAGCTTTTGGAAAGAACCAAGAAATGAGATGGCCAAATTTCGTAC 256
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1577 CGGCTGCTGTTGAGAGAAAGCCCTCGGTCAACGAGTGAAGCTTTGAGGGCCGAGCC 1636
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RESULT 12

COJ31804
LOCUS COJ31804 2499 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 17738 from Patent WO02068579.
ACCESSION COJ31804
VERSION COJ31804.1 GI:42309361
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 17738 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
ORIGIN
Query Match 56.3%; Score 2173.2; DB 6; Length 2499;
Best Local Similarity 94.0%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 146; Gaps 3;
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Oy	845	-----CAAGAAATTAATCTTGTGAAACCGAGACCTGTGTGAAGACCTGATGAC	892
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Oy	953	GTTGTGCTGTGGAGGCTCAAGCGGGGCTCTGCCCCACCTTGATTAACGTAAGAGCTC	1012
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Oy	1312	CTGTGCACTTGAACAGCGGTGCGACGCTGTGCACTTGCGCGGTGAGAGGCGGGCAAGAGGA	1371
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Db	1500	GTTGCGCAAGTGGCTGTGCTCAACAATGCAACCCCAACTGAGCAACTTAAAGGGCTC	1559
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Oy	1552	CCAGAAACGGGGATGTAGTCTAGACACAGGCTGTGTTTGGAGAAAGACGCTCGCTCAACGA	1611
Db	1680	CCAGAAACGGGGATGTAGTCTAGACACAGGCTGTGTTTGGAGAAAGACGCTCGCTCAACGA	1739
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Db	1980	ACAAGCGGGGACATACCGCGCTGTGCGCCGATCTCATTTGACCTGTGTCTCCAGCTCAAGCT	2039
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Db	2220	GAAAGCCGATGTGCTGGCCCGGGGACCCCTTGACACCAAGCGCGCTTGACACTTGGCTTGC	2279
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Qy	2212	CGAGCAGGGGCTCAGCGCGCTGCACTTGCGCGCCAGAGGCCGAGCAGCAGACGAGCGTGA	2271
Db	2340	CGAGCAGGGGCTCAGCGCGCTGCACTTGCGCGCCAGAGGCCGAGCAGCAGACGAGCGTGA	2399
Qy	2272	GACTCTGCTCAGGCAATGGGGCCCAATTCACCTGCAAGAGCTTCAAGTTCCAGGGCGGCGCA	2331
Db	2400	GACTCTGCTCAGGCAATGGGGCCCAATTCACCTGCAAGAGCTTCAAGTTCCAGGGCGGCGCA	2459
Qy	2332	TGGCCCCGCGCGCACAATCTCGGCGGCGAGCAAGACCTAG	2371
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AX166548			
LOCUS	AX166548	2499 bp	DNA
DEFINITION	Sequence 39 from Patent WO0138503.		
ACCESSION	AX166548		
VERSION	AX166548.1	GI:14546893	
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,		
AUTHORS	Flanagan,P. and Clary,D.S.		
TITLE	Novel human protein kinases and proteic kinase-like enzymes		
JOURNAL	Patent; WO 0138503-A 39 31-MAY-2001;		
FEATURES	Sugen, Inc. (US)		
source	Location/Qualifiers		
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ORIGIN

Query Match 56.3%; Score 2173.2; DB 6; Length 2499;
 Best Local Similarity 94.0%; Pred. No. 0;
 Matches 2351; Conservative 0; Mismatches 3; Indels 146; Gaps 3;

17 ATGAGGGGCGACGGGGGAGCCCGCATGGGCGCTGGCGGCACTTGAGAGCGGGG 76
 1 ATGAGGGGCGACGGGGGAGCCCGCATGGGCGCTGGCGGCACTTGAGAGCGGGG 60
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RESULT 14
AF302127 3559 bp mRNA linear ROD 08-JAN-2002
LOCUS Mus musculus PKC-regulated kinase PKK mRNA, complete cds.
DEFINITION AF302127
ACCESSION AF302127
VERSION AF302127.3 GI:18087895
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE 1 (bases 1 to 3559)
AUTHORS Chen, J., Haider, K., Ponda, M., Cariappa, A., Rowitch, D. and Pillai, S.
JOURNAL Protein kinase C-associated, ankyrin repeat-containing protein kinase
MEDLINE J. Biol. Chem. 276 (24), 21737-21744 (2001)
PUBMED 11278382
REFERENCE 2 (bases 1 to 3559)
AUTHORS Chen, J., Haider, K., Cariappa, A. and Pillai, S.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-2000) Cancer Center, Massachusetts General
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
REFERENCE 3 (bases 1 to 3559)
AUTHORS Chen, J., Haider, K., Cariappa, A. and Pillai, S.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Cancer Center, Massachusetts General
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
REMARK 4 (bases 1 to 3559)
AUTHORS Sequence update by submitter
JOURNAL
REMARK 5
AUTHORS Chen, J., Haider, K., Cariappa, A. and Pillai, S.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2002) Cancer Center, Massachusetts General
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
REMARK 6
AUTHORS Nucleotide sequence update by submitter
JOURNAL
REMARK 7
AUTHORS On Jan 8, 2002 this sequence version replaced gi:18086161.
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DB 646 GTTTGACCAAGACAGATGATTAAGCTTTGCGATGCTGAGGCGTCTGCTGCTGCTGCTGCTGCT 705
QY 673 GAAAGAGCGTTTGGCAAGATGATTAAGCTTTGCGATGCTGAGGCGTCTGCTGCTGCTGCTGCTGCT 732
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Db	1246	AGGCGACCTGGGGCCCCAC-AGACATCAAGAAAGAAAGACTGATGTCATCATATCAG	1300
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Db	1305	GGGACACCGAGCGCTGATGAAATCTTACAGCCCAAGATGTGTGAACTTGTGTTTAAACA	1366
Oy	1326	GGGATCCAGGCTGTGCGACCTTGCGGGTGAAGGCCGGGCAAGAGAGTGGCCCAAGTGGC	1388
Db	1365	GCAATCCAGGCTGTGCGACTTGTGAGAGGCCGGAACAGAGAGATGTGTCAAGTGGC	1422
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Db	1605	AGGCCAGCAACAAGCTGTCTGTAGAGAAAGATGTTTGTCAATGAAGTGGACTTTGAGG	1666
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Db	1665	GCCGAACACCCATGCACTGTGCTTGCAGCATGACAGAGAAACATTGTGCGCACCTTGC	1722
Oy	1686	TGGCCGAGCGGTGGAAGTGAAGCTGAGGGGCAAGATGTCTGCTGCACTGGACCTAAG	1744
Db	1725	TCCGCGGTGTGTGAATGTGGAGCTTGAAGGGAAGAGATGCTGTGCTCTTGTGACTATG	1788
Oy	1746	CTGCTTGAAGGACCACTGCTCATCTCAAGCTGTGGCCAAAGCAACCGGGGGTGAAGT	1800
Db	1785	CTGCTTGAAGGACCACTTCCATTTGTAAAGCTGTGAAGCCAAAGCAACCTGGGGTGAAGT	1866
Oy	1806	TGAAGCCCAAGACGCTGATGGAGAGCGCAATTGCACTTGGCCGCAAGCGCGGCACT	1866

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Db	1965	CACAGACACCTGTGCAGATGTGTCTGCAGAGACTGGACACACTAGTACTGGCCAGGCTACTCT	2024
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RESULT 15				
BC057871				
LOCUS				
DEFINITION	Mus musculus receptor-interacting serine-threonine kinase 4, mRNA			
ACCESSION	BC057871			
VERSION	BC057871.1			
KEYWORDS	GI:37046719			
ORGANISM	Mus musculus (house mouse)			
REFERENCE	Mus musculus			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3558)			
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stempleton, M., Soares, K.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uebelin, T.B., Toshitsuki, S., Carinini, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mollahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wootley, K.C., Hale, S., Garcia, A.M., Gay, L.U., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shcherenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywnicki, M.I., Skalska, U., Smalins, D.E.,			
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 QY 2406 GCTCTGTCTGTCTGTGTTCTCTGTGGGATGGAACGATCTGCG 2452
 DB 2402 GCTTCTGACATCTTGTCTTCTCATGTGGGACAGAAATGTCTCGG 2448

Search completed: September 16, 2005, 01:18:20
 Job time : 15989.8 secs

BS Claim 1; SEQ ID NO 1; 62pp; English.

XX The invention provides novel human 14171 protein kinase polypeptides and
CC polymucleotides. The methods and compositions of the present invention
CC are useful for the diagnosis and/or treatment of diseases or conditions
CC associated with aberrant expression or activity of a 14171 protein kinase
CC such as cancer, immunological disorder, inflammation, heart failure,
CC hypertension, atrial fibrillation, viral disorder and apoptotic disorder.
CC The invention can also be used in chromosome mapping, tissue typing,
CC predictive medicine, forensic biology and prognostic assays. The present
CC sequence is human 14171 protein kinase cDNA.

XX Sequence 3860 BP; 810 A; 1066 C; 1167 G; 816 T; 0 U; 1 Other;

Query Match 100.0%; Score 3859; DB 12; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCACGCGTCCGGCGGATGAGAGGCGAGCGGAGCCCATGAGGCGCTGCGCTGCG 60
Qy 61 CACCTTCGACGCGGCGGAGTTCACGCGGCTGAGAGAGTGGGCTCGCGGCTTGGGCA 120
Db 61 CACCTTCGACGCGGCGGAGTTCACGCGGCTGAGAGAGTGGGCTCGCGGCTTGGGCA 120
Qy 121 GGTGTACAAAGGTGCGCATGTTCACCTGAGAACCTGGCTGAGCAATGCTGCGCCAG 180
Db 121 GGTGTACAAAGGTGCGCATGTTCACCTGAGAACCTGGCTGAGCAATGCTGCGCCAG 180
Qy 131 CCGTGAACGTCGACGAGGAGGAGGATGAGAGCTTTTGAAGAAAGCAAGAAATGAGAT 240
Db 131 CCGTGAACGTCGACGAGGAGGAGGATGAGAGCTTTTGAAGAAAGCAAGAAATGAGAT 240
Qy 181 CCGTGAACGTCGACGAGGAGGAGGATGAGAGCTTTTGAAGAAAGCAAGAAATGAGAT 240
Db 181 CCGTGAACGTCGACGAGGAGGAGGATGAGAGCTTTTGAAGAAAGCAAGAAATGAGAT 240
Qy 241 GGCCTAAGTTTGGCTATCATCTGCTGTATGAGCATCTGCGCGAAGCTGTGCGCTGAT 300
Db 241 GGCCTAAGTTTGGCTATCATCTGCTGTATGAGCATCTGCGCGAAGCTGTGCGCTGAT 300
Qy 301 CATGAGTACATGAGAGCGGGCTCCCTGAGAAAGCTGCTGGAGCCATTGGCATG 360
Db 301 CATGAGTACATGAGAGCGGGCTCCCTGAGAAAGCTGCTGGAGCCATTGGCATG 360
Qy 361 GATATCTCCGGTCCGAAATATCAGAGAGCGGCGGATGAGAACTTCCTGCACTGAT 420
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Qy 421 GGCCTGCGGCTCTGCACTGAGCTCAAGCCCGGAAACATCTGCTGATGCCACTA 480
Db 421 GGCCTGCGGCTCTGCACTGAGCTCAAGCCCGGAAACATCTGCTGATGCCACTA 480
Qy 481 CCAAGTCAAGATTTTCTGATTTTGTGCTGAGCAAGTGCAGCGGCTGTCCACTCCATGA 540
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Qy 541 CCGTGAAGTGAAGTGGCTGTGTTGAGCAATCCGCTACCTCCCTCAAGAGCGGATGAGGA 600
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Qy 601 GAAAGAGCGGCTCTTGCACCAAGACGATGATATACAGCTTTGGATGATGATGAGGA 660
Db 601 GAAAGAGCGGCTCTTGCACCAAGACGATGATATACAGCTTTGGATGATGATGAGGA 660
Qy 661 CGTGTCTCAACAGAGAGCCGTTTTCAGATGAGAGAAACATCTGCAATGATGATGA 720
Db 661 CGTGTCTCAACAGAGAGCCGTTTTCAGATGAGAGAAACATCTGCAATGATGATGA 720
Qy 721 GGTGTGAAGGCGACCGGCGGAGCTGGCGCGCGTGTGACAGAGCGGCGGCGGCTG 780
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Qy 781 CAGCCACTGATAGCGCTCATGACAGGCGGTGTGTGCAAGGCGGATCCCGAGTTAGCCAC 840
Db 781 CAGCCACTGATAGCGCTCATGACAGGCGGTGTGTGCAAGGCGGATCCCGAGTTAGCCAC 840

Qy 841 CTTCGAGAAATTAATTCTTGTGAACCGAGACCTGTGTGAAAAAGCTGTATGACGAAATGA 900
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Db 901 AGAAGTGTCTATGATGTGACGTGAAGAGCCCGGAGCCGAGAGGAGTGTGCC 960
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Db 1021 TCTCTCAACGCTGAGCTCTGAGTTTCCAGGCTGTGAGAGGCGCCGAGAGCTCAAGCG 1080
Qy 1081 CAGCTCTCTGAGTTCAGAGCTGACATGCTCGGAGTGGAGAGAGCTCTCGGAGTGTGC 1140
Db 1081 CAGCTCTCTGAGTTCAGAGCTGACATGCTCGGAGTGGAGAGAGCTCTCGGAGTGTGC 1140
Qy 1141 CTGCGTGAATCTCGGCTTTCTCTTCCAGAGATCACTGTGCTGCTTTGAGCGGAAAC 1200
Db 1141 CTGCGTGAATCTCGGCTTTCTCTTCCAGAGATCACTGTGCTGCTTTGAGCGGAAAC 1200
Qy 1201 TTCAACCAAGCATCTGGGTACCAAGACGTCGAGAGAGAAAGAACTTGTGATGACATTC 1260
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DB 2101 TGTGCTGGGCGCGGGGACCCCTGAAACGACGGCGCTGCACTGGCTGCGCCGCAAGGCA 2160
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DB 3061 TGAACAACACACACAGTGTCCCACTGATCTAGCTGCCCTTGTGTTGCGCCCAA 3120
QY 3121 GATGTTTTGGCACTTGAAGCCACAGGCTTGAAGTCAATTAATAAATTCCTCCCTTTGTA 3180
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DB 3181 ACTCAGTCTGAGGACCTGAGCGAGCCCTCAAGTGTGCTGAGGTGCAACAATCTTGGG 3240
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DB 3241 GAAAGGTGCAAGAGAGCTGTTTTTATCTCAACAGAGATGAAGTAAATTAAC 3300
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QY 3361 TCCAGCTCTGATTTTTGTAGTGAATTTGGATAGGATAGTGTGTTGGGTATGGGG 3420
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QY 3421 GAGTGTCTGACCTGCTTTGACAGCTGCTCCGACCTCAGACGTTTGGGTTGCGCC 3480
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QY 3481 CCAAGGCGGTTCTGGATGTAAGAATGGGCATCTAGCCCTGTAACCTTCACTGCAAC 3540
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QY 3721 TTGAACCTGCTATGTTTTAATATGCTCATTTGCTCTTACTGTTGTGTGACCTGCTG 3780
DB 3721 TTGAACCTGCTATGTTTTAATATGCTCATTTGCTCTTACTGTTGTGTGACCTGCTG 3780
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DB 3841 TGAATAAAAAAAAAAAGG 3860

RESULT 2
ADE38376
ID ADE38376 strand, DNA; 3860 BP.
XX
XX ADE38376;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human protein 14171 gene sequence.
XX
XX tumorigenic disorder; angiogenic disorder; aberrant gene expression;
XX tumourigenic activity; cytostatic; antihypertoid; antidiabetic;
XX aberrant protein activity; cancer; breast cancer; lung cancer;
XX ophthalmological; cancer; breast cancer; colon cancer; lung cancer;

KM		prostatic cancer; Grave's disease; diabetic retinopathy; gene; ds;
XV		protein 14171.
XX	Homo sapiens.	
XX	Key CDS	Location/Qualifiers 14..2371 /*tag= a /product= "Human protein 14171"
FT		
XX	MO2003065006-A2.	
PN		
PD	07-Aug-2003.	
PF		
XP	30-JAN-2003; 2003WO-US002588.	
XX		
PR	31-JAN-2002; 2002US-0353600P.	
PR	15-MAR-2002; 2002US-0364517P.	
PR	09-APR-2002; 2002US-0371075P.	
PR	10-APR-2002; 2002US-0371507P.	
PR	16-APR-2002; 2002US-0372984P.	
PR	19-APR-2002; 2002US-0374194P.	
PR	24-MAY-2002; 2002US-0382995P.	
PR	31-MAY-2002; 2002US-0385023P.	
PR	14-JUN-2002; 2002US-0388853P.	
PR	17-JUN-2002; 2002US-0389395P.	
PR	25-JUN-2002; 2002US-0391324P.	
PR	15-JUL-2002; 2002US-0395944P.	
PR	22-JUL-2002; 2002US-0397726P.	
PR	13-AUG-2002; 2002US-0403046P.	
PR	22-AUG-2002; 2002US-0405155P.	
PR	27-AUG-2002; 2002US-0406361P.	
PR	25-OCT-2002; 2002US-0421195P.	
PR	12-NOV-2002; 2002US-0425456P.	
PR	19-NOV-2002; 2002US-0427626P.	
PR	10-DEC-2002; 2002US-0432122P.	
XX	(MILL-) MILLENNIUM PHARM INC.	
PA		
PI	Hunter JJ, Macbeth KJ, Tsai F, Leeson A, Lightcap ES; Williamson MW, Rudolph-Owen LA; WPL; 2003-646176/61. P-PDB; ADS38377.	
XX		
PT	Treating subject having tumorigenic disorder or angiogenic disorder caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic acid, by administering a modulator.	
PT		
XX		
PS	Disclosure; SEQ ID NO 37; 454bp; English.	
XX		
CC	This invention relates to a novel method of treating a human subject having a tumorigenic disorder or angiogenic disorder, caused by aberrant gene expression or activity of an isolated protein, by administering a modulator. The modulator may have cytostatic, antihypoid, anti-diabetic or ophthalmological activity. The method is useful for treating a subject having a tumorigenic or angiogenic disorder, in particular for treating cancer (for example breast cancer, colon cancer, lung cancer or prostatic cancer) and, for example, Grave's disease and diabetic retinopathy. The present sequence is a DNA sequence which encodes the novel isolated human protein 14171 of the invention.	
CC		
CC		
SQ	Sequence 3860 BP; 809 A; 1066 C; 1169 G; 816 T; 0 U; 0 Other;	
Query Match	99.4%; Score 3836; DB 10; Length 3860;	
Best Local Similarity	99.9%; Pred. No. 0;	
Matches 3858; Conservative	0; Mismatches 1; Indels 2; Gaps 2	
OY	1 CCACGCGTCCGGCGCATGAGAGCGAACCATTGAGCCTGTGCCTGTGC 60 Ddb 1 CCACGCCGTCCGGCGCATGAGAGCGAACCATTGAGCCTGTGCCTGTGC 60 61 CACTTCGACGCGGCGCAATTCAGGACTTGGAAGAAGTTGGAGCTCGAGCGGCTTGGAGCA 120	

Db	61	CACCTTCGACGCGGCGAGTTCA	CGGGCTGSGAGAAAGTGGGCTCGGGCGGCTTTCGGGCA	120
QY	121	GGTGTACAAAGTGTGGCCATGTCC	CTGGGAAGACTGGCTGTGCCATCAAGTGTCTCGCCAG	180
Db	121	GGTGTACAAAGTGTGGCCATGTTC	CTGGGAAGACTGGCTGTGCCATCAAGTGTCTCGCCAG	180
QY	181	CTTCGACGTGACGACAGAGGAGCG	CATGGAAGCTTTTGGAAAGGCCAAGAAAGTGAAGAT	240
Db	181	CTTCGACGTGACGACAGGAGCGCA	TGGAAGCTTTTGGAAAGGCCAAGAAAGTGAAGAT	240
QY	241	GGCCCAAGTTTTCGTACATCTCTG	CTGTGTATGGCATCTGCGCGCAACTGTCTGGCTGTGT	300
Db	241	GGCCCAAGTTTTCGTACATCTCTG	CTGTGTATGGCATCTGCGCGCAACTGTCTGGCTGTGT	300
QY	301	CATGGAAGTACATGGAAGCGGGCT	TCCCTGGAAAAGCTGTGGCTTTCGGAGGCATTTGGCATG	360
Db	301	CATGGAAGTACATGGAAGCGGGCT	TCCCTGGAAAAGCTGTGGCTTTCGGAGGCATTTGGCATG	360
QY	361	GGATCTCCGGTTCGGAATTCATCC	ACAGAGCGGCGGTGGAGATGAACTTCTGTGCACTGTCAAT	420
Db	361	GGATCTCCGGTTCGGAATTCATCC	ACAGAGCGGCGGTGGAGATGAACTTCTGTGCACTGTCAAT	420
QY	421	GGCCCGCGCACTCTCTGCACTCTG	CAAGCCCGGCAACATCTGTCTGAATGCCCCACTA	480
Db	421	GGCCCGCGCACTCTCTGCACTCTG	CAAGCCCGGCAACATCTGTCTGAATGCCCCACTA	480
QY	481	CCACGTCAAGATTTCTGATTTTGG	TCTGGCCAAATGCAACGGGCTGTGCCATCTGGCATGA	540
Db	481	CCACGTCAAGATTTCTGATTTTGG	TCTGGCCAAATGCAACGGGCTGTGCCATCTGGCATGA	540
QY	541	CCTCAGCATGGAATGGCCGTTTGG	CATCAATCGCTCACTCCCTCCAGAGCGCATCAAGGGA	600
Db	541	CCTCAGCATGGAATGGCCGTTTGG	CATCAATCGCTCACTCCCTCCAGAGCGCATCAAGGGA	600
QY	601	GAAAGCGCGGCTCTTTCGACAC	CAAGCAAGATGTATACAGCTTTTGCATCTGTCAATCTGGGG	660
Db	601	GAAAGCGCGGCTCTTTCGACAC	CAAGCAAGATGTATACAGCTTTTGCATCTGTCAATCTGGGG	660
QY	661	CTGTCTCAACAGAAAGAAAGCCG	TTTGCATGAGAAAGACATCTGTGCATCATATGTGTGA	720
Db	661	CTGTCTCAACAGAAAGAAAGCCG	TTTGCATGAGAAAGACATCTGTGCATCATATGTGTGA	720
QY	721	GGTGTGAAGGGCCACCGGCCCGG	AGCTGGCGCGGTGTGCAGAACCCGGCGCGGCGCTGTG	780
Db	721	GGTGTGAAGGGCCACCGGCCCGG	AGCTGGCGCGGTGTGCAGAACCCGGCGCGGCGCTGTG	780
QY	781	CAGCCACCTGTATAGCGCTCATG	CAGCGGTGTGTGCAGAGGGGAGTCCGCGATTTAGGCCAC	840
Db	781	CAGCCACCTGTATAGCGCTCATG	CAGCGGTGTGTGCAGAGGGGAGTCCGCGATTTAGGCCAC	840
QY	841	CTTCCAGAAATTAATTCTGAAACC	GAGGACTCTGTGTGAAAAGCTGTGATGACGAATGTAA	900
Db	841	CTTCCAGAAATTAATTCTGAAACC	GAGGACTCTGTGTGAAAAGCTGTGATGACGAATGTAA	900
QY	901	AGAAACGTCTATATCTGGAAGT	GAAAGCCCCCGGAGGCCAGAGCGAGGTGTGCC	960
Db	901	AGAAACGTCTATATCTGGAAGT	GAAAGCCCCCGGAGGCCAGAGCGAGGTGTGCC	960
QY	961	TGCGAGGCTCAAGCGGGGCTCTG	CCCCCACTTTCGATTAACAATCAAGCTCTCCGAGCT	1020
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QY	1021	TCTCTCAAGCTTGAATCTGTGA	ATTTCCAGGCTGTGCAGAGGCCCCGAGAGCTCAAGCCG	1080
Db	1021	TCTCTCAAGCTTGAATCTGTGA	ATTTCCAGGCTGTGCAGAGGCCCCGAGAGCTCAAGCCG	1080
QY	1081	CAGCTCTCTGTAGTGTCAAGCTG	CCATGTCTCCGCGATGTGGAAAGAGGCTCTCTGGGGGTGTCC	1140
Db	1081	CAGCTCTCTGTAGTGTCAAGCTG	CCATGTCTCCGCGATGTGGAAAGAGGCTCTCTGGGGGTGTCC	1140
QY	1141	CTCGGTGGAATCCGGCTTCTCTT	CCAGAGGATCACTGTGCTGTCTTGAAGCGGGAATC	1200
Db	1141	CTCGGTGGAATCCGGCTTCTCTT	CCAGAGGATCACTGTGCTGTCTTGAAGCGGGAATC	1200

Db 1141 CTGGGTGAGCTCGCCCTTCTCTTCCAGAGGATCATGTCGCTGCTTTGAGCGGGAACC 1200
Qy 1201 TTCAACACAGCGATCTGGGTATCCAAGACGTCCTAGAGAAAGACTTGTGATGCCATGCG 1260
Db 1201 TTCAACACAGCGATCTGGGTATCCAAGACGTCCTAGAGAAAGACTTGTGATGCCATGCG 1259
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Qy 1320 TGGACACGCGTTCACAGCTGCTGCACTGGCGGTGGAGCGCGGCAAGAGATGCGCCA 1379
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Db 2160 ACTCGAGAGGTGTGAGAGAGTGTGTACAGCCCGATGCTATTGACCTGTTGACAGACAG 2219
Qy 2220 GGGCTACGCGGCTGCACTGGCCGCGCCAGGGCCGGACAGCAAGAGGTGAGAGCTCTG 2279
Db 2220 GGGCTACGCGGCTGCACTGGCCGCGCCAGGGCCGGACAGCAAGAGGTGAGAGCTCTG 2279

Qy 2280 TCAAGCAGGGGCGCCATCAACCTGACAGAGCTCAAGTTCCAGAGGCGGCCATGGCCCG 2339
Db 2280 TCAAGCAGGGGCGCCATCAACCTGACAGAGCTCAAGTTCCAGAGGCGGCCATGGCCCG 2339
Qy 2340 CCGCACAATCTCGCGGGAAGAAAGCTAGCTGGCTGCTCGGAGACCGGGGCTCA 2399
Db 2340 CCGCACAATCTCGCGGGAAGAAAGCTAGCTGGCTGCTCGGAGACCGGGGCTCA 2399
Qy 2400 CGTGGGCTCTTGTCTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGT 2459
Db 2400 CGTGGGCTCTTGTCTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGTCTGTGT 2459
Qy 2460 CGGTGGGCTTACCTTAATGTTAAACAGAGAGGTGACATGTTGATCATGAGAGCGG 2519
Db 2460 CGGTGGGCTTACCTTAATGTTAAACAGAGAGGTGACATGTTGATCATGAGAGCGG 2519
Qy 2520 CTGCTGACAGCGAGGTGCTCCCTCCAGGTGAAGCTGCTAGGTGACATGCTGCTCC 2579
Db 2520 CTGCTGACAGCGAGGTGCTCCCTCCAGGTGAAGCTGCTAGGTGACATGCTGCTCC 2579
Qy 2580 ATCATGATCTAGGCACTGCTGTGTAAGGACCGTGGTCAAGATCAATTCGTTGTC 2639
Db 2580 ATCATGATCTAGGCACTGCTGTGTAAGGACCGTGGTCAAGATCAATTCGTTGTC 2639
Qy 2640 TCTTAATGGGTCTGAGAGGCTGTCTCAAGTGAAGGCCAGCGGTGAAAGATCCA 2699
Db 2640 TCTTAATGGGTCTGAGAGGCTGTCTCAAGTGAAGGCCAGCGGTGAAAGATCCA 2699
Qy 2700 CTCTCTCTGAGAGGAGCCACTTGGGTTGCTGAGCTCACAGTCTTTAGGGAGTCA 2759
Db 2700 CTCTCTCTGAGAGGAGCCACTTGGGTTGCTGAGCTCACAGTCTTTAGGGAGTCA 2759
Qy 2760 GGGGAACTGTGTTTTATCTTCAATAGACGTTGGGCAAGAGGCTGTCTTAAAGT 2819
Db 2760 GGGGAACTGTGTTTTATCTTCAATAGACGTTGGGCAAGAGGCTGTCTTAAAGT 2819
Qy 2820 TTTCAATGAAATTTGTTTAAATATCTTAAGATGAATCTTATGAGCTGTTGCTTG 2879
Db 2820 TTTCAATGAAATTTGTTTAAATATCTTAAGATGAATCTTATGAGCTGTTGCTTG 2879
Qy 2880 AAACTGTTAAATATGTTCAATTAATGATGATGATGATGATGATGATGATGATGATG 2939
Db 2880 AAACTGTTAAATATGTTCAATTAATGATGATGATGATGATGATGATGATGATGATG 2939
Qy 2940 TGGGTTGGCTTTGAAAACAATGTTTATGCAACAGGAAAGAAATGATGACAGCTT 2999
Db 2940 TGGGTTGGCTTTGAAAACAATGTTTATGCAACAGGAAAGAAATGATGACAGCTT 2999
Qy 3000 TGGGGGGGTATGTTGGCCAGCTCTTAAACATTCAGCTTATTACTTGGGAGATCTT 3059
Db 3000 TGGGGGGGTATGTTGGCCAGCTCTTAAACATTCAGCTTATTACTTGGGAGATCTT 3059
Qy 3060 GTGGAACAACAACAAGTGGCCATGATGATGATGATGATGATGATGATGATGATGATG 3119
Db 3060 GTGGAACAACAACAAGTGGCCATGATGATGATGATGATGATGATGATGATGATGATG 3119
Qy 3120 AGATGTTTGGCACTTAAAGCCACAGGCTTAAAGTCAATTAATAATTCCTCTTGT 3179
Db 3120 AGATGTTTGGCACTTAAAGCCACAGGCTTAAAGTCAATTAATAATTCCTCTTGT 3179
Qy 3180 AACCTGATGCTGGGAGCTGAGGCGAGCCCTCAAGTGTGCTGAGTGCACAGCTTGG 3239
Db 3180 AACCTGATGCTGGGAGCTGAGGCGAGCCCTCAAGTGTGCTGAGTGCACAGCTTGG 3239
Qy 3240 GGAAGAGGTGAGAGAGCTGTGTTTATCTTCAACAGAGATGATGATGATGATGATGATG 3299
Db 3240 GGAAGAGGTGAGAGAGCTGTGTTTATCTTCAACAGAGATGATGATGATGATGATGATG 3299
Qy 3300 CATAGTATTAATTAAGCATAGCATGATTAATTAAGTATGATGATGATGATGATGATGATG 3359
Db 3300 CATAGTATTAATTAAGCATAGCATGATTAATTAAGTATGATGATGATGATGATGATGATG 3359

QY	3360	ITCCACGCTTCATCTTTTGGTAGAGTATTTGGAGATAGGATAGTGTTTGGGGTATAGGG	3413
Db	3360	TTCCACGCTTCATCTTTTGGTAGAGTATTTGGAGATAGGATAGTGTTTGGGGTATAGGG	3419
QY	3420	GGAGTGTTTCGACCTGCTTTGCACAGCGTCGCCGACCTCAGCAGTTTGAGGATGCGC	3479
Db	3420	GGAGTGTTTCGACCTGCTTTGCACAGCGTCGCCGACCTCAGCAGTTTGAGGATGCGC	3479
QY	3480	CCCAAGGCGGTTCTTGATGTAAAAAGATGTGGCCATCTAGCCTCGTAACTTCACTGTAC	3539
Db	3480	CCCAAGGCGGTTCTTGATGTAAAAAGATGTGGCCATCTAGCCTCGTAACTTCACTGTAC	3539
QY	3540	CTGTGTCCCATAGGGTGCCTCTGAAATCTGTTATTGAATAAAGTTGTTCAGAAAGCTG	3599
Db	3540	CTGTGTCCCATAGGGTGCCTCTGAAATCTGTTATTGAATAAAGTTGTTCAGAAAGCTG	3599
QY	3600	ACCCGCGGCGAAACATGATACCGTGGCCGGATATATGATAGATGTATTAATGTAC	3659
Db	3600	ACCCGCGGCGAAACATGATACCGTGGCCGGATATATGATAGATGTATTAATGTAC	3659
QY	3660	ATGTATGTTAAATGTGAATCTGTGGCAGAGATACCTTTCCATGCGCAGAAATATCCAACT	3719
Db	3660	ATGTATGTTAAATGTGAATCTGTGGCAGAGATACCTTTCCATGCGCAGAAATATCCAACT	3719
QY	3720	GTTGAACCTGCTATGTTTAAATATGCTCATTTGCTCTTACTGTTGTGACCTGCT	3779
Db	3720	GTTGAACCTGCTATGTTTAAATATGCTCATTTGCTCTTACTGTTGTGACCTGCT	3779
QY	3780	GAGGAGCAAGAGTCCCATTTGATGTCATAAAGCAAGTCTTGCCATCTTTTGGAN	3839
Db	3780	GAGGAGCAAGAGTCCCATTTGATGTCATAAAGCAAGTCTTGCCATCTTTTGGAN	3839
QY	3840	CTGAATAAAAAAAAAAAAAAGG 3860	
Db	3840	CTGAATAAAAAAAAAAAAAAGG 3860	
RESULT 3			
ADL61092			
ID	ADL61092	standard; DNA; 3879 BP.	
AC	ADL61092;		
DT	03-JUN-2004	(first entry)	
DE	Human protein tyrosine kinase biomarker ankyrin repeat domain 3 DNA.		
KM	predictor set, protein tyrosine kinase; cytosolic; antiangiogenic;		
KW	vasculotopic; vulnery; pharmacogenomic; drug sensitivity; breast cancer;		
KW	hypervascular disease; angiogenesis; wound healing scar; human;		
OS	biomarker; ds; gene; ankyrin repeat domain 3.		
OS	Homo sapiens.		
PN	WO2004020583-A2.		
PD	11-MAR-2004.		
PR	26-AUG-2003; 2003WO-US026491.		
PR	27-AUG-2002; 2002US-0406385P.		
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.		
PI	Huang F, Han X, Reeves KA, Amier L, Fairchild CR, Lee FY,		
PI	Shaw P;		
DR	WPI; 2004-239171/22.		
DR	P-PSDB; ADL61229.		
PT	New predictor sets with a plurality of polynucleotides and/or		
PT	polypeptides whose expression pattern predicts cell response to a		
PT	compound that modulates protein tyrosine kinase activity, useful in		

Pt	treating breast cancer.
Xx	Claim 2; SEQ ID NO 16; 649pp; English.
Cc	The invention relates to a novel predictor set comprising a plurality of polynucleotides and/or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. The molecules of the invention demonstrate cytosolic, antiangiogenic, vasotropic and vulnary activities and may be useful in the field of pharmacogenomics, in particular for determining drug sensitivity and in treating breast cancer, hypervascular diseases, angiogenesis and scars in wound healing. The current sequence is that of a human protein tyrosine kinase biomarker DNA of the invention.
Sq	Sequence 3879 BP, 807 A; 1074 C; 1178 G; 820 T; 0 U; 0 Other;
Query Match	98.6%; Score 3804.2; DB 12; Length 3879;
Best Local Similarity	99.7%; Pred. No. 0;
Matches 3831; Conservative	0; Mismatches 9; Indels 2; Gaps 2
Db	7 GTCCGCGCCCATGTAGAGGGCGAACGGCGGACCCTCATGGGCCCTTGCCTGCACCTT 66
Oy	39 GACGTGCCCATGTAGAGGGCGAACGGCGGACCCTCATGGGCCCTTGCCTGCACCTT 98
Oy	67 CGACGGGGCGAGTTCAACGGGCTGGGAAGAAGTGGGCTTCGGGGCCTTCGGCAGGTGA 126
Db	99 CGACGGGGCGAGTTCAACGGGCTGGGAAGAAGTGGGCTTCGGGGCCTTCGGCAGGTGA 158
Oy	127 CAAGGTGGGCCATGTCCACTGGAACAACCTGGCTGGCCATCAAAGTCTGGCCAGCTGCA 186
Db	159 CAAGGTGGGCCATGTCCACTGGAACAACCTGGCTGGCCATCAAAGTCTGGCCAGCTGCA 218
Oy	187 CGTCGACGACAGGAGCGCATGAGACTTTTGGAAAGCCAAAGAAATGAGATGGCCAA 246
Db	219 CGTCGACGACAGGAGCGCATGAGACTTTTGGAAAGCCAAAGAAATGAGATGGCCAA 278
Oy	247 GTTTCGTAATCTCTGCTGTGTATGGAATCTGCGCGCAACTGTGGCTTGGTCAATGA 306
Db	279 GTTTCGTAATCTCTGCTGTGTATGGAATCTGCGCGCAACTGTGGCTTGGTCAATGA 338
Oy	307 GTAACATGGAAGCGGGCTCCCTGGAAAACCTGTGGCTTCGAGGCCATTGGSCCANPSSATCT 366
Db	339 GTAACATGGAAGCGGGCTCCCTGGAAAACCTGTGGCTTCGAGGCCATTGGSCCANPSSATCT 398
Oy	367 CGGGTTCGGAATCATCCACAGACCGGCGGTGGGCATGAATCTCTGCACCTGATGGCCCC 426
Db	399 CGGGTTCGGAATCATCCACAGACCGGCGGTGGGCATGAATCTCTGCACCTGATGGCCCC 458
Oy	427 GCCACTCTCTGCACTTGAACCTTCAAGCCCGCGAACAATCTGTGTGATGCCACTTACCACT 486
Db	459 GCCACTCTCTGCACTTGAACCTTCAAGCCCGCGAACAATCTGTGTGATGCCACTTACCACT 518
Oy	487 CAAGATTTCTGATTTTTGGCTTGGCCAAATGGAACGGGCTGTGCCACTGSCATGACCTCAG 546
Db	519 CAAGATTTCTGATTTTTGGCTTGGCCAAATGGAACGGGCTGTGCCACTGSCATGACCTCAG 578
Oy	547 CATGATGAGCCGTTTGGCACAAATGCGCTTACTCCCTCAGAGGCCATATAGGAGAGAG 606
Db	579 CATGATGAGCCGTTTGGCACAAATGCGCTTACTCCCTCAGAGGCCATATAGGAGAGAG 638
Oy	607 CCGGCTCTTCGACACCAAGCAAGATGTATACAGCTTTTGGATCGTCAATCTGGGGCGTGTCT 666
Db	639 CCGGCTCTTCGACACCAAGCAAGATGTATACAGCTTTTGGATCGTCAATCTGGGGCGTGTCT 698
Oy	667 CACACAGAGAAAGCCGTTTGCAGATGAGAAACAATCTCTGCACATCATGTGTAAAGTGTGT 726
Db	699 CACACAGAGAAAGCCGTTTGCAGATGAGAAACAATCTCTGCACATCATGTGTAAAGTGTGT 758
Oy	727 GAAGGGCCACCGCCCAGATGGCGCCGCTGTGAGAGCCGCGCGCGGCTCTGCAGCCA 786
Db	759 GAAGGGCCACCGCCCAGATGGCGCCGCTGTGAGAGCCGCGCGCGGCTCTGCAGCCA 818

QY 787 CCTGATAGCCTCATGACGCGTGTGCGACGCGGGATCCGAGATTAGAGCCCACTTCC 846
DB 819 CTTGATAGCCTCATGACGCGTGTGCGACGCGGGATCCGAGATTAGAGCCCACTTCC 878
QY 847 AGAATTTACTTCTGAAACCGAGACCTGTGTGAAAGCCTGATGACGAGATGAAAGAAC 906
DB 879 AGAATTTACTTCTGAAACCGAGACCTGTGTGAAAGCCTGATGACGAGATGAAAGAAC 938
QY 907 TGCCTGATGATGACGAGAAAGCCCGGAGCCGAGAGCGAGAGTGTGCTGCGAG 966
DB 939 TGCCTGATGATGACGAGAAAGCCCGGAGCCGAGAGCGAGAGTGTGCTGCGAG 998
QY 967 GCTCAAGGCGGCTCTGCGCCCACTTGTGATTAAGACTTAAGCCTTCCGAGCTTCTTC 1026
DB 999 GCTCAAGGCGGCTCTGCGCCCACTTGTGATTAAGACTTAAGCCTTCCGAGCTTCTTC 1058
QY 1027 ACAGCTGAGCTCTGAGGTTTCCAGAGCTGTGAGGGCCCGGAGAGCTCAAGCCGAGCTC 1086
DB 1059 ACAGCTGAGCTCTGAGGTTTCCAGAGCTGTGAGGGCCCGGAGAGCTCAAGCCGAGCTC 1118
QY 1087 CTCTGATGTCAGAGCTGACATCGTCCGACGTGGAAGAGGCTCTGCGGGGTGTCTCGGT 1146
DB 1119 CTCTGATGTCAGAGCTGACATCGTCCGACGTGGAAGAGGCTCTGCGGGGTGTCTCGGT 1178
QY 1147 GGAATCCGCTTCTCTTCAAGAGATCACTGTGCTTCTTGAACGGGAACTTTCAAC 1206
DB 1179 GGAATCCGCTTCTCTTCAAGAGATCACTGTGCTTCTTGAACGGGAACTTTCAAC 1238
QY 1207 CAGCGATCTGAGGTAACAAGAGCTGCAAGAGAGAGGCTTGTGATGCACTGCTGC- 1265
DB 1239 CAGCGATCTGAGGTAACAAGAGCTGCAAGAGAGAGGCTTGTGATGCACTGCTGC- 1297
QY 1266 GGAACAACAAGAGATGATCTGACGCGGACGAGAGCTGTGACCTGTGACCTGTGACA 1325
DB 1298 GGAACAACAAGAGATGATCTGACGCGGACGAGAGCTGTGACCTGTGACCTGTGACA 1357
QY 1326 GCGGTGCGAGCTGCTGACCTGTGAGGAGGCGGGCAAGAGAGTGTGCAATGTGC 1385
DB 1358 GCGGTGCGAGCTGCTGACCTGTGAGGAGGCGGGCAAGAGAGTGTGCAATGTGC 1417
QY 1386 TGCCTGTCAGCAATGCAACCCCACTGAGCAACGTAAGGGCTCAACCCGTTGACA 1445
DB 1418 TGCCTGTCAGCAATGCAACCCCACTGAGCAACGTAAGGGCTCAACCCGTTGACA 1477
QY 1446 TGCCTGTCAGCAATGCAACCCCACTGAGCAACGTAAGGGCTCAACCCGTTGACA 1505
DB 1478 TGCCTGTCAGCAATGCAACCCCACTGAGCAACGTAAGGGCTCAACCCGTTGACA 1537
QY 1506 TCAAGGCCAAGATGAGACCAAGTGAAGAGCTTGTGCGACGGAAGATCAAGT 1565
DB 1538 TCAAGGCCAAGATGAGACCAAGTGAAGAGCTTGTGCGACGGAAGATCAAGT 1597
QY 1566 ACTCTAGCACAGGCGCTGTTGAGAAAGAGCCTCGGTCAACAGAGTGAAGCTTTGAGG 1625
DB 1598 ACTCTAGCACAGGCGCTGTTGAGAAAGAGCCTCGGTCAACAGAGTGAAGCTTTGAGG 1657
QY 1626 GCGGAGCGCCATGACGAGCTGTGCAACGCGGACGAGAAATATCTGCGCATCTGC 1685
DB 1658 GCGGAGCGCCATGACGAGCTGTGCAACGCGGACGAGAAATATCTGCGCATCTGC 1717
QY 1686 TGCCTGAGAGGCTGAGCTGAGCTGTGAGGCAAGATGCTGTGCTGCACTGTAGG 1745
DB 1718 TGCCTGAGAGGCTGAGCTGAGCTGTGAGGCAAGATGCTGTGCTGCACTGTAGG 1777
QY 1746 CTGCTGAGAGGCGCACTGCGCATGTCAAGCTGTGCGCAAGCAGCGGAGGTGAGT 1805
DB 1778 CTGCTGAGAGGCGCACTGCGCATGTCAAGCTGTGCGCAAGCAGCGGAGGTGAGT 1837
QY 1806 TGAAGCCCAAGACGCTGATGAGAGAGCCATGTGACCTGTGCGGACAGCGCGGCACT 1865
DB 1838 TGAAGCCCAAGACGCTGATGAGAGAGCCATGTGACCTGTGCGGACAGCGCGGCACT 1897
QY 1866 ACCGCTGCGCCGATCTCATGACCTGTGCTCGACGTCAGAGCTCAAGCTGTGACGCTGTGCTG 1925

DB 1925 ACCGCTGCGCCGATCTCATGACCTGTGCTCGACGTCACAGCTGTGACGCTGTGCGG 1957
QY 1926 CACAGACCCCTGACAGTGTGCGCGGAGACGCGGACACAGAGACCTGTGCGGCTGCC 1985
DB 1958 CACAGACCCCTGACAGTGTGCGCGGAGACGCGGACACAGAGACCTGTGCGGCTGCC 2017
QY 1986 TGCATCGGAGCGCTGTGAGAGAGGCGGTGAACCTGACGCGCTACACGCGCTGTGACCTG 2045
DB 2018 TGCATCGGAGCGCTGTGAGAGAGGCGGTGAACCTGACGCGCTACACGCGCTGTGACCTG 2077
QY 2046 CTGCGCCGACAGACCACTGTGCGCACTGTCAAGCTTGTGTGAGAGAGAGCCGATGTGC 2105
DB 2078 CTGCGCCGACAGACCACTGTGCGCACTGTCAAGCTTGTGTGAGAGAGAGCCGATGTGC 2137
QY 2106 TGCCTCGGAGAGCCCTGTAACAGAGCGGCTGTGACCTGTGCGCCCAAGGACCTGCG 2165
DB 2138 TGCCTCGGAGAGCCCTGTAACAGAGCGGCTGTGACCTGTGCGCCCAAGGACCTGCG 2197
QY 2166 AGGTGTGAGAGAGTGTGTGAGCGGCGATGTGATCTGATCTGATGACGAGAGGAGCTCA 2225
DB 2198 AGGTGTGAGAGAGTGTGTGAGCGGCGATGTGATCTGATCTGATGACGAGAGGAGCTCA 2257
QY 2226 GCGGCTGTGACCTGTGCGCGCCAGAGGCGGACAGACAGAGCGGTGAGACTGTGCTCAGGC 2285
DB 2258 GCGGCTGTGACCTGTGCGCGCCAGAGGCGGACAGACAGAGCGGTGAGACTGTGCTCAGGC 2317
QY 2286 ATGAGGCCCATCATACCTGTGAGAGCTCAAGTTTCAGAGGCGGCACTGTGCTCAGGC 2345
DB 2318 ATGAGGCCCATCATACCTGTGAGAGCTCAAGTTTCAGAGGCGGCACTGTGCTCAGGC 2377
QY 2346 CACTCTGCGGCGGAGAGAGAGCTGAGCTGTGCTGTGAGAGCGGAGGCTCAAGTGG 2405
DB 2378 CACTCTGCGGCGGAGAGAGAGCTGAGCTGTGCTGTGAGAGCGGAGGCTCAAGTGG 2437
QY 2406 GCTCTGTGCTGTGCTGTGCTGTCTGTGAGAGAGAGAGTGTGAGAGGCGGCTGTG 2465
DB 2438 GCTCTGTGCTGTGCTGTGCTGTCTGTGAGAGAGAGAGTGTGAGAGGCGGCTGTG 2497
QY 2466 TGCCTTACCTAATGTTAACAGAGAGAGTGAAGTGTGCTGACATGAGAGGCGGCTGTG 2525
DB 2498 TGCCTTACCTAATGTTAACAGAGAGAGTGAAGTGTGCTGACATGAGAGGCGGCTGTG 2557
QY 2526 TGAACCGGAGTGTGCTGTGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2585
DB 2558 TGAACCGGAGTGTGCTGTGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2617
QY 2586 GATCTAGGCACTGTGCTGTGAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2645
DB 2618 GATCTAGGCACTGTGCTGTGAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2677
QY 2646 TGCCTGTGAGAGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2705
DB 2678 TGCCTGTGAGAGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2737
QY 2706 CTTGAGGAGAGCCACTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2765
DB 2738 CTTGAGGAGAGCCACTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2797
QY 2766 ACTGTGTTTGTATCTTATCATATGACGAGTGTGAGAGAGGCTGTCTTAAAGTTTCAT 2825
DB 2798 ACTGTGTTTGTATCTTATCATATGACGAGTGTGAGAGAGGCTGTCTTAAAGTTTCAT 2857
QY 2826 GGAATTTGTTTATTAATAATATCTTAAAGATTAACCTTATGAGTGTGTTGTTGAAACT 2885
DB 2858 GGAATTTGTTTATTAATAATATCTTAAAGATTAACCTTATGAGTGTGTTGTTGAAACT 2917
QY 2886 GTTAAATTTGTTTATTAATAATATCTTAAAGATTAACCTTATGAGTGTGTTGTTGAAACT 2945
DB 2918 GTTAAATTTGTTTATTAATAATATCTTAAAGATTAACCTTATGAGTGTGTTGTTGAAACT 2977
QY 2946 TGCCTTGAAGAAATGTTTATGCAACAGAGAGAGTGTGAGAGCAGCTTGTGCGG 3005

Db 2978 TGGCTTGAACAAATGTTTATGCAACAGAAAGATGATGAGCAGCTTTGGCGG 3037
Qy 3006 GCGTATGTGTGGCCAGCTCTTAACCATTCAGTCTATTACTTTGGTGAGTCTTGTGGAC 3065
Db 3038 GCGTATGTGTGGCCAGCTCTTAACCATTCAGTCTATTACTTTGGTGAGTCTTGTGGAC 3097
Qy 3066 AACCAACACAGCGTGGCCACATGGTACTAGTGGCGGTCGTTTCGTTGCTGCTAAGATGT 3125
Db 3098 AACCAACACAGCGTGGCCACATGGTACTAGTGGCGGTCGTTTCGTTGCTGCTAAGATGT 3157
Qy 3126 TTTGGCACTCTAGAGCCACAGGCGCTTAAGAGTCAATTAATAAATCTCCCTTTGTAACCTC 3185
Db 3158 TTTGGCACTCTAGAGCCACAGGCGCTTAAGAGTCAATTAATAAATCTCCCTTTGTAACCTC 3217
Qy 3186 AGTGTGGGGACGTAGAGGCGAGCCCTCAAGTCCGTGAGATGACCAAGCTTTGGGGAAGA 3245
Db 3218 AGTGTGGGGACGTAGAGGCGAGCCCTCAAGTCCGTGAGATGACCAAGCTTTGGGGAAGA 3277
Qy 3246 GGTGAGAGAGAGCGTGTGTTTATCTCAACAGCAGTATGAGAATAAATTAACATAGT 3305
Db 3278 GGTGAGAGAGAGCGTGTGTTTATCTCAACAGCAGTATGAGAATAAATTAACATAGT 3337
Qy 3306 ATTAACCTAGACATAGACAGATATTAACCTAGATAGTCACTGCTCACTGCAACCTTCCCA 3365
Db 3338 ATTAACCTAGACATAGACAGATATTAACCTAGATAGTCACTGCTCACTGCAACCTTCCCA 3397
Qy 3366 GCTCTCATTTTGTAGGTGATTTGGGATAGGAGATAGTGTGTTGGGGTATAGGGGGAGTG 3425
Db 3398 GCTCTCATTTTGTAGGTGATTTGGGATAGGAGATAGTGTGTTGGGGTATAGGGGGAGTG 3457
Qy 3426 TTTTCGACCTGCTTTGAGAGCGTGCCTCGACCTCAGACAGTTTGGGGTGTGGCCCCAGG 3485
Db 3458 TTTTCGACCTGCTTTGAGAGCGTGCCTCGACCTCAGACAGTTTGGGGTGTGGCCCCAGG 3517
Qy 3486 GCGGTTCTTGTAGATTAAGATGTGGCCATCTAGCCTGTGAATCACTGTCACTGTGT 3545
Db 3518 GCGGTTCTTGTAGATTAAGATGTGGCCATCTAGCCTGTGAATCACTGTCACTGTGTGT 3577
Qy 3546 CCCATAGGCTGCTCTGAAATCTGTATTTAGAAATTAAGTTTGTTCAGAAAGTGAACCTTG 3605
Db 3578 CCCATAGGCTGCTCTGAAATCTGTATTTAGAAATTAAGTTTGTTCAGAAAGTGAACCTTG 3637
Qy 3606 CGTGCAAAATGTACCGTGGCCCTGATATGATAGATTAATTAATTAATTAATTAATTAAT 3665
Db 3638 CGTGCAAAATGTACCGTGGCCCTGATATGATAGATTAATTAATTAATTAATTAATTAAT 3697
Qy 3666 GTTAATGTAAATCTGTGGGAGAGATCTTTTCATGAGCAAGAAATATCAAGCTGTGAA 3725
Db 3698 GTTAATGTAAATCTGTGGGAGAGATCTTTTCATGAGCAAGAAATATCAAGCTGTGAA 3757
Qy 3726 ACTGCTATGTTTAAATATGCTCATTTGTGCTTTACTGTTGTGTGAGCTGTGAGGGA 3785
Db 3758 ACTGCTATGTTTAAATATGCTCATTTGTGCTTTACTGTTGTGTGAGCTGTGAGGGA 3817
Qy 3786 CAAGAAGTTCATTTGATGTCAATAAGCAAAAGTACTTGTCTACTTTTGTGAANTGAAA 3845
Db 3818 CAAGAAGTTCATTTGATGTCAATAAGCAAAAGTACTTGTCTACTTTTGTGAANAAAAA 3877
Qy 3846 AA 3847
Db 3878 AA 3879

RESULT 4
ID ADR25979 standard; DNA; 3879 BP.
XX ADR25979;
AC ADR25979;
DT 21-OCT-2004 (first entry)
XX
DE Breast cancer prognosis marker #1840.
XX

KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS Homo sapiens.
XX
PN MO2004065545-A2.
XX
PD 05-AUG-2004.
XX
PE 15-JAN-2004; 2004NO-US001100.
XX
PR 15-JAN-2003; 2003US-00342887.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
XX
PI Van't Veer LJ, He Y;
XX
DR WPI; 2004-593473/57.
XX
PT Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX
PS Disclosure; SEQ ID NO 1840; 226bp; English.
XX
PS The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
XX
SQ Sequence 3879 BP; 807 A; 1074 C; 1178 G; 820 T; 0 U; 0 Other;
Qy 7 GTCCGGCGCGATGAGGAGGCGCACGCGGAGACCCCATGAGGACCTGAGCTGCGCACCTT 66
Db 39 GACGTGCGCATGAGAGGCGCACGCGGAGACCCCATGAGGACCTGAGCTGCGCACCTT 98
Qy 67 CGACGCGGCGCATGAGGAGGCGCACGCGGAGACCCCATGAGGACCTGAGCTGCGCACCTT 126
Db 99 CGACGCGGCGCATGAGGAGGCGCACGCGGAGACCCCATGAGGACCTGAGCTGCGCACCTT 158
Qy 127 CAAGTGTGCGCATGAGGAGGCGCACGCGGAGACCCCATGAGGACCTGAGCTGCGCACCTT 186
Db 159 CAAGTGTGCGCATGAGGAGGCGCACGCGGAGACCCCATGAGGACCTGAGCTGCGCACCTT 218
Qy 187 CGTGAAGACAGGAGGCGCATGAGGAGGCGCACGCGGAGACCCCATGAGGACCTGAGCTGCGCACCTT 246
Db 219 CGTGAAGACAGGAGGCGCATGAGGAGGCGCACGCGGAGACCCCATGAGGACCTGAGCTGCGCACCTT 278
Qy 247 GTTTCGCTACATCTGCTGTGTATGAGCATGTGCGGGAACCTGTGCGGCTGTGATGGA 306
Db 279 GTTTCGCTACATCTGCTGTGTATGAGCATGTGCGGGAACCTGTGCGGCTGTGATGGA 338
Qy 307 GTACATGAGAGCGGAGCTCCCTGGAAGCTGCTGCTGCGAGCATTTGCGATGGATCT 366
Db 339 GTACATGAGAGCGGAGCTCCCTGGAAGCTGCTGCTGCGAGCATTTGCGATGGATCT 398
Qy 367 CGGTTCCGAATCATTCACAGAGAGCGGCGGTGGGATGAATCTTCTGCACTGCAATGAGCCC 426
Db 399 CGGTTCCGAATCATTCACAGAGAGCGGCGGTGGGATGAATCTTCTGCACTGCAATGAGCCC 458
Qy 427 GCCACTCTGTGACCTGAGCTCAAGCCCGGCAACATCTGTGTGATGCCCACTACAGCT 486
Db 459 GCCACTCTGTGACCTGAGCTCAAGCCCGGCAACATCTGTGTGATGCCCACTACAGCT 518

QY 487 CAAAGTTTCTGATTTTGGTCTGGCCCAAGTGCACCGGCGTGTCTCCACTGCGCATGACCTCAG 546
DB 519 CAAAGTTTCTGATTTTGGTCTGGCCCAAGTGCACCGGCGTGTCTCCACTGCGCATGACCTCAG 578
QY 547 CATTGATGAGCGGTTTGGCACAATGCGCCACGCTCCCGAGAGCGCATCAGGGAAGAG 606
DB 579 CATTGATGAGCGTGTGGCACAATGCGCTACCTCCCTCAGAGCGCATCAGGGAAGAG 638
QY 607 CCGGCTCTTGCACACCAAGCAGATGTATATACGCTTTGGCATGTCATCTGGGCGTGTCT 666
DB 639 CCGGCTCTTGCACACCAAGCAGATGTATATACGCTTTGGCATGTCATCTGGGCGTGTCT 698
QY 667 CACAAGAGAGAGCGGTTTGGCAGATGAGAGAAACATCTTGCACTATCTGTGAAGTGT 726
DB 699 CACAAGAGAGAGCGTGTGGCAGATGAGAGAAACATCTTGCACTATCTGTGAAGTGT 758
QY 727 GAAAGGCGCACCGCCCGAGCTGCGCGGTGTGCAGAGCGCGGCGCGCTGCAGACCA 786
DB 759 GAAAGGCGCACCGCCCGAGCTGCGCGGTGTGCAGAGCGCGGCGCGCTGCAGACCA 818
QY 787 CCTGATACGCTCATGTCAGCGGTGTGCAGAGGAGATCCGCGAGTTAGGCCCACTTCCA 846
DB 819 CCTGATACGCTCATGTCAGCGGTGTGCAGAGGAGATCCGCGAGTTAGGCCCACTTCCA 878
QY 847 AGAAATTAATTTCTGAAACCGAGAGCCTGTGTGAAACCTGTATGACGAAAGTGAAGAAC 906
DB 879 AGAAATTAATTTCTGAAACCGAGAGCCTGTGTGAAACCTGTATGACGAAAGTGAAGAAC 938
QY 907 TECTCATGATCTGAGAGTGAAGAAAGCCCCCGAGGCCAGAGCGAGGTGTCTGCGAG 966
DB 939 TECTCATGATCTGAGAGTGAAGAAAGCCCCCGAGGCCAGAGCGAGGTGTCTGCGAG 998
QY 967 GCTCAAGCGGCGCTCTGCCCCCACTTGCATTAACGACTACGCTCTCCGAGCTTCTCTC 1026
DB 999 GCTCAAGCGGCGCTCTGCCCCCACTTGCATTAACGACTACGCTCTCCGAGCTTCTCTC 1058
QY 1027 ACAGCTGGAATCTGAGATTCCAGAGCTGTGCAGGGCCCCAGAGAGCTCAGCCGAGCTC 1086
DB 1059 ACAGCTGGAATCTGAGATTCCAGAGCTGTGCAGGGCCCCAGAGAGCTCAGCCGAGCTC 1118
QY 1087 CTCTGAGTCCAAAGCTCCCAATCTGTCGCGCAGTGGGAAGAGGCTCTCGGGGAGTGTCCCGGT 1146
DB 1119 CTCTGAGTCCAAAGCTCCCAATCTGTCGCGCAGTGGGAAGAGGCTCTCGGGGAGTGTCCCGGT 1178
QY 1147 GGAAGCTCGGCTCTCTTCCAGAGAGATCACTGTGCTGTCTTGTGAGCGGGAACCTTCAAC 1206
DB 1179 GGAAGCTCGGCTCTCTTCCAGAGAGATCACTGTGCTGTCTTGTGAGCGGGAACCTTCAAC 1238
QY 1207 CAGCGATCTGGGTACCAAGAGCGTCCAGAGAGAGAGCTTGTGATGTCATCTGTCTC- 1265
DB 1239 CAGCGATCTGGGTACCAAGAGCGTCTGAGAGAGAGCTTGTGATGTCATCTGTCTC- 1297
QY 1266 GGGACACCAAGCAAACTGATGAAATCTCTGACGCCGAGAGCGTGCACCTGCACCTGGA 1325
DB 1298 GGGACACCAAGCAAACTGATGAAATCTCTGACGCCGAGAGCGTGCACCTGCACCTGGA 1357
QY 1326 GGGGTGACGCGCTGTCACCTGAGCGTGAAGGCGGAGCAAGAGAGTGCAGCAATGAG 1385
DB 1358 GGGGTGACGCGCTGTCACCTGAGCGTGAAGGCGGAGCAAGAGAGTGCAGCAATGAG 1417
QY 1386 TGTGCTCTCAACATGACCAACCCCAACCTGAGCAACCGTGAAGGCTCACCCGTTGACA 1445
DB 1418 TGTGCTCTCAACATGACCAACCCCAACCTGAGCAACCGTGAAGGCTCACCCGTTGACA 1477
QY 1446 TGGCGTGTGAGAGAGAGGTGTGAGAGTCTCTGCGTGCAGAGAGAGAGTGAAGTGAAG 1505
DB 1478 TGGCGTGTGAGAGAGAGGTGTGAGAGTCTCTGCGTGCAGAGAGAGAGTGAAGTGAAG 1537
QY 1506 TCAACGCCAAGAGATGAGAGCAAGCTGCACAGCCTTCCACTTTGGACGCCAAGAGCGGAGT 1565
DB 1538 TCAACGCCAAGAGATGAGAGCAAGCTGCACAGCCTTCCACTTTGGACGCCAAGAGCGGAGT 1597

QY 1566 AGTCTAGCAGCAGGCTGTGTTGGAGAGAAACGCTCGGTCTCAAGAGTGAAGCTTTGAG 1625
DB 1598 AGTCTAGCAGCAGGCTGTGTTGGAGAGAAACGCTCGGTCTCAAGAGTGAAGCTTTGAG 1657
QY 1626 GCCGAGCGCCCATGACGCTGACGACACCGGCGAGAGATATGCTGCGCATCTGCG 1685
DB 1658 GCCGAGCGCCCATGACGCTGACGACACCGGCGAGAGATATGCTGCGCATCTGCG 1717
QY 1686 TGGCGGAGGCGTGAAGTGAAGCTTGCAGGCGCAAGATGCTGCGTGCACCTGACCTAG 1745
DB 1718 TGGCGGAGGCGTGAAGTGAAGCTTGCAGGCGCAAGATGCTGCGTGCACCTGACCTAG 1777
QY 1746 CTGCGCTGACAGGCGCACTGCGCAATGCTCAAGCTGTGCGCAAGACGCGGAGTGAAGT 1805
DB 1778 CTGCGCTGACAGGCGCACTGCGCAATGCTCAAGCTGTGCGCAAGACGCGGAGTGAAGT 1837
QY 1806 TGAAGCGCCAGACGCTGAGTGAAGAGAGCCATTGCACTGACCTGCGCAGACGCGGAGCT 1865
DB 1838 TGAAGCGCCAGACGCTGAGTGAAGAGAGCCATTGCACTGACCTGCGCAGACGCGGAGCT 1897
QY 1866 ACCGCTGAGCGCGCATCTTCACTGACCTGTGTCTCCAGAGTGAAGTGAAGTGAAGT 1925
DB 1898 ACCGCTGAGCGCGCATCTTCACTGACCTGTGTCTCCAGAGTGAAGTGAAGTGAAGT 1957
QY 1926 CACAGACACCCCTGACGCTGACGCGGAGAGACGCGGAGACACAGACACTGCGAGCTGCC 1985
DB 1958 CACAGACACCCCTGACGCTGACGCGGAGAGACGCGGAGACACAGACACTGCGAGCTGCC 2017
QY 1986 TGCATCGGAGCGCTGAGAGAGAGCGGTGACCTGACAGCGGCTACACCGCTCTGACCTGG 2045
DB 2018 TGCATCGGAGCGCTGAGAGAGAGCGGTGACCTGACAGCGGCTACACCGCTCTGACCTGG 2077
QY 2046 CTGCGCGACAGAGACCTTGCACCTGTGCATGACCTGTGTGTGAGAGAGAGCCGATGTGCG 2105
DB 2078 CTGCGCGAGAGACCACTGCGCACTGTCAAGCTGTGTGTGAGAGAGAGCCGATGTGCG 2137
QY 2106 TGGCGCGGAGAGCCCTGAGACAGAGCGGCGTGCACCTGAGTGCAGCGGAGCTGCGG 2165
DB 2138 TGGCGCGGAGAGCCCTGAGACAGAGCGGCGTGCACCTGAGTGCAGCGGAGCTGCGG 2197
QY 2166 AGTGTGAGAGAGTGTGTCAGCGCGCAATGTCATTTGACCTGTTGACAGAGAGGAGCTCA 2225
DB 2198 AGTGTGAGAGAGTGTGTCAGCGCGCAATGTCATTTGACCTGTTGACAGAGAGGAGCTCA 2257
QY 2226 GCGCGCTGACCTGCGCGCCAGAGGCGCGCACACAGACGCTGAGACTGTGCTCAAGC 2285
DB 2258 GCGCGCTGACCTGCGCGCCAGAGGCGCGCACACAGACGCTGAGACTGTGCTCAAGC 2317
QY 2286 ATGGGCGCCACATCAACCTGAGAGGCTCAAGTTCCAGGGCGGCGATGAGCCCGCGCA 2345
DB 2318 ATGGGCGCCACATCAACCTGAGAGGCTCAAGTTCCAGGGCGGCGATGAGCCCGCGCA 2377
QY 2346 CACTCTGCGGAGAGCAAGACTTGAAGTGTGCTGCGGAGACCGGAGGCTTCAAGTGGG 2405
DB 2378 CACTCTGCGGAGAGCAAGACTTGAAGTGTGCTGCGGAGACCGGAGGCTTCAAGTGGG 2437
QY 2406 GCTCTGTGCTGTGCTGTGTCTCTGAGGAGATGAAACGATCTGCGTGGGCGCCGTTTG 2465
DB 2438 GCTCTGTGCTGTGCTGTGTCTCTGAGGAGATGAAACGATCTGCGTGGGCGCCGTTTG 2497
QY 2466 TGGCTTAATCTTAATTTAAACAGAGAGAGTGAACATGTTGCATGAGAGGCGGTGCG 2525
DB 2498 TGGCTTAATCTTAATTTAAACAGAGAGAGTGAACATGTTGCATGAGAGGCGGTGCG 2557
QY 2526 CTGACCGAGAGTGTCCCTTCCAGAGTGAAGCTGAGTGCATGAGTGCATCTCAATC 2585
DB 2558 CTGACCGAGAGTGTCCCTTCCAGAGTGAAGCTGAGTGCATGAGTGCATCTCAATC 2617
QY 2586 GATCTTAAGCACTGTGTGTGAAGAGACGCTGGGTCAAGATCAATTTGCTGTGCTCTAA 2645
DB 2618 GATCTTAAGCACTGTGTGTGAAGAGACGCTGGGTCAAGATCAATTTGCTGTGCTCTAA 2677
QY 2646 TGGGTGCTGAGGCTGTGTCTCAATGATGAAGCCCAAGGCGTGAAGCATCTCTCT 2705


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Db      2678 TGGGTCGTGAGGCTGCTCTCTCACTGATGAAGCCCGGCGGTGAGACATCCTCTCT 2737
Oy      2706 CCTGAGCGAGCCACTTGGGTGCTGAGACTCACAGCTCTTGAAGAGGTGCAGGAGAA 2765
Db      2738 CCTGAGCGAGCCACTTGGGTGCTGAGACTCACAGCTCTTGAAGAGGTGCAGGAGAA 2797
Oy      2766 ACTGCTTTTATCTTATCATACATGACGTGGGCGAGAGGCGTGTCTTAAAGTTCCAT 2825
Db      2798 ACTGCTTTTATCTTATCATATATGACGTGGGCGAGAGGCGTGTCTTAAAGTTCCAT 2857
Oy      2826 GGAATTTTATTAATAATCTTAAAGATGAATCCTTATCAGCTGTGCTTGAACCT 2885
Db      2858 GGAATTTTATTAATAATCTTAAAGATGAATCCTTATCAGCTGTGCTTGAACCT 2917
Oy      2886 GTTAAAAATGTTCAATACATTTGATGATGCTCTCTTAAATGATGCTTAAAGTGGGT 2945
Db      2918 GTTAAAAATGTTCAATACATTTGATGATGCTCTCTTAAATGATGCTTAAAGTGGGT 2977
Oy      2946 TGGCTTTGAAAAATGTTTATATGACAGAGGAGATGATGAGGACGCTTGGGGG 3005
Db      2978 TGGCTTTGAAAAATGTTTATATGACAGAGGAGATGATGAGGACGCTTGGGGG 3037
Oy      3006 GCGTATGCTGGGCGAGCTCTTACCATTTCAAGTCTATTACTTGGGTGAGTCTTGGAC 3065
Db      3038 GCGTATGCTGGGCGAGCTCTTACCATTTCAAGTCTATTACTTGGGTGAGTCTTGGAC 3097
Oy      3066 AACCAACAACAATGCTCCCAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3125
Db      3098 AACCAACAACAATGCTCCCAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3157
Oy      3126 TTTGGCACTCTAGAGCCACAGGCGCTAAGATGATTTAAATAATTCCTCTTGTAACTC 3185
Db      3158 TTTGGCACTCTAGAGCCACAGGCGCTAAGATGATTTAAATAATTCCTCTTGTAACTC 3217
Oy      3186 AGTGTGGGAGCTGAGGCGAGGCGCCCTCAAGTGTGCTGAGTGCACAGTCTTGGGAGAA 3245
Db      3218 AGTGTGGGAGCTGAGGCGAGGCGCCCTCAAGTGTGCTGAGTGCACAGTCTTGGGAGAA 3277
Oy      3246 GGTGACAGAGAAAGCTGTGTTTTTATCTTCACAGCGATGATGAATTAATCATAGT 3305
Db      3278 GGTGACAGAGAAAGCTGTGTTTTTATCTTCACAGCGATGATGAATTAATCATAGT 3337
Oy      3306 ATTACTAGACATACAGATATTAATCTAGATGATGACCTGCTACCTGACCTTCCCA 3365
Db      3338 ATTACTAGACATACAGATATTAATCTAGATGATGACCTGCTACCTGACCTTCCCA 3397
Oy      3366 GCTCTCATTTTGTAGGTGATTTGGAGTAGGATAGTGTGTTGGGATAGGGGAGAGTG 3425
Db      3398 GCTCTCATTTTGTAGGTGATTTGGAGTAGGATAGTGTGTTGGGATAGGGGAGAGTG 3457
Oy      3426 TTTCTGACCTGCTTTGACAGAGTGTCTCCGACCTCAGACATTTGGGGTGTGCCCCAGG 3485
Db      3458 TTTCTGACCTGCTTTGACAGAGTGTCTCCGACCTCAGACATTTGGGGTGTGCCCCAGG 3517
Oy      3486 GGGGTCTTGTGATGAATGAAGATGAGGCGATCAGCTGTATCTTCACTGACCTGTGT 3545
Db      3518 GGGGTCTTGTGATGAATGAAGATGAGGCGATCAGCTGTATCTTCACTGACCTGTGT 3577
Oy      3546 CCCATAGGAGTCCCTCTGATATCTGTATTAGATTAAGTTGTTGTCAGAACCTGACCTG 3605
Db      3578 CCCATAGGAGTCCCTCTGATATCTGTATTAGATTAAGTTGTTGTCAGAACCTGACCTG 3637
Oy      3606 CGTGAACACATGATCCGTGGCTGTGATATGATGATGATGATGATGATGATGATGATGAT 3665
Db      3638 CGTGAACACATGATCCGTGGCTGTGATATGATGATGATGATGATGATGATGATGATGAT 3697
Oy      3666 GTTAAATGATATCTGTGGGCGAGATATCTTTCATGAGGAGAAATATCCACCTGTGAA 3725
Db      3698 GTTAAATGATATCTGTGGGCGAGATATCTTTCATGAGGAGAAATATCCACCTGTGAA 3757
Oy      3726 ACTGCTATGTTTATATATGCTCATATGCTTACTGTTGTGTCAGTGGGTGAGGGA 3785

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Db      3758 ACTGCTATGTTTATATATGCTCATTTGCTTACTGTTGTGTCAGTGGGAGGA 3817
Oy      3786 CAAGAATTCATTTGATATGTCATTAAGCAAAAGACTTGGCTACTTTTGAATCGAAA 3845
Db      3818 CAAGAATTCATTTGATATGTCATTAAGCAAAAGACTTGGCTACTTTTGAATCGAAA 3877
Oy      3846 AA 3847
Db      3878 AA 3879

RESULT 5
AAH15762
ID AAH15762 standard; cDNA, 3876 BP.
XX
AC AAH15762;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14188.
XX
KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Ito gai T, Nishikawa T, Hayashi K, Saio K, Yamamoto J;
PI Ishi S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 14188; 2537bp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC oligonucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

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QY	2106	TGGCCCGGGGACCCTGAAACCAAGGCGTGTCACTGGCTGCGGCCCAAGGGCACTGCGG	2105
Db	2155	TGGCCCGGGGACCCTGAAACCAAGAGGCGGTGTCACTGGCTGCGGCCCAAGGGCACTGCGG	2214
QY	2166	AGGTGTGGAAGAATTGTGTCAAGCGCCGATGTCAATGACCTGTGTGACGACGAGGAGGCTCA	2225
Db	2215	AGGTGTGTGAAGAAATTGTGTCAAGCGCCGATGTCAATGACCTGTGTGACGACGAGGAGCTCA	2274
QY	2226	GCGGCTGTGCACTGTGCGCCGCCAAGGGCCGGCACGCAAGAAGTGTGAACCTGTCTCAAGGC	2285
Db	2275	GCGGCTGTGCACTGTGCGCCGCCAAGGGCCGGCACGCAAGAAGTGTGAACCTGTCTCAAGGC	2334
QY	2286	ATGGGGGCCCAATCAACTCAAGCTGACGAGCTCAAGTTCCAGGGCGGCATATGGCCCGCGGCA	2345
Db	2335	ATGGGGGCCCAATCAACTCAAGAGCTCTCAAGTTCCAGGGCGGCATATGGCCCGCGGCA	2394
QY	2346	CACCTCTGCGGCGAAGCAAGACTGAGCTGTGCGGAGACCGGGGGTTCACATGTGGG	2405
Db	2395	CACCTCTCTGCGGCGAAGCAAGACTGAGCTGTGCGGAGACCGGGGGTTCACATGTGGG	2454
QY	2406	GCTCTTGTCTCTGTCTGTGTCTCTGTGTGGGGAATGGAAGAATCTGTGTGGGGCCCGGTTG	2465
Db	2455	GCTCTTGTCTCTGTCTGTGTCTCTGTGTGGGGAATGGAAGAATCTGTGTGGGGCCCGGTTG	2514
QY	2466	TGGCTTACCTTAATTTTAAACGACGAGGTGACATGTGTGCATCAGAGAGGCGGTGCTG	2525
Db	2515	TGGCTTACCTTAATTTTAAACGACGAGGTGACATGTGTGCATCAGAGAGGCGGTGCTG	2574
QY	2526	CTGACCGGAGTGTCCCCCTTCAGGTGAAGCTGGCTAGGTGCACATGCCCGCTCATATTC	2585
Db	2575	CTGACCGGAGTGTCCCCCTTCAGGTGAAGCTGGCTAGGTGCACATGCCCGCTCATATTC	2634
QY	2586	GATCTAGGCACTGTCTGTCTGTGAAGGGAACGTGGGTCAGAAATCATTTCTGTGTCCTAA	2645
Db	2635	GATCTAGGCACTGTCTGTCTGTGAAGGGAACGTGGGTCAGAAATCATTTCTGTGTCCTAA	2694
QY	2646	TGGGTCGCTGAGGCTGTCTCTCAGTGATGAAGCCCGAGGCGGTGGAACATCACTCTCT	2705
Db	2695	TGGGTCGCTGAGGCTGTCTCTCAGTGATGAAGCCCGAGGCGGTGGAACATCACTCTCT	2754
QY	2706	CCTGAGGCGAGCGACACTTGGGTTGTGTGAAGCTCAACAATCTTGAAGGAGGTGTGAGGGGAA	2765
Db	2755	CCTGAGGCGAGCGACACTTGGGTTGTGTGAAGCTCAACAATCTTGAAGGAGGTGTGAGGGGAA	2814
QY	2766	ACTGTGTTTTTATCTTCATACATGACGGTGGGCGAGAGGCGCTGTCTTAAAGTTTCAT	2825
Db	2815	ACTGTGTTTTTATCTTCATACATGACGGTGGGCGAGAGGCGCTGTCTTAAAGTTTCAT	2874
QY	2826	GGAATTTGTTTTATAAATATCTTAAAGATGAATACCTTATACAGCTGTGTGCTTGAACCT	2885
Db	2875	GGAATTTGTTTTATAAATATCTTAAAGATGAATACCTTATACAGCTGTGTGCTTGAACCT	2934
QY	2886	GTTAAAAAATGTTCAATCAATTTGGAATAGTCTAGTCTCTAAATGATGGCTAAAGTAGGGGT	2945
Db	2935	GTTAAAAAATGTTCAATCAATTTGGAATAGTCTAGTCTCTAAATGATGGCTAAAGTAGGGGT	2994
QY	2946	TGGCTTTGAAAACAATGTTTTATGCAACAAGGAAGAAATGTTAGCAGCCGACTTTGCCGG	3005
Db	2995	TGGCTTTGAAAACAATGTTTTATGCAACAAGGAAGAAATGTTAGCAGCCGACTTTGCCGG	3054
QY	3006	GCGTATGTGTGGCCGACTTAAACAATTCAGCTTAATCACTTGGGTGAGTCCCTGTGGAC	3065
Db	3055	GCGTATGTGTGGCCGACTTAAACAATTCAGCTTAATCACTTGGGTGAGTCCCTGTGGAC	3114
QY	3066	AAACAACAACAAGTCCCAATGTACTAGCTGCAGTTGCTTCTCGTGTGCTTAAGATGT	3125
Db	3115	AAACAACAACAAGTCCCAATGTACTAGCTGCAGTTGCTTCTCGTGTGCTTAAGATGT	3174
QY	3126	TTTGGCAACTCTAGAGCCAAGAGCCTTAAGATCATTTAAAAAATCTCCCTTTGTATCCTC	3185
Db	3175	TTTGGCAACTCTAGAGCCAAGAGCCTTAAGATCATTTAAAAAATCTCCCTTTGTATCCTC	3234

QY	3186	AGTGTGGGGACTGAGGCGAGCCCCCTTCAGTCCCTGTGGAGTGCACAGCTTTGGGGAA	3245
Db	3235	AGTGTGGGGACTGAGGCGAGCCCCCTTCAGTCCCTGTGGAGTGCACAGCTTTGGGGAA	3294
QY	3246	GGTGAAGGAAGGCTGTGTTTTTATCTCCACAGCAGTATGAGATPAAATTAATCAATAGT	3305
Db	3255	GGTGAAGGAAGGCTGTGTTTTTATCTCCACAGCAGTATGAGATPAAATTAATCAATAGT	3354
QY	3306	ATTACCTAGACATAGACAGTATTACTTAGTAGATGCACTGCTCACTGCACCCCTTCCCA	3365
Db	3355	ATTACCTAGACATAGACAGTATTACTTAGTAGATGCACTGCTCACTGCACCCCTTCCCA	3414
QY	3366	GCTCTCATTTTTTTGTTAGGTGATTTTGGATPAGGATPAGTTTTTGGGGATATGGGGGAGTGTG	3425
Db	3415	GCTCTCATTTTTTTGTTAGGTGATTTTGGATPAGGATPAGTTTTTGGGGATATGGGGGAGTGTG	3474
QY	3426	TTTCTGACCTGCTTTTGACAGAGTGCCTCGACACTCAGCAGTGTGGGGTGTGGCCACAG	3485
Db	3475	TTTCTGACCTGCTTTTGACAGAGTGCCTCGACACTCAGCAGTGTGGGGTGTGGCCACAG	3534
QY	3486	GCGGTTCTTGATGTAAAAAGATGTGTGGCCATCTAGCCTTGTAATCTCACTGTCACTGTGT	3545
Db	3535	GCGGTTCTTGATGTAAAAAGATGTGTGGCCATCTAGCCTTGTAATCTCACTGTCACTGTGT	3594
QY	3546	CCCATAGGGTGCCCTTCGATACACTGTTATTGATTAAGTTTGTGGCAGAAAGTGAACCTTG	3605
Db	3595	CCCATAGGGTGCCCTTCGATACACTGTTATTGATTAAGTTTGTGGCAGAAAGTGAACCTTG	3654
QY	3606	CGTGCAAAACATGTACCGTGCGCTGGTATGATPAGATGTAGATTTAATGTATCCATGTAT	3665
Db	3655	CGTGCAAAACATGTACCGTGCGCTGGTATGATPAGATGTAGATTTAATGTATCCATGTAT	3714
QY	3666	GTTAATGTGAATCTGTGTGGCAGAGTACTTTTCCATGTGCAGGAAATATCAAGCTGTGAA	3725
Db	3715	GTTAATGTGAATCTGTGTGGCAGAGTACTTTTCCATGTGCAGGAAATATCAAGCTGTGAA	3774
QY	3726	ACTGGCTATGTTTTAATATGCTCTCATTTGTGCTTTACTGTTGTGTGACCTGCTGAGGGA	3785
Db	3775	ACTGGCTATGTTTTAATATGCTCTCATTTGTGCTTTACTGTTGTGTGACCTGCTGAGGGA	3834
QY	3786	CAAGAGTTCCATTTTGATGTCAATPAAAGCAAGTACTTGCC	3826
Db	3835	CAAGAGTTCCATTTTGATGTCAATPAAAGCAAGTACTTGCC	3875

XX (HISE-) HISEQ INC.

XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao Q, Ren F,
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M,
PI Wehrman T, Wang J, Wang D, Drmanac RT;XX WPI, 2002-759812/82.
DR P-PSDB; ABP69806.XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.

XX Claim 1, SEQ ID NO 905; 1012bp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (1) comprising a
XX nucleotide sequence selected from any of 948 sequences (AB211119-
XX AB212066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
XX platelet or coagulation disorders (bacterial, viral, fungal, parasitic),
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
XX arthritis, etc. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIFO at ftp.wipo.int/pub/published_pcl_sequences

SQ Sequence 3981 BP; 829 A; 1105 C; 1205 G; 842 T; 0 U; 0 Other;

Query Match 94.4%; Score 3643; DB 6; Length 3981;
Best Local Similarity 96.1%; Pired. No. 0;
Matches 3825; Conservative 0; Mismatches 11; Indels 146; Gaps 3;

QY	17	ATGGAGGGGCGAGCGGGGAGCCCATGGGCGCTGGCGCTGCGACCTTTCAGCGGGAC	76
DB	1	ATGGAGGGGCGAGCGGGGAGCCCATGGGCGCTGGCGCTGCGACCTTTCAGCGGGAC	60
QY	77	GAGTTCACTGGGCTGGGAGAGTGAGCTGGGCGGCTTGGGCGAGGTGTACAAAGTGCGC	136
DB	61	GAGTTCACTGGGCTGGGAGAGTGAGCTGGGCGGCTTGGGCGAGGTGTACAAAGTGCGC	120
QY	137	CATGTCACCTGGAAGACCTGGCTGGCCATGATGCTCCGCCGCTGCACTGCAAGAC	196
DB	121	CATGTCACCTGGAAGACCTGGCTGGCCATGATGCTCCGCCGCTGCACTGCAAGAC	180
QY	197	AGGAGCGGATGAGAGCTTTTGAAGAAGCCAGAAGATGAGATGGCAAGTTTCGCTAC	256
DB	181	AGGAGCGGATGAGAGCTTTTGAAGAAGCCAGAAGATGAGATGGCAAGTTTCGCTAC	240
QY	257	ATCTCTCTGTGTATGAGCATCTGCGCGAATCTGTGGCTGTGTATGAGATCATGAG	316
DB	241	ATCTCTCTGTGTATGAGCATCTGCGCGAATCTGTGGCTGTGTATGAGATCATGAG	300
QY	317	ACGGGCTCCCTGGAAAAAGCTGTGGCTTGGAGCCATTTGCAATGGATCTTCGGTTCCGA	376
DB	301	ACGGGCTCCCTGGAAAAAGCTGTGGCTTGGAGCCATTTGCAATGGATCTTCGGTTCCGA	360
QY	377	ATCATCCAGAGACGGCGGTGGGATGAATCTTCGATCGATGAGGCCCGGCACTCTG	436
DB	361	ATCATCCAGAGACGGCGGTGGGATGAATCTTCGATCGATGAGGCCCGGCACTCTG	420
QY	437	CACCTGGAAGCTCAAGCCCGGAAATCTCTGTGATGATCCCACTCAAGATTTCT	496
DB	421	CACCTGGAAGCTCAAGCCCGGAAATCTCTGTGATGATCCCACTCAAGATTTCT	480
QY	497	GATTTTGCTGGCGAAGTGAACGGGCTGTCCCACTCGCATGACCTCAGCATGATGAGC	556

DB	481	GATTTTGCTGGCGAAGTGAACGGGCTGTCCCACTCGCATGACCTCAGCATGATGAGC	540
QY	557	CTGTTTGCAATGCGCTTCACTCTCCAGAGGCACTCAGGAGAAAGCCGCTCTTC	616
DB	541	CTGTTTGCAATGCGCTTCACTCTCCAGAGGCACTCAGGAGAAAGCCGCTCTTC	600
QY	617	GACACCAAGACGATGTATACAGCTTTGCGATGCTGATCTGGGGGCTGTCAACAGAG	676
DB	601	GACACCAAGACGATGTATACAGCTTTGCGATGCTGATCTGGGGGCTGTCAACAGAG	660
QY	677	AAGCGTTTGGAGATGAGAAAGAAATCTGTGACATCATGTGAAAGTGTGAAGGCGAC	736
DB	661	AAGCGTTTGGAGATGAGAAAGAAATCTGTGACATCATGTGAAAGTGTGAAGGCGAC	720
QY	737	CGCCCGAGCTGGCGCCGCTGTGAGAGCCGCGCGGCTGTGAGCCACTGTATAGC	796
DB	721	CGCCCGAGCTGGCGCCGCTGTGAGAGCCGCGCGGCTGTGAGCCACTGTATAGC	780
QY	797	CTCATGACGCGTGTGCGAGGGGATTCGGAGTTAGGCCCACTTC-----	844
DB	781	CTCATGACGCGTGTGCGAGGGGATTCGGAGTTAGGCCCACTTC-----	840
QY	845	-----	844
DB	841	CTGAATGGGAGCTCATCCGCCAAGTGTGGCAGCTGCTCCCTGTGATGGCAGTGG	900
QY	845	-----	844
DB	901	CGCTCCCGGGGAAAGCTTCCGCTTGTAGTCTGAAATCATATCCAGTGCATGATGCC	960
QY	845	-----	844
DB	961	CTTTCTTCCCAAGAAATTAATTCTGAAACCGAGACCTGTGTAAAGCTTATGAC	1020
QY	893	GAAAGTGAAGAACTGTCTATGATCTGAGACGTGAAGACCCCGGAGCCCAAGAGCAG	952
DB	1021	GAAAGTGAAGAACTGTCTATGATCTGAGACGTGAAGACCCCGGAGCCCAAGAGCAG	1080
QY	953	GTGATGCTGGAGGCTCAAGCGGCGCTTGTGCGCCCACTTGTGATATGACTACGCTTC	1012
DB	1081	GTGATGCTGGAGGCTCAAGCGGCGCTTGTGCGCCCACTTGTGATATGACTACGCTTC	1140
QY	1013	TCCGAGCTTTCTTCAACATGAGACCTGGAAGTTTCCAGGCGTGTGAGGGCCGAGAG	1072
DB	1141	TCCGAGCTTTCTTCAACATGAGACCTGGAAGTTTCCAGGCGTGTGAGGGCCGAGAG	1200
QY	1073	CTCAGCCGAGCTCTCTGAGTCAAGCTGCAATGCTCCGCGAGTGGAGAGGCTCTCG	1132
DB	1201	CTCAGCCGAGCTCTCTGAGTCAAGCTGCAATGCTCCGCGAGTGGAGAGGCTCTCG	1260
QY	1133	GGGATGCTCTGAGTCAAGCTGCTCTTCTTCAAGGATCACTGTCCGTCTTTGAG	1192
DB	1261	GGGATGCTCTGAGTCAAGCTGCTCTTCTTCAAGGATCACTGTCCGTCTTTGAG	1320
QY	1193	CGGAACTTTCAACAGAGGATCTGGGTATCAACAAGCTTCAGAGAGAGCTTGTGA	1252
DB	1321	CGGAACTTTCAACAGAGGATCTGGGTATCAACAAGCTTCAGAGAGAGCTTGTGA	1379
QY	1253	TGCGATGCTGTC--GGGACACAGAGAACTGATGAATCTCTGAGCGCGAGAGCTGGA	1311
DB	1380	TGCGATGCTGTC--GGGACACAGAGAACTGATGAATCTCTGAGCGCGAGAGCTGGA	1439
QY	1312	CCTGGCACTGACACAGGCTGCAAGCTGTGCACTTGTGAGAGGCTGGCAAGAGA	1371
DB	1440	CCTGGCACTGACACAGGCTGCAAGCTGTGCACTTGTGAGAGGCTGGCAAGAGA	1499
QY	1372	GTGCGCAAGTGGCTGTCTCAAAATGCGCAACCCCAACCTGAGCAACCGTGAAGGCGTC	1431
DB	1500	GTGCGCAAGTGGCTGTCTCAAAATGCGCAACCCCAACCTGAGCAACCGTGAAGGCGTC	1559
QY	1432	CACCCGTTTGCATGAGCGTGTGAGAGAGGAGGCTGTGAGAGCTTCTGCTGAC	1491

Db 1560 CACCCGTTTGCACTATGACCGCTGAGAGAGAGGCTGCGGGGTGTCTGAGAGCTCTTGCTGAC 1619
Qy 1492 ACGGAAGATCAAGTGTCAACGCCAAGAGATGAGGACAGATGACAGCCCTTCACTTTGCGAC 1551
Db 1620 GCGGAAGATCAAGTGTCAACGCCAAGAGATGAGGACAGATGACAGCCCTTCACTTTGCGAC 1679
Qy 1552 CCAGAACGGGGATGAGTCTAGACAACGGCTGCTGTTTGGAGAAAGACGGCTCGTCAACGA 1611
Db 1680 CCAGAACGGGGACGAGTCTAGACAACGGCTGCTGTTTGGAGAAAGACGGCTCGTCAACGA 1739
Qy 1612 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 1671
Db 1740 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 1799
Qy 1672 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 1731
Db 1800 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 1859
Qy 1732 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 1791
Db 1860 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 1919
Qy 1792 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 1851
Db 1920 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 1979
Qy 1852 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 1911
Db 1980 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2039
Qy 1912 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 1971
Db 2040 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2099
Qy 1972 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2031
Db 2100 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2159
Qy 2032 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2091
Db 2160 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2219
Qy 2092 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2151
Db 2220 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2279
Qy 2152 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2211
Db 2280 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2339
Qy 2212 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2271
Db 2340 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2399
Qy 2272 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2331
Db 2400 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2459
Qy 2332 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2391
Db 2460 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2519
Qy 2392 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2451
Db 2520 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2579
Qy 2452 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2511
Db 2580 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2639
Qy 2512 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2571
Db 2640 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2699

Qy 2572 CCGCTCCATCATCATGATCTAGGACCTGCTGTCTGAAGGACCGTGGGTGAGAAATCATTT 2631
Db 2700 CCGCTCCATCATCATGATCTAGGACCTGCTGTCTGAAGGACCGTGGGTGAGAAATCATTT 2759
Qy 2632 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2691
Db 2760 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2819
Qy 2692 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2751
Db 2820 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2879
Qy 2752 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2811
Db 2880 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2939
Qy 2812 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2871
Db 2940 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2999
Qy 2872 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2931
Db 3000 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3059
Qy 2932 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 2991
Db 3060 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3119
Qy 2992 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3051
Db 3120 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3179
Qy 3052 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3111
Db 3180 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3239
Qy 3112 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3171
Db 3240 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3299
Qy 3172 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3231
Db 3300 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3359
Qy 3232 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3291
Db 3360 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3419
Qy 3292 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3351
Db 3420 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3479
Qy 3352 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3411
Db 3480 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3539
Qy 3412 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3471
Db 3540 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3599
Qy 3472 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3531
Db 3600 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3659
Qy 3532 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3591
Db 3660 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3719
Qy 3552 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3651
Db 3720 GGTGACCTTTGAGGGCCGGAACGCCATGCACTGTGCTTCCAGCAACGGGACAGAGAAATAT 3779

QY 3652 AATGACCATGATGTAATGTAATCTGAGGAGAGATACCTTTCCATGGAGGAATA 3711
DB 3780 AATGACCATGATGTAATGTAATCTGAGGAGAGATACCTTTCCATGGAGGAATA 3839
QY 3712 TCCAGGCTGTGAAGTGGCTATGTTTAAATAGCTCATTTGCTTACTGTGTG 3771
DB 3840 TCCAGGCTGTGAAGTGGCTATGTTTAAATAGCTCATTTGCTTACTGTGTG 3899
QY 3772 GACTGCTGAGGAGCAAGAGTTCCATTTGATGTCAATAAGCAAGTACTGCTACTT 3831
DB 3900 GACTGCTGAGGAGCAAGAGTTCCATTTGATGTCAATAAGCAAGTACTGCTACTT 3959
QY 3832 TTTTGAAGTGAAGAAAAAAA 3853
DB 3960 TTTTGAAGTGAAGAAAAAAA 3981
RESULT 7
ADM44541
ID ADM44541 standard, cDNA, 3981 BP.
AC ADM44541;
XX
XX
DT 03-JUN-2004 (first entry)
DE Novel human arginine-rich protein cDNA #905.
XX
XX ss; gene; human; arginine-rich protein; cancer; inflammation;
KM genetic disorder.
XX
XX Homo sapiens.
XX
XX US2004053250-A1.
XX
PD 18-MAR-2004.
XX
PP 21-NOV-2002; 2002US-00302172.
XX
XX 05-MAR-2001; 2001US-00799451.
PR 05-MAR-2002; 2002WO-US000595.
PR 20-AUG-2002; 2002US-00252521.
XX
XX (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
XX
PI Tang YT, Xue A, Drmanac RT;
XX
DR WPI, 2004-238579/22.
XX
XX
PT New isolated arginine-rich protein-like polynucleotides and polypeptides,
PT useful for diagnosing and/or treating conditions associated with aberrant
PT activity of the arginine-rich polypeptides, such as cancer and
PT inflammation.
XX
PS Disclosure; SEQ ID NO 905; 51pp; English.
XX
XX The invention relates to an isolated polynucleotide. The methods and
CC compositions of the present invention are useful for the diagnosis and/or
CC treatment of diseases or conditions associated with aberrant expression
CC or activity of the arginine-rich protein-like polypeptides, such as
CC cancer and inflammation. They can also be used in forensics, gene
CC mapping, identification of mutations responsible for genetic disorders,
CC and in assessing biodiversity. The present sequence represents a novel
CC human arginine-rich protein cDNA.
XX
SQ Sequence 3981 BP; 829 A; 1105 C; 1205 G; 842 T; 0 U; 0 Other;
Query Match 94.4%; Score 3643; DB 12; Length 3981;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 3825; Conservative 0; Mismatches 11; Indels 146; Gaps 3;
QY 17 ATGAGAGGCGACGCGGAGCCCATGGCCCTGCGCTGCGCACCTTCGACGCGGCG 76

DB 1 ATGAGAGGCGACGCGGAGCCCATGGCCCTGCGCTGCGCACCTTCGACGCGGCG 60
QY 77 GAGTTACAGGCGCTGGAGAAAGTGGGCTCGGGCCGCTTCGGGAGGTGTAAAGGTGGCG 136
DB 61 GAGTTACAGGCGCTGGAGAAAGTGGGCTCGGGCCGCTTCGGGAGGTGTAAAGGTGGCG 120
QY 137 CATGTCATGGAAGACCTGGCTGGCCATCAAGTGTCTGCCACGCTGACGTGACGAC 196
DB 121 CATGTCATGGAAGACCTGGCTGGCCATCAAGTGTCTGCCACGCTGACGTGACGAC 180
QY 197 AGGAGCGCATGAGAGCTTTTGAAGAACCAAGAAATGAGATGGCCAGTTTGTCTAC 256
DB 181 AGGAGCGCATGAGAGCTTTTGAAGAACCAAGAAATGAGATGGCCAGTTTGTCTAC 240
QY 257 ATCTGCTGTGTATGAGCATCTCCCGGCAACTGTCCGCTGTGTATGAGTACATGGAG 316
DB 241 ATCTGCTGTGTATGAGCATCTCCCGGCAACTGTCCGCTGTGTATGAGTACATGGAG 300
QY 317 ACGGCTCCCTGGAAAGCTGTGCTGGAGGCATTGGCCATGGGATCTCCGTTCCGA 376
DB 301 ACGGCTCCCTGGAAAGCTGTGCTGGAGGCATTGGCCATGGGATCTCCGTTCCGA 360
QY 377 ATCATCCAGAGACGCGCGTGGAGCAATCTTCTGCACTGCAATGACCCTGCTCTG 436
DB 361 ATCATCCAGAGACGCGCGTGGAGCAATCTTCTGCACTGCAATGACCCTGCTCTG 420
QY 437 CACTGGAAGCTTGAAGCCCGGCAACATCTGCTGAGTCCCACTACAGTCAAGTTTCT 496
DB 421 CACTGGAAGCTTGAAGCCCGGCAACATCTGCTGAGTCCCACTACAGTCAAGTTTCT 480
QY 497 GATTTTGTCTGGCCAAATGCAAGCGGCTGTCCCATGCGCATGAGATGAGTGGC 556
DB 481 GATTTTGTCTGGCCAAATGCAAGCGGCTGTCCCATGCGCATGAGATGAGTGGC 540
QY 557 CTGTTTGGCAAGTGGCTTACCTCCCTCAGAGGCGATCAGGAGAAAGCGGCTCTTC 616
DB 541 CTGTTTGGCAAGTGGCTTACCTCCCTCAGAGGCGATCAGGAGAAAGCGGCTCTTC 600
QY 617 GACACCAAGCAAGATGTATACAGCTTTGCGATTCGTATCTGGGCGGTCTACACAGAG 676
DB 601 GACACCAAGCAAGATGTATACAGCTTTGCGATTCGTATCTGGGCGGTCTCTCACAGAG 660
QY 677 AAGCGTTTGAAGTGAAGAAACAATCTGCAATCATGTGAAGGTGTGAAGGCGCAC 736
DB 661 AAGCGTTTGAAGTGAAGAAACAATCTGCAATCATGTGAAGGTGTGAAGGCGCAC 720
QY 737 CGCCCCGAGCTGCGCCGCTGTGAGAGCCCGCGCGGCTGCGAGCACTGTATAGC 796
DB 721 CGCCCCGAGCTGCGCCGCTGTGAGAGCCCGCGCGGCTGCGAGCACTGTATAGC 780
QY 797 CTGATGACGCGGTGTGCAAGGAGATCGGAGTTAGGCCCACTTC----- 844
DB 781 CTGATGACGCGGTGTGCAAGGAGATCGGAGTTAGGCCCACTTCCAAGAAACGCG 840
QY 845 ----- 844
DB 841 CTGAATGGGAGCTCATCCGCGAGGTGTGCGACGCTTCTCTGTGACTGGCAGGTGG 900
QY 845 ----- 844
DB 901 CGCTCCCGCGGAAAGGCTTCGCGCTTGAAGTCTGAAGTCATCATCCGATGACATGTCC 960
QY 845 -----CAAGAAATTACTTCTGAACCGAGACCTGTGTGAAGAGCTGTATGAC 892
DB 961 CTTCCTCCCAAGAAATTACTTCTGAACCGAGACCTGTGTGAAGAGCTGTATGAC 1020
QY 893 GAAGTGAAGAAACCTGCTCATGATGTGACGTGAAGAACCCCGGAGGCCAGAGCGAG 952
DB 1021 GAAGTGAAGAAACCTGCTCATGATGTGACGTGAAGAACCCCGGAGGCCAGAGCGAG 1080
QY 953 GTGTGCTGCGAGGCTCAAGCGGCTCTGCGCCCACTTCGATTAAGACTTACAGCTTC 1012

Db	1081	GTGGTGCCTGGAGGCGCTCAAGCGGGGCTCTGCGCCCACTTCGATTAACGACTACAGCTTC	1140
Qy	1043	TCCGAGCTTCTCTCAACAGCTGAGACTTGAAGTTTCCAGAGCTGTGAGAGGCCCGCAGAGAG	1072
Db	1141	TCCGAGCTGCTCTCAACAGCTGAGACTTGAAGTTTCCAGAGCTGTGAGAGGCCCGCAGAGAG	1200
Qy	1073	CTCAGCCGCAAGCTCCTTGAAGTCCAGCTGCATCTGTCCGCAATGGGAAGAGGCTTTCG	1132
Db	1201	CTCAGCCGCAAGCTCCTTGAAGTCCAGCTGCATCTGTCCGCAATGGGAAGAGGCTTTCG	1260
Qy	1133	GGGGGTCTCGAGTGAATCCGCGCTTCCTTCCAGAGGATACATCTGCGCTGTCTTTGAG	1192
Db	1261	GGGGGTCTCGAGTGAATCCGCGCTTCCTTCCAGAGGATACATCTGCGCTGTCTTTGAG	1320
Qy	1193	CGGGAACCTTCAACCAAGGATCTGGGTACCAAGACGTCAGGAAGAAAGTGTGGA	1252
Db	1321	CGGGAACCTTCAACCAAGGATCTGGGTACCAAGACGTCAGGAAGAAAGTGTGGA	1379
Qy	1253	TGCCATCGTGTCC-GGGACACAGCAAACTGATGAAGTCTTGACGCCGCAAGACGTGGA	1311
Db	1380	TGCCATCGTGTCCGGGGGACACAGCAAACTGATGAAGTCTTGACGCCGCAAGACGTGGA	1439
Qy	1312	CCTGGCACTGGAACAAGGGTGCAGCGTGCCTGACCTGCGGTGGAAGGCCGGGGCAAGAGA	1371
Db	1440	CCTGGCACTGGAACAAGGGTGCAGCGTGCCTGACCTGCGGTGGAAGGCCGGGGCAAGAGA	1499
Qy	1372	GTGCGCCAAAGTGGCTGTCTCAACAATAGCCAAACCCAACTGAGCAACGTAAGGGCTC	1431
Db	1500	GTGCGCCAAAGTGGCTGTCTCAACAATAGCCAAACCCAACTGAGCAACGTAAGGGCTC	1559
Qy	1432	CACCCCGTTGCACATGSCCGTGGAGAGAGAGGGTGCAGGAGTCTGTGAGCTCTGTGCGC	1491
Db	1560	CACCCCGTTGCACATGSCCGTGGAGAGAGAGGGTGCAGGAGTCTGTGAGCTCTGTGCGC	1619
Qy	1492	ACGGAAGATCAAGTGTCAACGCCAAGATGAGGACCAAGTGAACAGCCCTTCCACTTTGAGC	1551
Db	1620	ACGGAAGATCAAGTGTCAACGCCAAGATGAGGACCAAGTGAACAGCCCTTCCACTTTGAGC	1679
Qy	1552	CCAGAACCGGGAGTGAAGTCTAGCACACGCGCTGTGTTGAGAGAAAGACGCTTCGTCAACGA	1611
Db	1680	CCAGAACCGGGAGTGAAGTCTAGCACACGCGCTGTGTTGAGAGAAAGACGCTTCGTCAACGA	1739
Qy	1612	GGTGGACTTTGAGGGCCGGAAGCCCATGCACTGTGCTTGCACGACCGGGCAGAGAAATAT	1671
Db	1740	GGTGGACTTTGAGGGCCGGAAGCCCATGCACTGTGCTTGCACGACCGGGCAGAGAAATAT	1799
Qy	1672	CGTGGGCAATCTGCTGCGCCCGCAAGGGGTGAGAGGTGACCGTGAAGGGCAAGATGCGGGCT	1731
Db	1800	CGTGGGCAATCTGCTGCGCCCGCAAGGGGTGAGAGGTGACCGTGAAGGGCAAGATGCGGGCT	1859
Qy	1732	GSCACTGCACTACGCTGCTGGCAAGGGCAACTGCGCAATCGTCAAGACTGTGGCAAGCA	1791
Db	1860	GSCACTGCACTACGCTGCTGGCAAGGGCAACTGCGCAATCGTCAAGACTGTGGCAAGCA	1919
Qy	1792	GCGGGGGGTGAAGTGTGAAGCCCGAGAGGCTGATGGAGAGAGCCGCAATTGCACTTGGCGGC	1851
Db	1920	GCGGGGGGTGAAGTGTGAAGCCCGAGAGGCTGATGGAGAGAGCCGCAATTGCACTTGGCGGC	1979
Qy	1852	ACAAGGCGGGGCACTACCGGCTGAGCCCGCACTCTCATCGACTGTGCTCCAGCTTCACAGT	1911
Db	1980	ACAAGGCGGGGCACTACCGGCTGAGCCCGCACTCTCATCGACTGTGCTCCAGCTTCACAGT	2039
Qy	1912	CTGCAAGCTGTGGGCAAGACACCCCTGCAAGTGGCCGCGGAGACGGGGCAAGAGAC	1971
Db	2040	CTGCAAGCTGTGGGCAAGACACCCCTGCAAGTGGCCGCGGAGACGGGGCAAGAGAC	2099
Qy	1972	TGCGAAGCTGTCTTGAATCGGAGGCGCTTGGCAAGAGAGGCGGTGACTTCAGACGGCTACAC	2031
Db	2100	TGCGAAGCTGTCTTGAATCGGAGGCGCTTGGCAAGAGAGGCGGTGACTTCAGACGGCTACAC	2159
Qy	2032	CGCTCTTGCACTTGGCTGCCCGCAAGGACACTTGGCACTGTCAAGCTGTCTTGTGAGGA	2091
Db	2160	CGCTCTTGCACTTGGCTGCCCGCAAGGACACTTGGCACTGTGTGAGCTGTGTGAGGA	2219

QY	2092	GAAAGCCGATGTGCTGGCCCGGGAAACCCCTGAACCAAGACGGCGCTGCACCTGGCTCCGC	2151
Db	2220	GAAAGCCGATGTGCTGGCCCGGGAAACCCCTGAACCAAGACGGCGCTGCACCTGGCTCCGC	2279
QY	2152	CCACGGGGCACTCGAGAGTGTGTGGAGAGATGTGTGACGGCGGAGTGTGATTCGACCTGTTCGA	2211
Db	2280	CCACGGGGCACTCGAGAGTGTGTGGAGAGATGTGTGACGGCGGAGTGTGATTCGACCTGTTCGA	2339
QY	2212	CGAGCAGGGGGCTCAAGCGGCTGCACCTGGCCGCCCAAGGCGGACGCAACAGCGTGA	2271
Db	2340	CGAGCAGGGGGCTCAAGCGGCTGCACCTGGCCGCCCAAGGCGGACGCAACAGCGTGA	2399
QY	2272	GACTGTGCTCAGGCAATGGGGCCCAATCACTGCAGAGCTCAAGTTCAGGGCGGCCA	2331
Db	2400	GACTGTGCTCAGGCAATGGGGCCCAATCACTGCAGAGCTCAAGTTCAGGGCGGCCA	2459
QY	2332	TGGCCCCCGCCGACAACCTCGTGGGGGAGAGCAAGACTAGCGTGGCCGTGGGAGACCG	2391
Db	2460	TGGCCCCCGCCGACAACCTCGTGGGGGAGAGCAAGACTAGCGTGGCCGTGGGAGACCG	2519
QY	2392	GGGGTCCACAGTGGGGCTCTTGTCTGTCTGTCTGTCTGTCTGTGGAGATGGAACATCTGC	2451
Db	2520	GGGGTCCACAGTGGGGCTCTTGTCTGTCTGTCTGTCTGTCTGTGGAGATGGAACATCTGC	2579
QY	2452	GTGGGGCCCGCTTGTGTGCTTACCTAAATGTAAACCAAGCAGGTGACATGTGCATCA	2511
Db	2580	GTGGGGCCCGCTTGTGTGCTTACCTAAATGTAAACCAAGCAGGTGACATGTGCATCA	2639
QY	2512	GGAGCGCGCTGTGCTGACCCGAGAGTCCCCCGCAGGTGAAGCTGGCTCAGGGGCATG	2571
Db	2640	GGAGCGCGCTGTGCTGACCCGAGAGTCCCCCGCAGGTGAAGCTGGCTCAGGGGCATG	2699
QY	2572	CCCGCTCCATCATGCATCAGGACACCTGCTGTCTGAAGGGAACCGTGGGTCAAGATCATTT	2631
Db	2700	CCCGCTCCATCATGCATCAGGACACCTGCTGTCTGAAGGGAACCGTGGGTCAAGATCATTT	2759
QY	2632	CGTTGTGCTCTTAATGGGTGCGTGAAGCTGTCTCAAGTGAAGAACCCCAAGCGTGA	2691
Db	2760	CGTTGTGCTCTTAATGGGTGCGTGAAGCTGTCTCAAGTGAAGAACCCCAAGCGTGA	2819
QY	2692	AGCATCCACTCTCTCCTGAGGGAGGACACCTGGGGTGGCGAGCTCACCAAGCTTGAAG	2751
Db	2820	AGCATCCACTCTCTCCTGAGGGAGGACACCTGGGGTGGCGAGCTCACCAAGCTTGAAG	2879
QY	2752	GAGGTGACGGGGAAACTGTGTTTTTATCTTCATACATGACGCTGGGACAGAGGCTGT	2811
Db	2880	GAGGTGACGGGGAAACTGTGTTTTTATCTTCATACATGACGCTGGGACAGAGGCTGT	2939
QY	2812	CTTAAAGTTTCATGGAATTGTTTATTAATAAATATCTTAAGAGATGAATACCTTATCAGCT	2871
Db	2940	CTTAAAGTTTCATGGAATTGTTTATTAATAAATATCTTAAGAGATGAATACCTTATCAGCT	2999
QY	2872	GTTGCTTGAACCTGTTAATAATGTTCAATPAACATTGGATGTAGTCTTAAATGATGG	2931
Db	3000	GTTGCTTGAACCTGTTAATAATGTTCAATPAACATTGGATGTAGTCTTAAATGATGA	3059
QY	2932	CTAAGTAGGGGGTGGCTTTGAAACAAATGTTTTTATGCAACAAGAACAAATGATGA	2991
Db	3060	CTAAGTAGGGGGTGGCTTTGAAACAAATGTTTTTATGCAACAAGAACAAATGATGA	3119
QY	2992	GCCAGCTTGCAGGGCGTATGTGTGGCCAGCTCTTAACCAATTCAGTCTATTACTTGGGT	3051
Db	3120	GCCAGCTTGCAGGGCGTATGTGTGGCCAGCTCTTAACCAATTCAGTCTATTACTTGGGT	3179
QY	3052	GAGTCTTGTGCAACAACAACAACAGTGGCCCATGTATCTAGCTGCGGTTGTTCTC	3111
Db	3180	GAGTCTTGTGCAACAACAACAACAGTGGCCCATGTATCTAGCTGCGGTTGTTCTC	3239
QY	3112	GTTGCTTAAGATGTTTGGCAACTCTAAGAGCCACAGGCCCTAAGACATTAATAAATTC	3171
Db	3240	GTTGCTTAAGATGTTTGGCAACTCTAAGAGCCACAGGCCCTAAGACATTAATAAATTC	3299

Db	695	CGTGGCCCGCAATCCATTCAGACCTGTGCTCCGACGTCAACCTCTGCAGCCTGCGGCA	754
OY	1930	GACACCCCTGCACGTCGGCCGCGAGACAACGAGCACTGCACAGCTGCTCTGCA	1989
Db	755	GACACCCCTGCACGTCGGCCGCGAGACAACGAGCACTGCACAGCTGCTCTGCA	814
OY	1990	TCCGGGCGCTGCAGAGAGCCGTGACCTCAGAAGCTTACAACGCTCTGCACCTGCTGC	2049
Db	815	TCCGGGCGCTGCAGAGAGCCGTGACCTCAGAAGCTTACAACGCTCTGCACCTGCTGC	874
OY	2050	CCGCAACGGACACCTGGCCACTGTAAACTGTGTGAGAGAAAGCCGATTTGTCGTGC	2109
Db	875	CCGCAACGGACACCTGGCCACTGTAAACTGTGTGAGAGAAAGCCGATTTGTCGTGC	934
OY	2110	CCGGGGACCCCTGAAACAGACCGGCGCTGCACTGGCTCCCGCCACCGGGCACTCGAGAGT	2169
Db	935	CCGGGGACCCCTGAAACAGACCGGCGCTGCACTGGCTCCCGCCACCGGGCACTCGAGAGT	994
OY	2170	GGTGGAGAGTTGTGTCAGCGCGGATGTCAATTGACCTGTTCGACGACGGGGCTCAAGCGC	2229
Db	995	GGTGGAGAGTTGTGTCAGCGCGGATGTCAATTGACCTGTTCGACGACGGGGCTCAAGCGC	1054
OY	2230	GCTGCACTGCGCCGCCCGGCAAGCAACAGCGGTGGAGACTCTGCTCAGGCATAG	2289
Db	1055	GCTGCACTGCGCCGCCCGGCAAGCAACAGCGGTGGAGACTCTGCTCAGGCATAG	1114
OY	2290	GGCCCAATCAACCTGACAGAGCTCAAGTTCAGAGGCGGACCATGAGCCCGCGCAACT	2349
Db	1115	GGCCCAATCAACCTGACAGAGCTCAAGTTCAGAGGCGGACCATGAGCCCGCGCAACT	1174
OY	2350	CCTGCGGCGAAGCAAGACCTTAGCTGCTGCTGCGAGACCGGGGGTTCACGTGGGCTC	2409
Db	1175	CCTGCGGCGAAGCAAGACCTTAGCTGCTGCTGCGAGACCGGGGGTTCACGTGGGCTC	1234
OY	2410	TTGTCTCTGCTCTGTGTTCTCTGTCGGGAGTGAACGATCTCTGCTGTGGGCCCTCTTGTGGC	2469
Db	1235	TTGTCTCTGCTCTGTGTTCTCTGTCGGGAGTGAACGATCTCTGCTGTGGGCCCTCTTGTGGC	1294
OY	2470	TTACCTTAATGTTTAAACAAGCAGAGGTATCAATGTCATCAGAGGCGGCTGCTGTA	2529
Db	1295	TTACCTTAATGTTTAAACAAGCAGAGGTATCAATGTCATCAGAGGCGGCTGCTGTA	1354
OY	2530	CCGAGGTGTCCTCCCTCAGGTGAAGCTGACTCAGTGCACATGCCCTCCATCATCATC	2589
Db	1355	CCGAGGTGTCCTCCCTCAGGTGAAGCTGACTCAGTGCACATGCCCTCCATCATCATC	1414
OY	2590	TAGGCACTGCTGTCTGAAAGGGAACGTCGGGTACAAATCATTTCTGTTGCTCTTAATGGG	2649
Db	1415	TAGGCACTGCTGTCTGAAAGGGAACGTCGGGTACAAATCATTTCTGTTGCTCTTAATGGG	1474
OY	2650	TGCTGAGGCTGATCTCTCAGTGAAGAACCCAGGCGTGAAGCATCACTCTCTCTG	2709
Db	1475	TGCTGAGGCTGATCTCTCAGTGAAGAACCCAGGCGTGAAGCATCACTCTCTCTG	1534
OY	2710	AGCGAGGCCACTTGGGTTGCTGAGACTCACCACTTTGAGGGAGTGCAGGGGAACTG	2769
Db	1535	AGCGAGGCCACTTGGGTTGCTGAGACTCACCACTTTGAGGGAGTGCAGGGGAACTG	1594
OY	2770	TGTTTTTATCTTCAATACATGACGGTGGCAGAGAGGCTGTCTTAAAGTTTCCATGGA	2829
Db	1595	TGTTTTTATCTTCAATACATGACGGTGGCAGAGAGGCTGTCTTAAAGTTTCCATGGA	1654
OY	2830	TGTTTTTAAAAATCTTAAAGATGAAATACTTAATCAGCGTGTCTGAAACCTGTTA	2889
Db	1655	TGTTTTTAAAAATCTTAAAGATGAAATACTTAATCAGCGTGTCTGAAACCTGTTA	1714
OY	2890	AAAATGTTCAATAACATTTGATAGTCTAGTCTTAATATGAGCTTAAGTGTGGGTTGGC	2949
Db	1715	AAAATGTTCAATAACATTTGATAGTCTAGTCTTAATATGAGCTTAAGTGTGGGTTGGC	1774
OY	2950	TTTGAAGAACATGTTTATGCAACAGGAACGAATGTAGCAGCGCTTTGCGGGGCGT	3009

Db	1775	TTTGGAAAAGCATGTTTATATGCAACAAAGAAAGATGGTAGACGCACACTTTGCGGGCGCT	1894
QY	3010	ATGTGTGGCCAGCTCTTAACCAATCCAGTCTATTACTTGGGTAGTCCCTTGTGCAACC	3069
Db	1895	ATGTGTGGCCAGCTCTTAACCAATCCAGTCTATTACTTGGGTAGTCCCTTGTGCAACC	1894
QY	3070	ACACACACGTGCCCAATGTAATGAGTGGCTGCTTTCTCCGTTGGCTAAGATGTTTG	3129
Db	1895	ACACACACGTGCCCAATGTAATGAGTGGCTGCTTTCTCCGTTGGCTAAGATGTTTG	1954
QY	3130	GCAACTCTAGAGCCACAGGCCCTAAGAGTCATTAATAAAATTCCTCCCTTGTAACTCAGTG	3189
Db	1995	GCAACTCTAGAGCCACAGGCCCTAAGAGTCATTAATAAAATTCCTCCCTTGTAACTCAGTG	2014
QY	3190	CTGGGGAATGAGGCGAGGCCCTCAGGTGCTGGAGTGACCAAGTCTTGGGGAAGAGTG	3249
Db	2015	CTGGGGAATGAGGCGAGGCCCTCAGGTGCTGGAGTGACCAAGTCTTGGGGAAGAGTG	2074
QY	3250	CAGAGGAAGCTGTGTTTATTTTATCTCCCAACGCAATAGAAGATTAATTAATCATAGTTTA	3309
Db	2075	CAGAGGAAGCTGTGTTTATTTTATCTCCCAACGCAATAGAAGATTAATTAATCATAGTTTA	2134
QY	3310	CCTAGACATAGACAGTATTAACCTAAGATGATGACACTGTCACCTGCACACCTTCCACATC	3369
Db	2135	CCTAGACATAGACAGTATTAACCTAAGATGATGACACTGTCACCTGCACACCTTCCACATC	2194
QY	3370	TCATTTTGTATGAGTGATTTGGGATAGGGAATAGTGTTTTGGGGTATGCGGGAGATGTTTC	3429
Db	2195	TCATTTTGTATGAGTGATTTGGGATAGGGAATAGTGTTTTGGGGTATGCGGGAGATGTTTC	2254
QY	3430	TGACCTGCTTTGCAAGAGTGTCTCCGCACTCAGCAGTTTGGGGTGTGGCCCAAGGCGG	3489
Db	2255	TGACCTGCTTTGCAAGAGTGTCTCCGCACTCAGCAGTTTGGGGTGTGGCCCAAGGCGG	2314
QY	3490	TTCTTGAATGTAAGAAAGATGGGCAATGACCTGCTGTAACTTCACATGTCACCTGATGCCA	3549
Db	2315	TTCTTGAATGTAAGAAAGATGGGCAATGACCTGCTGTAACTTCACATGTCACCTGATGCCA	2374
QY	3550	TAGGGTGCCTTCTGAATATCTGTTATTAAGATTAAGTTTGTTCAGAAAGTGACCTGCGTG	3609
Db	2375	TAGGGTGCCTTCTGAATATCTGTTATTAAGATTAAGTTTGTTCAGAAAGTGACCTGCGTG	2434
QY	3610	CAACATATACCGTGGCTCGGTATATGATATAGATTTGATTAATATATACCATATATGTTA	3665
Db	2435	CAACATATACCGTGGCTCGGTATATGATATAGATTTGATTAATATATACCATATATGTTA	2494
QY	3670	ATGTGAATCTGTGGGACAGATTACTTTTCATGGGAGAAATATCAAGCTGTGAAACTG	3729
Db	2495	ATGTGAATCTGTGGGACAGATTACTTTTCATGGGAGAAATATCAAGCTGTGTAACTG	2554
QY	3730	GCTATGTTTATATATGCTCATATGTGCTTACTGTGTGTGGAATGCGTGAAGGACAAG	3789
Db	2555	GCTATGTTTATATATGCTCATATGTGCTTACTGTGTGTGGAATGCGTGAAGGACAAG	2614
QY	3790	AAGTTCATTTGATGTCAATTAAGCAAAAGTACTTGCCATCTTTTGAANCTGAAAAAA	3849
Db	2615	AAGTTCATTTGATGTCAATTAAGCAAAAGTACTTGCCATCTTTTGAANCTGAAAAAA	2674
QY	3850	AAAAAAAAAA 3858	
Db	2675	AAAAAAAAAA 2683	
RESULT 9			
ADE29194			
ID	ADE29194 standard; DNA, 2355 BP.		
AC	ADE29194;		
XX			
XX	29-JAN-2004 (first entry)		
DT			
DE	Human novel protein kinase 14171 gene coding sequence SegID3.		
XX			


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QY 1217 GGTACCAAGACGTCAGAAAGAAAGAGCTTGTGGATGCGATCGTGTCCGGGACACCGC 1276
DB 1201 GGTACCAAGACGTCAGAAAGAAAGAGCTTGTGGATGCGATCGTGTCCGGGACACCGC 1260
QY 1277 AAACGTATGAAGATCTGTCAGCGCCGAGGACGTGACCTGGACCTGGACAGCGGTGCCAGC 1336
DB 1261 AAACGTATGAAGATCTGTCAGCGCCGAGGACGTGACCTGGACCTGGACAGCGGTGCCAGC 1320
QY 1337 CTGCTGCACTTGGCGGTGGAGGCGCGGCAAGAGAGTGGCCCAAGTGGCTGTGTCAAC 1396
DB 1321 CTGCTGCACTTGGCGGTGGAGGCGCGGCAAGAGAGTGGCCCAAGTGGCTGTGTCAAC 1380
QY 1397 AATGCCAACCCCAACCTGAGCAACCGTAGGGGCTCCACCCGTTGCATAGGCGGTGAG 1456
DB 1381 AATGCCAACCCCAACCTGAGCAACCGTAGGGGCTCCACCCGTTGCATAGGCGGTGAG 1440
QY 1457 AGGAGGAGTGGCGGGGTGTGTGTGAGTCTGTGTCGACGGAAGATGATGTCACGCGCAAG 1516
DB 1441 AGGAGGAGTGGCGGGGTGTGTGTGAGTCTGTGTCGACGGAAGATGATGTCACGCGCAAG 1500
QY 1517 GATGAGACCAATGAGCAGGCTCTCACTTTGCAAGCCCAAGAGGGGATGAGTCTTGACA 1576
DB 1501 GATGAGACCAATGAGCAGGCTCTCACTTTGCAAGCCCAAGAGGGGATGAGTCTTGACA 1560
QY 1577 CGGCTGCTGTTGGAGAGAAAGCGCTCGGTCAACGAGGTGACCTTTGAGGGCCGAGCGCC 1636
DB 1561 CGGCTGCTGTTGGAGAGAAAGCGCTCGGTCAACGAGGTGACCTTTGAGGGCCGAGCGCC 1620
QY 1637 ATGCACTGTGCTGTCAGACGCGGAGAGAAATATGTGCGCATCTGTGCGCGGAGGC 1696
DB 1621 ATGCACTGTGCTGTCAGACGCGGAGAGAAATATGTGCGCATCTGTGCGCGGAGGC 1680
QY 1697 GTGAGACGTGAGCGCTGCAAGGAGAGATGCTGCGGCACTAGCGTGCCTGGGAG 1756
DB 1681 GTGAGACGTGAGCGCTGCAAGGAGAGATGCTGCGGCACTAGCGTGCCTGGGAG 1740
QY 1757 GGCACACCTGCGCATGTGTCAGAGTGTGCGCAAGACCGGGGTGAGTGTGAACCGCCAG 1816
DB 1741 GGCACACCTGCGCATGTGTCAGAGTGTGCGCAAGACCGGGGTGAGTGTGAACCGCCAG 1800
QY 1817 AGCTGTGATGGAGAGACGCGCATTTGCACTGTGCGGACAGCGGGGCACTACCGCGTGGC 1876
DB 1801 AGCTGTGATGGAGAGACGCGCATTTGCACTGTGCGGACAGCGGGGCACTACCGCGTGGC 1860
QY 1877 CGCATCTTATGACCTGTGCTCCGACGTCAACGTCTGAGAGCTGTGCGCAACAGACCC 1936
DB 1861 CGCATCTTATGACCTGTGCTCCGACGTCAACGTCTGAGAGCTGTGCGCAACAGACCC 1920
QY 1937 CTGCACTGTGCGCGGAGACGCGGACCAAGACACTGCGAGGCTGCTCTTGATCGGGGC 1996
DB 1921 CTGCACTGTGCGCGGAGACGCGGACCAAGACACTGCGAGGCTGCTCTTGATCGGGGC 1980
QY 1997 GCTGGCAAGAGAGCGGTGACCTCAAGCGGCTACACCGCTCTGACCTGGCTGCCGCAAC 2056
DB 1981 GCTGGCAAGAGAGCGGTGACCTCAAGCGGCTACACCGGCTCTGACCTGGCTGCCGCAAC 2040
QY 2057 GGAACACCTGCGCACTGTCAAGTGTGTCGAGAGAGAGCGAGTGTGCGCGCGGGA 2116
DB 2041 GGAACACCTGCGCACTGTCAAGTGTGTCGAGAGAGAGCGAGTGTGCGCGCGGGA 2100
QY 2117 CCCCTGAACCAAGCGGCGCTGACCTGTGCGCGGCACTGCGAGGTGTGTGAG 2176
DB 2101 CCCCTGAACCAAGCGGCGCTGACCTGTGCGCGGCACTGCGAGGTGTGTGAG 2160
QY 2177 GAGTGTGTGAGCGCGCGATGTCATTGACCTGTTGACGAGCAGGGGCTCAGCGCGCTGAC 2236
DB 2161 GAGTGTGTGAGCGCGCGATGTCATTGACCTGTTGACGAGCAGGGGCTCAGCGCGCTGAC 2220
QY 2237 CTGGCGCGCCCAAGGCGCGGACGACGAGAGGTGAGACCTGTCTGAGGAGTGGGCGCAC 2296
DB 2221 CTGGCGCGCCCAAGGCGCGGACGACGAGAGGTGAGACCTGTCTGAGGAGTGGGCGCAC 2280
QY 2297 ATCAACTCTGACAGGCTCAAGTTCCAGGGCGGCGCATGGCCCGCGCCACACTCTCTGCG 2356

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DB 2281 ATCAACTCTGACAGGCTCAAGTTCCAGGGCGGCGCATGGCCCGCGCCACACTCTCTGCG 2340
QY 2357 CGAAGCAAGACCTTG 2371
DB 2341 CGAAGCAAGACCTTG 2355

RESULT 10
ADL67199
ID ADL67199 standard; DNA, 2355 BP.
XX
AC ADL67199;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human 14171 protein kinase coding region.
XX
KW Human, 14171 protein kinase; cancer; immunological disorder;
KW inflammation; heart failure; hypertension; atrial fibrillation;
KW viral disorder; apoptotic disorder; chromosome mapping; tissue typing;
KW predictive medicine; forensic biology; gene; ss.
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 1..2355
FT CDS /*tag=a
FT /product="Human 14171 protein kinase"
FT
PN US2004048305-A1.
XX
PD 11-MAR-2004.
XX
PF 10-SEP-2003; 2003US-06658904.
XX
PR 11-FEB-2000; 2000US-0182096P.
XX
PR 12-FEB-2001; 2001US-00781882.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Kapeller-Libermann R;
XX
DR MPI; 2004-226195/21.
XX
DR P-PSDB; ADL67198.
XX
PT New 14171 protein kinase and nucleic acid, useful for diagnosing or
PT treating diseases with aberrant expression of the 14171 protein kinase,
PT such as cancer, an immunological disorder, inflammation, heart failure
PT and hypertension.
XX
PS Claim 1; SEQ ID NO 3; 62pp; English.
XX
CC The invention provides novel human 14171 protein kinase polypeptides and
CC polynucleotides. The methods and compositions of the present invention
CC are useful for the diagnosis and/or treatment of diseases or conditions
CC associated with aberrant expression or activity of a 14171 protein kinase
CC such as cancer, immunological disorder, inflammation, heart failure,
CC hypertension, atrial fibrillation, viral disorder and apoptotic disorder.
CC The invention can also be used in chromosome mapping, tissue typing,
CC predictive medicine, forensic biology and prognostic assays. The present
CC sequence is human 14171 protein kinase coding region.
XX
SQ Sequence 2355 BP; 464 A; 738 C; 759 G; 394 T; 0 U; 0 Other;

Query Match 61.0%; Score 2355; DB 12; Length 2355;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ATGAGGGCGAGCGGCGGACCCCATGGGCGCTGGGCGTGTGCGGACCTTGACGCGGGC 76
DB 1 ATGAGGGCGAGCGGCGGACCCCATGGGCGCTGGGCGTGTGCGGACCTTGACGCGGGC 60

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QY	77	GAATTCAACGGGCTGGAGAGAGTGGGCTTCGGGCGGCTTTGGGCGAGGTGTACAAGGTGGC	136
Db	61	GAGTTCAACGGGCTGGAGAGAGTGGGCTTCGGGCGGCTTTGGGCGAGGTGTACAAGGTGGC	120
QY	137	CATGTCCACTGGAAAGACCTGGCTGGCCATCAAGTGCTCGCCAGCTGCACGTGACGAC	196
Db	121	CATGTCCACTGGAAAGACCTGGCTGGCCATCAAGTGCTCGCCAGCTGCACGTGACGAC	180
QY	197	AGGAGCCCATGAGAGCTTTTGGAAAGACCAGAAGATGAGATGAGCAAGTTTCGCTAC	256
Db	181	AGGAGCCCATGAGAGCTTTTGGAAAGACCAGAAGATGAGATGAGCAAGTTTCGCTAC	240
QY	257	ATCTGCTGTGTATGGCATCTGCCGCAACTGTCCGCTGTGTATGAGTACATGAG	316
Db	241	ATCTGCTGTGTATGGCATCTGCCGCAACTGTCCGCTGTGTATGAGTACATGAG	300
QY	317	AACGGCTCCCTGGAAAGACTGTGGCTTCGGAGCCATTGGCCATGGGATTCCTCGGTTCCGA	376
Db	301	AACGGCTCCCTGGAAAGACTGTGGCTTCGGAGCCATTGGCCATGGGATTCCTCGGTTCCGA	360
QY	377	ATCATCCACAGACGGCGGTGGGACATGAATCTTCGCACTGCATGAGCCCGCCACCTCTG	436
Db	361	ATCATCCACAGACGGCGGTGGGACATGAATCTTCGCACTGCATGAGCCCGCCACCTCTG	420
QY	437	CACCTGGAAGCTCAAGCCCGCGCAACTCTGCTGTGATGCCCACTACACGTCAAGATTTCT	496
Db	421	CACCTGGAAGCTCAAGCCCGCGCAACTCTGCTGTGATGCCCACTACACGTCAAGATTTCT	480
QY	497	GATTTTGGTCTGGCCAACTGCAACGGGGTGTCCACTCGCATGACCTCAGCATGGAATGGC	556
Db	481	GATTTTGGTCTGGCCAACTGCAACGGGGTGTCCACTCGCATGACCTCAGCATGGAATGGC	540
QY	557	CTGTTTGGCACAATGCGCTACCTCCCTCCAGAGCGCATCAGGAGAGAAAGCCGCTCTTC	616
Db	541	CTGTTTGGCACAATGCGCTACCTCCCTCCAGAGCGCATCAGGAGAGAAAGCCGCTCTTC	600
QY	617	GACACCAAGCAGATGTATACAGCTTTGCGATCGTCACTTGGGGCGTGTCTACACAGAAG	676
Db	601	GACACCAAGCAGATGTATACAGCTTTGCGATCGTCACTTGGGGCGTGTCTACACAGAAG	660
QY	677	AAGCGTTTGCAGATGAGAGAAACATCTTGACATCATGTGTGAAGGTGTGAAGGGCAC	736
Db	661	AAGCGTTTGCAGATGAGAGAAACATCTTGACATCATGTGTGAAGGTGTGAAGGGCAC	720
QY	737	CGCCCCAGAGCTCGCGCCGCTGTGCAGAGCCCGGCGCGGCTGACGCACTGTATACG	796
Db	721	CGCCCCAGAGCTCGCGCCGCTGTGTGCAGAGCCCGGCGCGGCTGACGCACTGTATACG	780
QY	797	CTCATGCAAGCGGTGTGCGACAGGGGATCCGCGAGTTAAGGCCACCTTTCAGAAATTAAT	856
Db	781	CTCATGCAAGCGGTGTGCGACAGGGGATCCGCGAGTTAAGGCCACCTTTCAGAAATTAAT	840
QY	857	TTTGAACCGAGAGACCTGTGTGAAGAAAGCTGTATGACGAATGGAAGAAACTGTCTATGAT	916
Db	841	TTTGAACCGAGAGACCTGTGTGAAGAAAGCTGTATGACGAATGGAAGAAACTGTCTATGAT	900
QY	917	CTGGAAGTGAAGAAAGCCCCCGGAGGCCAGAGAGCGAGTGTGCTGCGAGGCTCAAGCGG	976
Db	901	CTGGAAGTGAAGAAAGCCCCCGGAGGCCAGAGAGCGAGTGTGCTGCGAGGCTCAAGCGG	960
QY	977	GCGCTGCGCCCACTTGATTAACACTACAGCCTCTCCAGACTTCTCTCAAGACTGGAC	1036
Db	961	GCGCTGCGCCCACTTGATTAACACTACAGCCTCTCCAGACTTCTCTCAAGACTGGAC	1020
QY	1037	TTCTGAGATTTCCCAAGGCTGTCAAGGGCCCCGAGAGACTCAACCCCAAGTCTCTGAGATCC	1096
Db	1021	TTCTGAGATTTCCCAAGGCTGTCAAGGGCCCCGAGAGACTCAACCCCAAGTCTCTGAGATCC	1080
QY	1097	AAGCTGACCATCGTCCGGCAGTGGAGAAAGGCTCTGGGGGTGTCTCGTGGTGAATCCGCGC	1156
Db	1081	AAGCTGACCATCGTCCGGCAGTGGAGAAAGGCTCTGGGGGTGTCTCGTGGTGAATCCGCGC	1140
QY	1157	TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGAAACTTCAACAGCGATCTG	1216

Db	1141	TTCTCTTCAGAGATCACTGTCCCTGTCTCTTTAGCGGAACTTACAAGAGATCTG	1200
Qy	1217	GGTACCAACAGACGTCCAGAAAGAGCTTTGTGATGCACTGTTCCTGGACAACAAC	1276
Db	1201	GGTACCAACAGACGTCCAGAAAGAGCTTTGTGATGCACTGTTCCTGGACAACAAC	1260
Qy	1277	AAACTGATGAAGATCTTCACAGCCGACAGACGTGACCTTGGCACTGGACAAGCGGTGCCAGC	1336
Db	1261	AAACTGATGAAGATCTTCACAGCCGACAGACGTGACCTTGGCACTGGACAAGCGGTGCCAGC	1320
Qy	1337	CTGCTGCACCTGGGCGGTGGAGGCGGGACAAGAGAGTGCACAAGTGGCTCTCTCAAC	1396
Db	1321	CTGCTGCACCTGGGCGGTGGAGGCGGGACAAGAGAGTGCACAAGTGGCTCTCTCAAC	1380
Qy	1397	AATGCCAACCCCAACCTTGAGCAACCGTAGGGGCTCAACCCCGTTGCAATAGCCGTGTAG	1456
Db	1381	AATGCCAACCCCAACCTTGAGCAACCGTAGGGGCTCAACCCCGTTGCAATAGCCGTGTAG	1440
Qy	1457	AGAGAGGTGGCGGGGTGTGTGTGAAGCTCTGTGGCAAGGAAGATCACTGTCTAAAGCCAAAG	1516
Db	1441	AGAGAGGTGGCGGGGTGTGTGTGAAGCTCTGTGGCAAGGAAGATCACTGTCTAAAGCCAAAG	1500
Qy	1517	GATGAGGACCACTGGACAAGCCCTCACTTTGCAAGCCCAAGACGGGAGATGAATCTAGACA	1576
Db	1501	GATGAGGACCACTGGACAAGCCCTCACTTTGCAAGCCCAAGACGGGAGATGAATCTAGACA	1560
Qy	1577	CGGCTGCTGTTGGAGAAAGAACGCTTCGATCAACAGAGTGAATCTTTGAGGGCCGAGCC	1636
Db	1561	CGGCTGCTGTTGGAGAAAGAACGCTTCGATCAACAGAGTGAATCTTTGAGGGCCGAGCC	1620
Qy	1637	ATGCACTGTGCGCTTGCAAGCAAGGACAGAGAAATTCGTGCGCATCTCTGCGCCGAAGGC	1696
Db	1621	ATGCACTGTGCGCTTGCAAGCAAGGACAGAGAAATTCGTGCGCATCTCTGCGCCGAAGGC	1680
Qy	1697	GTGACACGTGAACCTGCAAGGCGAAGGATGCCGGCTGCCACTGCACTAACGCTGCCTGGAG	1756
Db	1681	GTGACACGTGAACCTGCAAGGCGAAGGATGCCGGCTGCCACTGCACTAACGCTGCCTGGAG	1740
Qy	1757	GGCCACCTGACCCTATGCTCAAGCTGTGCGCAAGAGCCGCGGGGTGAGTGTGAACGCCAG	1816
Db	1741	GGCCACCTGACCCTATGCTCAAGCTGTGCGCAAGAGCCGCGGGGTGAGTGTGAACGCCAG	1800
Qy	1817	ACGCTGATGAGGAGAGACGCCAATTGACCTTGGCCGCAAGCCGCGGCACTTACCGGTGGCC	1876
Db	1801	ACGCTGATGAGGAGAGACGCCAATTGACCTTGGCCGCAAGCCGCGGCACTTACCGGTGGCC	1860
Qy	1877	CGCATCTCTCACTGACCTGTGCTCCGACGCTCAACGCTGCAACCTGCTGGACAAGACCC	1936
Db	1861	CGCATCTCTCACTGACCTGTGCTCCGACGCTCAACGCTGCAACCTGCTGGACAAGACCC	1920
Qy	1937	CTGCACGTGACCGCGAGACCGGGGACAAGACACTGCAAGGCTGCTCTGCACTGAGGC	1996
Db	1921	CTGCACGTGACCGCGAGACCGGGGACAAGACACTGCAAGGCTGCTCTGCACTGAGGC	1980
Qy	1997	GCTGGCAAGAGAGCCGTGACCTCAAGCGGCTTACAACCGCTCTTGCACTTGGCTGCCCAAC	2056
Db	1981	GCTGGCAAGAGAGCCGTGACCTCAAGCGGCTTACAACCGCTCTTGCACTTGGCTGCCCAAC	2040
Qy	2057	GGACACCTGGGCACTGTCAAGCTGCTTGTCAAGAGAGAGGCGATATGTGCTGGCCCGGGGA	2116
Db	2041	GGACACCTGGGCACTGTCAAGCTGCTTGTCAAGAGAGAGGCGATATGTGCTGGCCCGGGGA	2100
Qy	2117	CCCTGAAACAGACGCGCGCTGCACTGTGCTGCCGCCCAAGGCACTCGAGAGTGGTGAAG	2176
Db	2101	CCCTGAAACAGACGCGCGCTGCACTGTGCTGCCGCCCAAGGCACTCGAGAGTGGTGAAG	2160
Qy	2177	GAGTTGTGTCAAGCGCGGATGTCAATTGACCTGTTTCAAGACAGGGGCTCAAGCGCTGTGAC	2236
Db	2161	GAGTTGTGTCAAGCGCGGATGTCAATTGACCTGTTTCAAGACAGGGGCTCAAGCGCTGTGAC	2220
Qy	2237	CTGGCGGCGCAAGGCGCGGCAAGCAAGCGGTGAAGACTCTGCTCAAGGCAATGGGCGCAC	2296

DB 2221 CTGCGCCGCCAAGGCGCGGACGACAGACGAGTGAAGACTGTGCTGACGAGGATGGGCGCAC 2280
QY 2297 ATCAACCTGCGAGAGGCTCAAGTTCCAGGGCGGCGCCATGCGCCCGCCACACTCTTGCGG 2356
DB 2281 ATCAACCTGCGAGAGGCTCAAGTTCCAGGGCGGCGCCATGCGCCCGCCACACTCTTGCGG 2340
QY 2357 CGAAGCAGAGCCTAG 2371
DB 2341 CGAAGCAGAGCCTAG 2355

RESULT 11
AAD64343
ID AAD64343 standard; DNA; 2355 BP.
XX
AC AAD64343;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human protein kinase C-associated kinase (PKK) variant DNA #5.
XX
KW Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN US2003199462-A1.
XX
PD 23-OCT-2003.
XX
PE 23-APR-2002; 2002US-00128174.
XX
PR 23-APR-2002; 2002US-00128174.
XX
PA (NDUNE/) NDUNEZ G.
PA (INOH/) INOHARA N.
PA (MUTO/) MUTO A.
XX
PI Nunez G, Inohara N, Muto A;
DR WPI; 2003-852808/79.
XX
PT New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKK induced NF-KB activation for treating hyperglycemia.
XX
PS Disclosure: SEQ ID NO 18; Opp; English.
XX
CC The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKK induced NF-kappaB activation for treating hyperglycemia.
CC The invention is also used in gene therapy. The present sequence is human
CC PKK variant DNA
XX
SQ Sequence 2355 BP; 463 A; 740 C; 761 G; 391 T; 0 U; 0 Other;

Query Match 60.3%; Score 2327.2; DB 10; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 17 ATGAGGGGAGCGCGGAGCCCAATGGGCGCTGGGCGTGTGCGACCTTGACGCGGCG 76
DB 1 ATGAGGGGAGCGCGGAGCCCAATGGGCGCTGGGCGTGTGCGACCTTGACGCGGCG 60
QY 77 GAGTTCAGCGGCTGGGAGGAGGTGGGCTGGGCGGCTTCGGCAGGTGACAAAGTGGCG 136
DB 61 GAGTTCAGCGGCTGGGAGGAGGTGGGCTGGGCGGCTTCGGCAGGTGACAAAGTGGCG 120
QY 137 CATGTCACTGAGAAAGCTGTGGCATCAAGTGTGCTGCGCAGGCTGCACTGACGAC 196

DB 121 CATGTCACTGAGAAAGCTGTGGCATCAAGTGTGCTGCGCAGGCTGCACTGACGAC 180
QY 197 AGGAGAGGCAATGAGGCTTTTGAAAGAGCCAGAAAGATGAGATGGCAAGTTTGGTAC 256
DB 181 AGGAGAGGCAATGAGGCTTTTGAAAGAGCCAGAAAGATGAGATGGCAAGTTTGGTAC 240
QY 257 ATCTGCTGTGTATGAGCATCTGCGCGGAACTGTGCGGCTGTGATGAGTACATGAG 316
DB 241 ATCTGCTGTGTATGAGCATCTGCGCGGAACTGTGCGGCTGTGATGAGTACATGAG 300
QY 317 ACGGAGCTCCCTGGAAGAGCTGTGCTTGAGAGCATTTGCCATGGATTCGGTTCGA 376
DB 301 ACGGAGCTCCCTGGAAGAGCTGTGCTTGAGAGCATTTGCCATGGATTCGGTTCGA 360
QY 377 ATCATCAAGAGAGCGGAGTGGAGTGAAGTCTGTCGATGAGTGGCCCGGCACTGCTG 436
DB 361 ATCATCAAGAGAGCGGAGTGGAGTGAAGTCTGTCGATGAGTGGCCCGGCACTGCTG 420
QY 437 CACCTGAGACTCAAGCCCGGCAATCTGCTGAGTCCGACTACAGTCAAGATTTCT 496
DB 421 CACCTGAGACTCAAGCCCGGCAATCTGCTGAGTCCGACTACAGTCAAGATTTCT 480
QY 497 GATTTGGTGTGGCAATGTCGACGAGCTGTCCCATCTGCAATGACTTCAGATGAGC 556
DB 481 GATTTGGTGTGGCAATGTCGACGAGCTGTCCCATCTGCAATGACTTCAGATGAGC 540
QY 557 CTGTTTGGCAATGCGCTACCTCCCTCCAGAGGCAATCAAGGAGAGCGGCTTC 616
DB 541 CTGTTTGGCAATGCGCTACCTCCCTCCAGAGGCAATCAAGGAGAGCGGCTTC 600
QY 617 GACACCAAGCAGATGTATACAGCTTTCGATCTGTCGAGGCTGTCTACACAGAG 676
DB 601 GACACCAAGCAGATGTATACAGCTTTCGATCTGTCGAGGCTGTCTACACAGAG 660
QY 677 AAGCGTTTGCAGATGAGAAAGACATCTCTGCACTCATGTGAAAGTGTGAGGCGCAC 736
DB 661 AAGCGTTTGCAGATGAGAAAGACATCTCTGCACTCATGTGAAAGTGTGAGGCGCAC 720
QY 737 CGCCCGAGGCTGGCGCGGAGTGCAGAGCCCGGCGGCGCTGCAGCAGCTGATAGC 796
DB 721 CGCCCGAGGCTGGCGCGGAGTGCAGAGCCCGGCGGCGCTGCAGCAGCTGATAGC 780
QY 797 CTCATGAGCGGCTGTGCGAGAGGAGATCCGCGAGTTAGGCGCACTTCCAGAAATTA 856
DB 781 CTCATGAGCGGCTGTGCGAGAGGAGATCCGCGAGTTAGGCGCACTTCCAGAAATTA 840
QY 857 TCTGAACCGAGAGCTGTGTGAAAGCTGATGACGAGTGAAGAAATGCTCATGAT 916
DB 841 TCTGAACCGAGAGCTGTGTGAAAGCTGATGACGAGTGAAGAAATGCTCATGAT 900
QY 917 CTGAGAGTGAAGAGCCCGCGGAGCCAGAGGAGGAGTGGCTGCGAGGCTCAAGCGG 976
DB 901 CTGAGAGTGAAGAGCCCGCGGAGCCAGAGGAGGAGTGGCTGCGAGGCTCAAGCGG 960
QY 977 GCTCTGCCCCCACTTGTGATACGACTACAGCTTCCAGAGCTTCTCAAGCTGAGC 1036
DB 961 GCTCTGCCCCCACTTGTGATACGACTACAGCTTCCAGAGCTTCTCAAGCTGAGC 1020
QY 1037 TCTGAGATTTCCAGAGCTGTGAGAGGCGCCGAGAGGCTCAAGCGGAGCTCTGAGTCC 1096
DB 1021 TCTGAGATTTCCAGAGCTGTGAGAGGCGCCGAGAGGCTCAAGCGGAGCTCTGAGTCC 1080
QY 1097 AAGCTGCATCTGTCGAGTGGAGAGAGGCTCTGAGGAGTCTGAGTGGAGCTCGGCC 1156
DB 1081 AAGCTGCATCTGTCGAGTGGAGAGAGGCTCTGAGGAGTCTGAGTGGAGCTCGGCC 1140
QY 1157 TTCTCTTCCAGAGGATCACTGTGCTCTTTTGAAGCGGAACTTCAACAGGAGATCTG 1216
DB 1141 TTCTCTTCCAGAGGATCACTGTGCTCTTTTGAAGCGGAACTTCAACAGGAGATCTG 1200
QY 1217 GGTACCAAGAGGCTCCAGAAAGAAAGCTTGTGATGTCATGTGTCC -GGACACGAG 1275
DB 1201 GGTACCAAGAGGCTCCAGAAAGAAAGCTTGTGATGTCATGTGTCCGGGAGACACGAG 1259

QY	1276	CAAACTGATGAAGATCTCTGCAGCGCCGACAGACCTGTGACACTTGGCACTGTGACAGCGGTTCAG	1335
Db	1260	CAAACTGATGAAGATCTCTGCAGCGCCGACAGAGTGTGACCTGTGACACTTGGCAAGCGGTTCAG	1319
QY	1336	CCTGCTGTCACCTGGCGGTGAGAGCGCGGACAAAGAGATGCGCCAAATGATGCTCTCTCAA	1395
Db	1320	CCTGCTGTCACCTGGCGGTGAGAGCGCGGACAAAGAGATGCGCCAAATGATGCTCTCTCAA	1379
QY	1396	CAATGCCAACTCCAACTGTAGCAACCGTAGGGGCTCCACCCGTTTGCACATGCGCTGTGA	1455
Db	1380	CAATGCCAACTCCAACTGTAGCAACCGTAGGGGCTCCACCCGTTTGCACATGCGCGTGTGA	1439
QY	1456	GAGGAGGGGTGGGGGTGTGCTGTGAGATCTCTGTGGCAACGGAAGATCAATGTCAACGCTCAA	1515
Db	1440	GAGGAGGGGTGGGGGTGTGCTGTGAGATCTCTGTGGCAAGGAAGATCAATGTCAACGCTCAA	1499
QY	1516	GGATGAGGACCAATGTGACAGCGCTTCACTTTTGCAGCGCCAGAACCGGAGATGATGTAGAC	1575
Db	1500	GGATGAGGACCAATGTGAGCAGCGCTTCACTTTTGCAGCGCCAGAACCGGAGATGATGTAGAC	1559
QY	1576	ACGGCTGCTGTTTGGAGAAAGACGCTCGGTCAACGAGGTGGAATTTTGAGGGCCGGAAGCC	1635
Db	1560	ACGGCTGCTGTTTGGAGAAAGACGCTCGGTCAACGAGGTGGAATTTTGAGGGCCGGAAGCC	1619
QY	1636	CATGCAAGTGGCTTCCGACAGCGGACAGAGAAATTCGTGGGCATTCCTGTGCGCCGAGG	1695
Db	1620	CATGCAAGTGGCTTCCGACAGCGGACAGAGAAATTCGTGGGCATTCCTGTGCGCCGAGG	1679
QY	1696	CGTGGACGTGAGCGCTTGCAGAGGCAAGAGATCTGTGCTGCACTTGCATACGCTGCTTGGCA	1755
Db	1680	CGTGGACGTGAGCGCTTGCAGAGGCAAGAGATCTGTGCTGCACTTGCATACGCTGCTTGGCA	1739
QY	1756	GGGCGCACTTCGCCCATTCGTCAAGCTGTGGCCAAAGACGCGGGGGATGTGAAACGCCA	1815
Db	1740	GGGCGCACTTCGCCCATTCGTCAAGCTGTGGCCAAAGACGCGGGGGATGTGAAACGCCA	1799
QY	1816	GACGCTGATGAGAGAGACGCCATTTCACCTGTGCGCACAGCGCGGGCACTAACGCGTGGC	1875
Db	1800	GACGCTGATGAGAGAGAGACGCCATTTCACCTGTGCGCACAGCGCGGGCACTAACGCGTGGC	1859
QY	1876	CCGCATCTCTCATGCACTGTGTCTCCGACGTCAACGTCTTGCAGCGCTTGGCAACAGACCC	1935
Db	1860	CCGCATCTCTCATGCACTGTGTCTCCGACGTCAACGTCTTGCAGCGCTTGGCAACAGACCC	1919
QY	1936	CCTGCAACGTGGCGCGGAGAACCGGGCAACAGAGCACTGCAGAGCTGTCTGTACATCGGGG	1995
Db	1920	CCTGCAACGTGGCGCGGAGAACCGGGCAACAGAGCACTGCAGAGCTGTCTGTACATCGGGG	1979
QY	1996	CGCTGGCAAGAGAGCGCTGACCTCAAGCGGCTAACCGCTGTGCACTTGGCTGCCCGCAA	2055
Db	1980	CGCTGGCAAGAGAGCGCTGACCTCAAGCGGCTAACCGCTGTGCACTTGGCTGCCCGCAA	2039
QY	2056	CGGACACCTTGGGCACTGTCAACATCTGTGTGAGAGAGAAAGCGAATGTGCTGGGCCCGGG	2115
Db	2040	CGGACACCTTGGGCACTGTCAACATCTGTGTGAGAGAGAAAGCGAATGTGCTGGGCCCGGG	2099
QY	2116	ACCCCTGAACCAAGACGAGCGCTGCACTGTGCTGCGCCCAACCGGACCTCGAGAGTGTGTGA	2175
Db	2100	ACCCCTGAACCAAGACGAGCGCGCTGCACTGTGCTGCGCCCAACCGGAGCTCGAGAGTGTGTGA	2159
QY	2176	GGAGTTTGTCAAGCGCCGATGTCAATTGACTGTTTTCAACAGACAGGGGCTCAAGCGCTGTCA	2235
Db	2160	GGAGTTTGTCAAGCGCCGATGTCAATTGACTGTTTTCAACAGACAGGGGCTCAAGCGCTGTCA	2219
QY	2236	CGTGGCGGCGCAAGGCGCGGCAACGACAGCGGTGAGACTTGTCTCAAGGCAATGGGGCCCA	2295
Db	2220	CGTGGCGGCGCAAGGCGCGGCAACGACAGCGGTGAGACTTGTCTCAAGGCAATGGGGCCCA	2279
QY	2296	CATCAACCTTGCAGAGGCTCAAGATTCCAGGGCGAGCATAGGCGCCGCGCGCCACACTCTTGC	2355
Db	2280	CATCAACCTTGCAGAGGCTCAAGATTCCAGGGCGAGCATAGGCGCCGCGCGCCACACTCTTGC	2339

QY	2356	GGGAAGCAAGCCTTAG	2371
Db	2340	GCGAAGCAAGCCTTAG	2355
RESULT 12			
ID	AAD64340	standard; DNA; 2355 BP.	
XX	AC	AAD64340;	
XX	DT	12-FEB-2004 (first entry)	
XX	DE	Human protein kinase C-associated kinase (PKC) variant DNA #2.	
XX	KW	Human; cellular signalling; protein kinase C-associated kinase; PKC; DIK;	
XX	RV	RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.	
XX	OS	Homo sapiens.	
XX	PN	US2003199462-A1.	
XX	PD	23-OCT-2003.	
XX	PF	23-APR-2002; 2002US-00128174.	
XX	PR	23-APR-2002; 2002US-00128174.	
XX	PA	(NUNEZ/) NUNEZ G.	
XX	PA	(INOCH/) INOHARA N.	
XX	PI	(MUTO/) MUTO A.	
XX	PI	Nunez G, Inohara N, Muto A;	
XX	DR	WPI; 2003-852808/79.	
PT	New nucleic acid encoding RICK3, useful in preparing a composition for		
PT	inhibiting PKC induced NF-KB activation for treating hyperglycemia.		
XX	Disclosure; SEQ ID NO 15; Opp; English.		
XX	The invention relates to methods and compositions for modulating cellular		
XX	signalling. In particular the present invention relates to protein kinase		
XX	C-associated kinase (PKC/DIK) and RICK3 proteins and nucleic acids		
XX	encoding such proteins. The invention further relates to the use of PKC		
XX	and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid		
XX	molecules of the invention are useful in preparing a composition for		
XX	inhibiting PKC induced NF-KappaB activation for treating hyperglycaemia.		
XX	The invention is also used in gene therapy. The present sequence is human		
XX	PKC variant DNA		
XX	Sequence 2355 BP; 462 A; 740 C; 761 G; 392 T; 0 U; 0 Other;		
QY	Query Match	60.3%; Score 2327.2; DB 10; Length 2355;	
Db	Best Local Similarity	99.8%; Pred. No. 0;	
Db	Matches 2351; Conservative	0; Mismatches 3; Indels 2; Gaps 2	
QY	17	ATGGAAGGCGAAGCGGGACCCCAATGGGCGCTGGCGGCGGACCTTGGACGCGGCG	76
Db	1	ATGGAAGGCGAAGCGGGACCCCAATGGGCGCTGGCGGCGGACCTTGGACGCGGCG	60
QY	77	GAGTTCACGCGGCTGGGAGAAGGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAGGTGCGC	136
Db	61	GAGTTCACGCGGCTGGGAGAAGGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAGGTGCGC	120
QY	137	CATGTCCACTGGAGAAGCTGGCTGCGCATCAAGTCTGCGCCAGCTTGACGTGACGAC	196
Db	121	CATGTCCACTGGAGAAGCTGGCTGCGCATCAAGTCTGCGCCAGCTTGACGTGACGAC	180
QY	197	AAGGAGCGGATGAGACTTTTGGAAAGCAAGCAAGATGAGATGAGGCGCAAGTTTGGCTAC	256
Db	181	AAGGAGCGGATGAGACTTTTGGAAAGCAAGCAAGATGAGATGAGGCGCAAGTTTGGCTAC	240

AAD64341	ID	AAD64341 standard; DNA; 2355 BP.
XX AC	AA	AAD64341;
XX DT	DT	12-FEB-2004 (first entry)
DE DE	DE	Human protein kinase C-associated kinase (PKK) variant DNA #3.
KW KW	KW	Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
XX XX	XX	RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; de.
OS OS	OS	Homo sapiens.
XX PN	PN	US200319462-A1.
PD PD	PD	23-OCT-2003.
XX PF	PF	23-APR-2002; 2002US-00128174.
XX PR	PR	23-APR-2002; 2002US-00128174.
XX PA	PA	(NINE/) NUNEZ G. (INOH/) INOHARA N. (MUTO/) MUTO A.
XX PI	PI	Nunez G, Inohara N, Muto A;
XX DR	DR	WPI; 2003-852808/79.
PT PT	PT	New nucleic acid encoding RICK3, useful in preparing a composition for inhibiting PKC induced NF-KB activation for treating hyperlycemia.
XX PS	PS	Disclosure; SEQ ID NO 16; Opp; English.
CC CC	CC	The invention relates to methods and compositions for modulating cellular signalling. In particular the present invention relates to protein kinase C-associated kinase (PKC/DIK) and RICK3 proteins and nucleic acids encoding such proteins. The invention further relates to the use of PKK and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid molecules of the invention are useful in preparing a composition for inhibiting PKC induced NF-kappaB activation for treating hyperglycaemia. The invention is also used in gene therapy. The present sequence is human PKK variant DNA
XX SQ	SQ	Sequence 2355 BP; 462 A; 739 C; 762 G; 392 T; 0 U; 0 Other;
Query Match		60.3%; Score 2327.2; DB 10; Length 2355;
Best Local Similarity		99.8%; Pred. No. 0;
Matches 2351; Conservative		0; Mismatches 3; Indels 2; Gaps 2
OY	17	ATGAGAGGGGAGCGCGCGGACCCCATGCGGCGCTGCGGCACCTTCGACGGCGGC 76
DB	1	ATGAGAGGGGAGCGCGCGGACCCCATGCGGCGCTGCGGCCTGCGCACCTTCGACGGCGGC 60
OY	77	GAGTTCAACGGGCTGGGAGAAGGTGGGCTCGGCGGCTTTCGGGACGGTGTAACAAGTGCGC 136
DB	61	GAGTTCAACGGGCTGGGAGAAGGTGGGCTCGGCGGCTTTCGGGACGGTGTAACAAGTGCGC 120
OY	137	CATGTCACATGGGAAGACTGGCTGGGCATCAAGTGCTGCCCCAGCCTGCACGTCGACGAC 196
DB	121	CATGTCACATGGGAAGACTGGCTGGGCATCAAGTGCTGCCCCAGCCTGCACGTCGACGAC 180
OY	197	AGGAGACCGCATGAGACTTTTGGAAAAGCAAGCAAGAAATGAGATGGCCAAAGTTGGCTAC 256
DB	181	AGGAGACCGCATGAGACTTTTGGAAAAGCAAGCAAGAAATGAGATGGCCAAAGTTGGCTAC 240
OY	257	ATCCTGCTGTGTATAGGCATCTGCACCAGAACCTGTGCGCTGGTCAATGAGTACATGAG 316
DB	241	ATCCTGCTGTGTATAGGCATCTGCACCAGAACCTGTGCGCTGGTCAATGAGTACATGAG 300
OY	317	ACGGGCTCCCTGGAAGACTGTGCGCTTGGAGCCATTGCAATGGGATCTCGGGTTCGGA 376

Db	301	ACGGGCTCCCTGGAAAAGCTGCTGCTTCGAGGCCATTGGCCATGGGATCTCCGGTTCCGA	360
Oy	377	ATCATTCACGAGACGGGCGGTGGGCAATGAACCTTCGCACTGCACTGAGTGGCCCGGCACCTCTG	436
Db	361	ATCATTCACGAGACGGGCGGTGGGCAATGAACCTTCGCACTGCACTGAGTGGCCCGGCACCTCTG	420
Oy	437	CACCTGGAAGCTCAGACCCCGGCAACATCTCTGCTGGATGGCCACTACCACTTCAAGATTTCT	496
Db	421	CACCTGGAAGCTCAGACCCCGGCAACATCTCTGCTGGATGGCCACTACCACTTCAAGATTTCT	480
Oy	437	GATTTTGGTCTGGCCCAAGTGCAGAGGGGCGTGTCCCACTGGCATGACCTCAGCATGATGGC	556
Db	481	GATTTTGGTCTGGCCCAAGTGCAGAGGGGCGTGTCCCACTGGCATGACCTCAGCATGATGGC	540
Oy	557	CTGTTTGGCACAATGCGCTACCTCCCTCCAGAGCGCATCGAGGAGAAAGACCGGCTCTTC	616
Db	541	CTGTTTGGCACAATGCGCTACCTCCCTCCAGAGCGCATCGAGGAGAAAGACCGGCTCTTC	600
Oy	617	GACACCAAGCAGATGTATACGCTTTGGGATGTATCTGGGGGGTGTCTCAACAGAA	676
Db	601	GACACCAAGCAGATGTATACGCTTTGGGATGTATCTGGGGGGTGTCTCAACAGAA	660
Oy	677	AAGCGGTTTGCAGATGAGAAAGAAACATCCGTCACATATGTTAAAGGTGTGAAGGGCCAC	726
Db	661	AAGCGGTTTGCAGATGAGAAAGAAACATCCGTCACATATGTTAAAGGTGTGAAGGGCCAC	720
Oy	737	CGCCCGGAGCTGCCCCCGCTGTGCAGAGCCCGGCGCGCTGCAGCCACTGATACGC	796
Db	721	CGCCCGGAGCTGCCCCCGCTGTGCAGAGCCCGGCGCGCTGCAGCCACTGATACGC	780
Oy	797	CTCATGCAAGCGGTGCTGCGAGGGGGGATCCGCGAGTTTAGGCCCACTTCCAGAAATTAAT	856
Db	781	CTCATGCAAGCGGTGCTGCGAGGGGGATCCGCGAGTTTAGGCCCACTTCCAGAAATTAAT	840
Oy	857	TCTGAAACCGAGGACCTGTGTGAAAAAGCCTGATGACGAAGTGAAGAAATCTGCTCATGAT	916
Db	841	TCTGAAACCGAGGACCTGTGTGAAAAAGCCTGATGACGAAGTGAAGAAATCTGCTCATGAT	900
Oy	917	CTGACAGTGAAGAGCCCCCGGAGGCCAGAGCGAGAGTGTGTCTGCGAGGCTCAAGCGG	976
Db	901	CTGACAGTGAAGAGCCCCCGGAGGCCAGAGCGAGAGTGTGTCTGCGAGGCTCAAGCGG	966
Oy	977	GCGTCTGCCCCCACTTGGATTAACGACTACAGCTTCCGAGCTTCTCAACAGCTGGAC	1033
Db	961	GCGTCTGCCCCCACTTGGATTAACGACTACAGCTTCCGAGCTTCTCAACAGCTGGAC	1020
Oy	1037	TCTGAGATTTCCCAAGGCTGTGAGGGGCCCCGAGAGGCTCAGCCGAGACTCTCTGAGTCC	1093
Db	1021	TCTGAGATTTCCCAAGGCTGTGAGGGGCCCCGAGAGGCTCAGCCGAGACTCTCTGAGTCC	1080
Oy	1097	AAGCTGCGCATCGTCCGGCAGTGGGAAAGGCTCTCGGGGGGTGTCTCGGTGACCTCGGC	1155
Db	1081	AAGCTGCGCATCGTCCGGCAGTGGGAAAGGCTCTCGGGGGGTGTCTCGGTGACCTCGGC	1144
Oy	1157	TTCTCTTTCAGAGATCACTGTGCTGTCTTTAGCGGGAACTTCAACAGCGATCTG	1221
Db	1141	TTCTCTTTCAGAGATCACTGTGCTGTCTTTAGCGGGAACTTCAACAGCGATCTG	1200
Oy	1217	GGTACCAAGACCTTCAGAAAGAAAGCTTGGATGTGCACTGTGTTC - GGGACACAG	1272
Db	1201	GGTACCAAC - AGACGTTCAGAAAGAAAGCTTGGATGTGCACTGTGTTC - GGGACACAG	1253
Oy	1276	CAAACTGATGATCTCTCAGCCCGCAGGACGTGACCTTGACCTTGACACAGCGGTGCAG	1333
Db	1260	CAAACTGATGATCTCTCAGCCCGCAGGACGTGACCTTGACCTTGACACAGCGGTGCAG	1313
Oy	1336	CCTGCTGCACCTGGCGGTGGAAGGCCGGGCAAGAGATGCGCCAAATGGCTGTGCTCA	1393
Db	1320	CCTGCTGCACCTGGCGGTGGAAGGCCGGGCAAGAGATGCGCCAAATGGCTGTGCTCA	1377
Oy	1396	CAATGCAACCCCAACCTGAGCAACGATGAGGGCTCAACCCCGTTCACATGGCCGTGGA	1451
Db	1380	CAATGCAACCCCAACCTGAGCAACGATGAGGGCTCAACCCCGTTCACATGGCCGTGGA	1433

QY 1456 GAGGAGGTTGCGGGGTGTCGTGAGCTCTCTGCGCAGGAAGATCACTGTCAAGCCAA 1515
DB 1440 GAGGAGGGGTGCGGGGTGTCGTGAGCTCTCTGCGCGGGAAGATCACTGTCAAGCCAA 1499
QY 1516 GGAATGAGGACGAGTGAAGAGCCCTCACTTTGACAGCCCGAAGCGGGAGATGAGTTCAGAC 1575
DB 1500 GGAATGAGGACGAGTGAAGAGCCCTCACTTTGACAGCCCGAAGCGGGAGATGAGTTCAGAC 1559
QY 1576 AGGCTGCTGTTGAGGAAGAACGCTCTGCTCAAGAGGTGACCTTTGAGGGCGGACGCGC 1635
DB 1560 AGGCTGCTGTTGAGGAAGAACGCTCTGCTCAAGAGGTGACCTTTGAGGGCGGACGCGC 1619
QY 1636 CATGACAGTGGCTGCTGACAGGAGGAGGAATATCGTGGCCATCTGCTGCGCGGAGG 1695
DB 1620 CATGACAGTGGCTGCTGACAGGAGGAGGAATATCGTGGCCATCTGCTGCGCGGAGG 1679
QY 1696 CGTGAAGTGAAGCTGACAGGAGGAGATGCTGGCTGCGCACTAGCACTAGCTGCTGACA 1755
DB 1680 CGTGAAGTGAAGCTGACAGGAGGAGATGCTGGCTGCGCACTAGCACTAGCTGCTGACA 1739
QY 1756 GGGGCACTGCGCCATCTGTCAGCTGCTGCGCAAGACCGGGGGTGAAGTGAACGCCCA 1815
DB 1740 GGGGCACTGCGCCATCTGTCAGCTGCTGCGCAAGACCGGGGGTGAAGTGAACGCCCA 1799
QY 1816 GACGCTGATGAGGAGGAGGAGCCCATTTGACCTGGCGCGCAGCGCGGCACTAACCGCTGGC 1875
DB 1800 GACGCTGATGAGGAGGAGGAGCCCATTTGACCTGGCGCGCAGCGCGGCACTAACCGCTGGC 1859
QY 1876 CCGCATCTCATGACCTGTGCTCGACGTCACAGCTGTGACAGCTGTGCGCAGACAGACACC 1935
DB 1860 CCGCATCTCATGACCTGTGCTCGACGTCACAGCTGTGACAGCTGTGCGCAGACAGACACC 1919
QY 1936 CCGTGAAGTGGCTGCGCGGAGACCGGGGACACAGACCTGCGAGGCTGCTCTGCTGCTGAGG 1995
DB 1920 CCGTGAAGTGGCTGCGCGGAGACCGGGGACACAGACCTGCGAGGCTGCTCTGCTGCTGAGG 1979
QY 1996 CGCTGGCAAGGAGGCGCTGACCTGACAGCGGCTACACCGCTGCGACCTGCGCGGCGACA 2055
DB 1980 CGCTGGCAAGGAGGCGCTGACCTGACAGCGGCTACACCGCTGCGACCTGCGCGGCGACA 2039
QY 2056 CCGAACAAGTGGCACTGTCAAGCTGCTGTCGAGGAGGAGCGGAGTGTGCTGCGCGGAGG 2115
DB 2040 CCGAACAAGTGGCACTGTCAAGCTGCTGTCGAGGAGGAGCGGAGTGTGCTGCGCGGAGG 2099
QY 2116 ACCCTCTGAACAGACGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2175
DB 2100 ACCCTCTGAACAGACGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2159
QY 2176 GGAATTTGTCACGCGCGATGTCATTTGACCTGTTTCAAGGAGGAGGCTCAAGGCGCTGCA 2235
DB 2160 GGAATTTGTCACGCGCGATGTCATTTGACCTGTTTCAAGGAGGAGGCTCAAGGCGCTGCA 2219
QY 2236 CCGTGGCGCGGAGGCGCGGACGCAAGACGCTGAGGAGCTGCTCAGGCACTGAGGAGGAGG 2295
DB 2220 CCGTGGCGCGGAGGCGCGGACGCAAGACGCTGAGGAGCTGCTCAGGCACTGAGGAGGAGG 2279
QY 2296 CATCAACCTGCAAGGCTCAAGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2355
DB 2280 CATCAACCTGCAAGGCTCAAGTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2339
QY 2356 GGGAGGCAAGACCTGAG 2371
DB 2340 GGGAGGCAAGACCTGAG 2355

RESULT 14
AAD64344
ID AAD64344 standard; DNA; 2355 BP.
XX
AC AAD64344;
XX
DT 12-FEB-2004 (first entry)

XX
DE Human protein kinase C-associated kinase (PKK) variant DNA #6.
XX
KW Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
OS Homo sapiens.
PN US2003199462-A1.
XX
PD 23-OCT-2003.
XX
PF 23-APR-2002; 2002US-00128174.
XX
PR 23-APR-2002; 2002US-00128174.
XX
PA (NUNEZ/) NUNEZ G.
PA (INOH/) INOHARA N.
XX (MUTO/) MUTO A.
PI Nunez G, Inohara N, Muto A;
XX
DR WPI; 2003-852808/79.
XX
PT New nucleic acid encoding RICK3, useful in preparing a composition for
XX inhibiting PKK induced NF-kB activation for treating hyperglycemia.
XX
PS Disclosure; SEQ ID NO 19; Opp; English.
XX
CC The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKK induced NF-kappaB activation for treating hyperglycaemia.
CC The invention is also used in gene therapy. The present sequence is human
XX PKK variant DNA
XX
SQ Sequence 2355 BP; 462 A; 739 C; 762 G; 392 T; 0 U; 0 Other;

Query Match 60.3%; Score 2327.2; DB 10; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 17 ATGAGGCGGAGCGGCGGAGCCCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 76
DB 1 ATGAGGCGGAGCGGCGGAGCCCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
QY 77 GAGTTCAAGGCGGCTGAGGAAGAGTGGGCTGCGGCGGCTTTCGAGGAGGATCAAGATGTCG 136
DB 61 GAGTTCAAGGCGGCTGAGGAAGAGTGGGCTGCGGCGGCTTTCGAGGAGGATCAAGATGTCG 120
QY 137 CATGTCACTGGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 196
DB 121 CATGTCACTGGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 197 AGGAGCGCATGAGAGCTTTTGAAGAAAGCCAAAGATGAGATGAGGCCAAGTTTCGCTAC 256
DB 181 AGGAGCGCATGAGAGCTTTTGAAGAAAGCCAAAGATGAGATGAGGCCAAGTTTCGCTAC 240
QY 257 ATTCGCTGCTGTATGAGATGCTGCGGAGACCTGTCGCGCGCTGTCATGAGATGATACATGAG 316
DB 241 ATTCGCTGCTGTATGAGATGCTGCGGAGACCTGTCGCGCGCTGTCATGAGATGATACATGAG 300
QY 317 AGGAGCTCCCTGGAAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 376
DB 301 AGGAGCTCCCTGGAAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 377 ATCATTCACGAGACGCGCGTGGGATGAATCTTCTGCACTGCACTGAGGCCCGGCACTCTCTG 436
DB 361 ATCATTCACGAGACGCGCGTGGGATGAATCTTCTGCACTGCACTGAGGCCCGGCACTCTCTG 420

QY 437 CACCTGACCTCAAGCCCGGAAACATCTGCTGATGATGCCCACTACCAAGTCAAGATTTCT 496
DB 421 CACCTGACCTCAAGCCCGGAAACATCTGCTGATGATGCCCACTACCAAGTCAAGATTTCT 480
QY 497 GATTTGATCTGGCAAGTGCACAGGGCTGTCCCACTCGATGACCTTCAGCATGATGAC 556
DB 481 GATTTGATCTGGCAAGTGCACAGGGCTGTCCCACTCGATGACCTTCAGCATGATGAC 540
QY 557 CTGTTTGGCAAAATGCGCTTACCTCCCTCGAAGCGCATCAAGGAAAGCCGGCTTTC 616
DB 541 CTGTTTGGCAAAATGCGCTTACCTCCCTCGAAGCGCATCAAGGAAAGCCGGCTTTC 600
QY 617 GACACCAAGCAGATGATACAGCTTTGGATGATGATCTGGGCGGTGCTCAACAGAG 676
DB 601 GACACCAAGCAGATGATACAGCTTTGGATGATGATCTGGGCGGTGCTCAACAGAG 660
QY 677 AAGCGCTTTGACAGATGAGAAACATCTGCAATCATGATGATGATGATGATGATGATGAT 736
DB 661 AAGCGCTTTGACAGATGAGAAACATCTGCAATCATGATGATGATGATGATGATGATGAT 720
QY 737 CGCGCCGAGCTGCGCCCGCTGTGCAAGAGCCCGCGCGCTGACAGCACTGATATGCG 796
DB 721 CGCGCCGAGCTGCGCCCGCTGTGCAAGAGCCCGCGCGCTGACAGCACTGATATGCG 780
QY 797 CTGATGACAGGCTGCTGGCAGGGGGATCCGCGATTAAGCCCACTTCAAGAAATTAAT 856
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XX Human; NF-kappaB activation; hyperglycaemia; gene therapy; gene; de.
KW RICK3;
XX

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XX
XX
XX New nucleic acid encoding RICK3, useful in preparing a composition for
XX inhibiting PKK induced NF-KB activation for treating hyperglycemia.
XX
XX Disclosure: SEQ ID NO 1; Opp; English.
XX
XX The invention relates to methods and compositions for modulating cellular
XX signaling. In particular the present invention relates to protein kinase
XX C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
XX encoding such proteins. The invention further relates to the use of PKK
XX and RICK3 proteins in modulating NF-kappaB signaling. Nucleic acid
XX molecules of the invention are useful in preparing a composition for
XX inhibiting PKK induced NF-kappaB activation for treating hyperglycemia.
XX The invention is also used in gene therapy. The present sequence is human
XX PKK DNA
XX
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ORIGIN

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Db	2435	CAAAATGTATACCGTGCGCTGTATATGATTAAGATTGATTAATATGATCATATATGTTA	2494
QY	3670	ATGTGAATCTGTGGGACAGATTACTTTTCCATAGGACGAAATATCCAACTGTGAACTG	3729
Db	2495	ATGTGAATCTGTGGGACAGATTACTTTTCCATAGGACGAAATATCCAACTGTGAACTG	2554
QY	3720	GCTATGTTTTTAATATGCTCATATGTCCTTACTGTGTGTGTGACCTGCTGAGGACAG	3789
Db	2555	GCTATGTTTTTAATATGCTCATATGTCCTTACTGTGTGTGTGACCTGCTGAGGACAG	2614
QY	3790	AAGTTCATTTGATGTCAATAAAGCAAAAGTACTTCTTTTGAATCTGAAAAAA	3849
Db	2615	AAGTTCATTTGATGTCAATAAAGCAAAAGTACTTCTTTTGAATCTGAAAAAA	2674
QY	3850	AAAAAAAAA 3858	
Db	2675	AAAAAAAAA 2683	
RESULT 2			
LOCUS	AY419490	2173 bp	DNA linear GSS 17-DEC-2003
DEFINITION			Homo sapiens ANKRD3 gene, VIRUAL TRANSCRIPT, partial sequence,
ACCESSION			AY419490
VERSION			AY419490.1 GI:39775447
KEYWORDS			GSS.
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
			1 (bases 1 to 2173)
TITLE			Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
			Todd,M.A., Tandenbaum,D.M., Civeleo,D.R., Lu,F., Murphy,B.,
			Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
			Adams,M.D. and Cargill,M.
			Inferring nonneutral evolution from human-chimp-mouse orthologous
			gene trios
JOURNAL			Science 302 (5652), 1960-1963 (2003)
PUBMED			14671302

REFERENCE	2 (bases 1 to 2173)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.O., Smirsky,J.O., Adams,M.D. and Carelli,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	1..2173
gene	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>2173 /gene="ANKRD3" /locus_tag="HCM6308"
ORIGIN	
Query Match	55.4%; Score 2138.8; DB 9; Length 2173;
Best Local Similarity	99.6%; Pred. No. 0;
Matches 2165; Conservative	0; Mismatches 7; Indels 2; Gaps 2
QY	199 GGAGGGCATGAGGCTTTTGGAAAGACCAAGAGATGAGATGGCAAGTTTCGCTACAT 258
DB	1 GGAGGGCATGAGGCTTTTGGAAAGACCAAGAGATGAGATGGCAAGTTTCGCTACAT 60
QY	259 CCTGCGCTGTGATGGCATCTGCGCGAACCCTGTGCGCTGTGTCATGAGTACATGAGAC 318
DB	61 CCTGCGCTGTGATGGCATCTGCGCGAACCCTGTGCGCTGTGTCATGAGTACATGAGAC 120
QY	319 GGGCTCCCTGAAAAAGCTGCTGGCTTGGAGCCATTGCCATGAGGATCTCCGGTCCGAAT 378
DB	121 GGGCTCCCTGAAAAAGCTGCTGGCTTGGAGCCATTGCCATGAGGATCTCCGGTCCGAAT 180
QY	379 CATCCAGAGACGGGGGATGGGATGAACCTTCGTACATGACATGAGCCGCGCACTCTGCA 438
DB	181 CATCCAGAGACGGGGGATGGGATGAACCTTCGTACATGACATGAGCCGCGCACTCTGCA 240
QY	439 CCTGAGACTCAAGCCCGCGAATCTCTGCTGATGCCATCCACTCAACAGTCAAGATTTCTGA 498
DB	241 CCTGAGACTCAAGCCCGCGAATCTCTGCTGATGCCATCCACTCAACAGTCAAGATTTCTGA 300
QY	499 TTTTGTCTGGCCAAATGCAAGCGGCTGTCCACTGCGATGACCTTCAGATGATGAGCCT 558
DB	301 TTTTGTCTGGCCAAATGCAAGCGGCTGTCCACTGCGATGACCTTCAGATGATGAGCCT 360
QY	559 GTTTGGCCAAATGCGCTACCTCCCTCCAGAGGCATCAGGGAGAGAGCGCGCTTTCGA 618
DB	361 GTTTGGCCAAATGCGCTACCTCCCTCCAGAGGCATCAGGGAGAGAGCGCGCTTTCGA 420
QY	619 CACCAAGACGATGATACAGCTTTGCGATCGTCACTGGGCGGTGCTTCAACAGAGAA 678
DB	421 CACCAAGACGATGATACAGCTTTGCGATCGTCACTGGGCGGTGCTTCAACAGAGAA 480
QY	679 GCCGTTTTCAGATGAGAGAAATCTCTGCATCATATGTTGAAAGTGTGAAGGGCCACCG 738
DB	481 GCCGTTTTCAGATGAGAGAAATCTCTGCATCATATGTTGAAAGTGTGAAGGGCCACCG 540
QY	739 CCGCGAGTCCCGCCCGGTGTGAGAGCCCGCGCGCGCGCTGCGACGACCTGATACGCCCT 798
DB	541 CCGCGAGTCCCGCCCGGTGTGAGAGCCCGCGCGCGCGCTGCGACGACCTGATACGCCCT 600
QY	799 CATGAGAGCGGTGCTGGCAGGGGGAATCCCGAGTTAGGCGCCACTTCCAAAGAAATTACTTC 858
DB	601 CATGAGAGCGGTGCTGGCAGGGGGAATCCCGAGTTAGGCGCCACTTCCAAAGAAATTACTTC 660
QY	859 TGAATCCGAGGACTGTGTGTAAGACCTGTATGACGAAAGTGAAGAAATCTGCTCATGATCT 918
DB	661 TGAATCCGAGGACTGTGTGTAAGACCTGTATGACGAAAGTGAAGAAATCTGCTCATGATCT 720
QY	919 GGAAGCTGAAAAGCCCCCGGAGCCAGGAGCGAGGATGGTGGCTTGGAGGCTCAAGCGGCG 978

Db	721	GGACGTAAGAAACCCCCCGGAGCCGAGAGCGAGGTGTGTGCTTGAGAGCTCAAGCGAGC	780
Qy	979	CTCTGGCCCCCACTTCGATTAACGACTAGACCTCTCCAGAGCTTCTCTCAAGCTGACTC	1038
Db	781	CTCTGCCCCCACTTCGATTAAGACTTACAGCTCTCCAGAGCTCTCAAGCTGACTC	840
Qy	1039	TGGAAGTTTCCAGGCTGTGAGAGGCCCCGAGAGGCTCAAGCCGACGCTCTCTGATGCCAA	1098
Db	841	TGGAAGTTTCCAGAGCTGTGAGAGGCCCCGAGAGGCTCAAGCCGACGCTCTCTGATGCCAA	900
Qy	1099	GCTGCGCATGTGTCCGCGCAGTGGGAAAGAGCTCTCCGAGGAGTGTCTCTCGGTGACTCCGCTT	1158
Db	901	GCTGCGCATGTGTCCGCGCAGTGGGAAAGAGCTCTCCGAGGAGTGTCTCTCGGTGACTCCGCTT	960
Qy	1159	CTCTTCCAGAGGATCACTGTGCTGTCTTGTGAGGGGGAACCTTCAACACAGACTTGGG	1218
Db	961	CTCTTCCAGAGGATCACTGTGCTGTCTTGTGAGGGGGAACCTTCAACACAGACTTGGG	1020
Qy	1219	TACCAACAAGACGTCCAGAAAGAAAGCTTGTGATGCCATGTGTCC - GGAGACAACA	1277
Db	1021	CACCAAC - AAGCGTCCAGAAAGAAAGCTTGTGATGCCATGTGTCCGAGGAGACAACA	1079
Qy	1278	AACCTGATGAAGTCTCTGACGCCGCGAGAGACTGGAACCTTGGCACTGGAACAGCGGTGCCAGCC	1337
Db	1080	AACCTGATGAAGTCTCTGACGCCGCGAGAGACTGGAACCTTGGCACTGGAACAGCGGTGCCAGCC	1139
Qy	1338	TGCTGCACTGGCGGGTGAAGGCGGAGCAAGAGAGTGGCCAAAGTGGCTGTCTCAACA	1397
Db	1140	TGCTGCACTGGCGGGTGAAGGCGGAGCAAGAGAGTGGCCAAAGTGGCTGTCTCTCAACA	1139
Qy	1398	ATGCCAACCCCAACCTGAGCAACGCTGAGGGCTCCACCCTGTGCACTAGGCGCTGGAGA	1457
Db	1200	ATGCCAACCCCAACCTGAGCAACGCTGAGGGCTCCACCCTGTGCACTAGGCGCTGGAGA	1259
Qy	1458	GGAAGGTGGGGGTGTCTGTGAGACTCTCTGTGGCACAGAAATCATGTTCAACGCCAAGG	1517
Db	1260	GGAAGGTGGGGGTGTCTGTGAGACTCTCTGTGGCACAGAAATCATGTTCAACGCCAAGG	1319
Qy	1518	ATGAGAGACAGTGGACAGGCTCTCACTTGTGACGCCAGAACGAGGAGATGACTAGCACAC	1577
Db	1320	ATGAGAGACAGTGGACAGGCTCTCACTTGTGACGCCAGAACGAGGAGATGACTAGCACAC	1379
Qy	1578	GAGTGTCTTGTGAGAAAGAACGAGCTCGGTCAACGAGGTGGACTTTGAGGGCGGAGACGCCA	1637
Db	1380	GAGTGTCTTGTGAGAAAGAACGAGCTCGGTCAACGAGGTGGACTTTGAGGGCGGAGACGCCA	1439
Qy	1638	TGCACTGTGGCTTGCCAGCACGCGGCGAGAGAAATATGTGTGGCATCTGTCTGTGGCGGAGCG	1697
Db	1440	TGCACTGTGGCTTGCCAGCACGCGGCGAGAGAAATATGTGTGGCATCTGTCTGTGGCGGAGCG	1499
Qy	1698	TGGACGTGAGCGCTGACGAGGCAAGAGATGCTGTGCTGCACTGACACTAGCGTGCCTGGACAGG	1757
Db	1500	TGGACGTGAGCGCTGACGAGGCAAGAGATGCTGTGCTGCACTGACACTAGCGTGCCTGGACAGG	1559
Qy	1758	GCCACCTGGCCATCTGTCAAGCTGTGCGCCAAACAGCCGAGGGGTGAGTGAACGCCGAGA	1817
Db	1560	GCCACCTGGCCATCTGTCAAGCTGTGCGCCAAACAGCCGAGGGGTGAGTGAACGCCGAGA	1619
Qy	1818	CGCTGGAATGGAGAGACGCAATTGCACTTGCGCGCACAGCGCGGAGCACTAACGCGTGGGCC	1877
Db	1620	CGCTGGAATGGAGAGACGCAATTGCACTTGCGCGCACAGCGCGGAGCACTAACGCGTGGGCC	1679
Qy	1878	GCAATCTCAATCGACCTGTGCTCGAGAGTGAAGSTGTGACAGCTGTGCGACAGACACCC	1937
Db	1680	GCAATCTCAATCGACCTGTGCTCGAGAGTGAAGSTGTGACAGCTGTGCGACAGACACCC	1739
Qy	1938	TGCACTGTGGCGCGAGAGCGGAGCAACAGAGACTTGCACAGCTGTCTCTGTGATCGGAGCG	1997
Db	1740	TGCACTGTGGCGCGAGAGCGGAGCAACAGAGACTTGTCCAGAGCTGTCTCTGTGATCGGAGCG	1799
Qy	1998	CTGGCAAGAGGCGGTGACCTTCAAGCGGCTTACACCGCTTGGCACTTGGCTGCGGCAAG	2057

Db	1800	CTGGCAAGAGAGCCGTBACTTCAGACCGCTACACCCGCTTCGACCTGGCTGGCCGCAAGC	1851
Qy	2058	GACACCTGGCCACTGTCAAGCTGCTTGTGCAAGAGAAAGCCGATGTCTGGCCCGGGGAC	2117
Db	1860	GACACCTGGCCACTGTCAAGCTGCTTGTGCAAGAGAAAGCCGATGTCTGGCCCGGGGAC	1919
Qy	2118	CCCTGAACCAAGACGGGCGCTGCACCTGGCTCCCGCCACGGGCACTCGAGAGTGGTGAAG	2177
Db	1920	CCCTGAACCAAGACGGGCGCTGCACCTGGCTCCCGCCACGGGCACTCGAGAGTGGTGAAG	1979
Qy	2178	AGTTGTCAGGGCCGATGTCAATTGACCTGTTTCGACGACGAGGGGCTCAGGCGCTGCACC	2237
Db	1980	AGTTGTCAGGGCCGATGTCAATTGACCTGTTTCGACGACGAGGGGCTCAGGCGCTGCACC	2039
Qy	2238	TGGCCGCCCGAAGGCGCGGACGACAGACGGTGAAGACTTCTGCTCAGGACATGGGGCCACA	2297
Db	2040	TGGCCGCCCGAAGGCGCGGACGACAGACGGTGAAGACTTCTGCTCAGGACATGGGGCCACA	2099
Qy	2298	TCAACCTGTCAGAGGCTTCAAGTTCCAGGGCGGGCCATGGCCCGCGCCACACTCTCGGGCG	2357
Db	2100	TCAACCTGTCAGAGGCTTCAAGTTCCAGGGCGGGCCACATGGCCCGCGCCACACTCTCGGGCG	2159
Qy	2358	GAGACAGAGACCTAG 2371	
Db	2160	GAGACAGAGACCTAG 2173	
RESULT 3	AY19491	1901 bp DNA linear GSS 17-DEC-2003	
LOCUS	AY19491		
DEFINITION	Pan troglodytes ANKRD3 gene, VIRUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY19491		
VERSION	AY19491.1 GI:39775448		
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.		
REFERENCE	1 (bases 1 to 1901)		
AUTHORS	Clark,A.G., Glanbaum,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Cavello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smnisky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Interfering nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1901)		
AUTHORS	Clark,A.G., Glanbaum,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Cavello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smnisky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	location/Qualifiers		
source	1..1901		
gene	/organism="Pan troglodytes"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9598"		
	<1..>1901		
	/gene="ANKRD3"		
	/locus_tag="HCM6908"		
ORIGIN			
Query Match	42.4%; Score 1637.2; DB 9; Length 1901;		
Best Local Similarity	86.7%; Pred. No. 0;		
Matches 1648; Conservative	0; Mismatches 253; Indels 0; Gaps 0;		
Qy	199	GGAGCGCATGAGCTTTTGAAGAAGCCAGAGAATGAGATGGCCAAAGTTTCCCTACAT	258

Db 1 GAGAGGCGATGAGCTTTTGAAGAAAGCCAGAAAGATGAGATGCGCAGTTTTCCTACAT 60
 Oy 259 CCTGCTGTGTATGATCATCTGCGCGAACTGTGCGCTGTGATGAGTACATGAGAGC 318
 Db 61 CTTGCTGTGTATGAGATCTGCGGGAACCTGTGCGGCTGTGATGAGTACATGAGAGC 120
 Oy 319 GGGGCTCCCTGGAAGAGCTGCTGCGAGCCATTGCGAGTATGAGTATCTCCGCTTCCGAT 378
 Db 121 GGGGCTCCCTGGAAGAGCTGCTGCGAGCCATTGCGAGTATGAGTATCTCCGCTTCCGAT 180
 Oy 379 CATCCACGAGAGCGGCGTGGGATGAACTTCTGCACTGCAATGAGCGCGCCCACTCTGCA 438
 Db 181 CATCCACGAGAGCGGCGTGGGATGAACTTCTGCACTGCAATGAGCGCGCCCACTCTGCA 240
 Oy 439 CTTGACCTCAAGCCCGCGCAATCTGTGATGAGCCCACTACCAAGTCAAGATTTTCTGA 498
 Db 241 CTTGACCTCAAGCCCGCGCAATCTGTGATGAGCCCACTACCAAGTCAAGATTTTCTGA 300
 Oy 499 TTTTGGTCTGGCCAAAGTGCACAGGCTGTCCCACTGCAATGACCTTCAAGATGAGCTTGA 558
 Db 301 TTTTGGTCTGGCCAAAGTGCACAGGCTGTCCCACTGCAATGACCTTCAAGATGAGCTTGA 360
 Oy 559 GTTTGGCAAAATGCGCTTACCTCCCTGCAAGGCGCATCAGGAGAAAGCGGCTTCTGA 618
 Db 361 GTTTGGCAAAATGCGCTTACCTCCCTGCAAGGCGCATCAGGAGAAAGCGGCTTCTGA 420
 Oy 619 CACCAAGACAGATGTATACAGCTTTGCGATGCTCATCTGCGGCGTGTCTCACAGAGAA 678
 Db 421 CACCAAGACAGATGTATACAGCTTTGCGATGCTCATCTGCGGCGTGTCTCACAGAGAA 480
 Oy 679 GCGGTTTGAGATGAGAGAAATCTGTGACATCATGTGAAAGTGTGAAGGCGCACCG 738
 Db 481 GCGGTTTGAGATGAGAGAAATCTGTGACATCATGTGAAAGTGTGAAGGCGCACCG 540
 Oy 739 CCGCGAGCTGCGCGCTGTGAGAGAGCCGCGCGCGCGCTGAGGCACTGATACGCT 798
 Db 541 CCGCGAGCTGCGCGCTGTGAGAGAGCCGCGCGCGCGCTGAGGCACTGATACGCT 600
 Oy 799 CATGACGCGTGTGAGAGGAGATCCGAGATTTAGGCCACCTTCCAGAAATTAATCTTC 858
 Db 601 CATGACGCGTGTGAGAGGAGATCCGAGATTTAGGCCATTTCCAGAAATTAATCTTC 660
 Oy 859 TGAACCGAGAGACTGTGTGAAAGCTGTGATGACAGATGAAAGAACTGTCTCATGATCT 918
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 Oy 919 GGAAGTGAAGAAAGCCCCCGAGGCGCGAGAGCGAGTGTGCTGCGAGGCTCAAGCGGCG 978
 Db 721 GGAAGTGAAGAAAGCCCCCGAGGCGCGAGAGCGAGTGTGCTGCGAGGCTCAAGCGGCG 780
 Oy 979 CTCTGCGCCCACTTGTGATGACAGCTCTCTGAGCTTCTCTCAAGCTGAGCTC 1038
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 Oy 1039 TGAAGTTTCCAGAGCTGTGAGAGGCGCGCGAGGCTCAAGCTGAGCTCTCTGAGCTCA 1098
 Db 841 TGAAGTTTCCAGAGCTGTGAGAGGCGCGCGAGGCTCAAGCTGAGCTCTCTGAGCTCA 900
 Oy 1099 GCTGCGCAATGCTCCGCGAGTGGAGAGAGCTCTGCGGCGTGTCTCGGTGAGCTCCGCTT 1158
 Db 901 GCTGCGCAATGCTCCGCGAGTGGAGAGAGCTCTGCGGCGTGTCTCGGTGAGCTCCGCTT 960
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 Db 961 CTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAACCTTCAACAGCGATCTGAG 1020
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 Oy 1279 ACTGATGAGATCTCTGAGCGCGAGAGAGCTGTGAGCTGTGAGCACTGAGCAAGCGGCTCAGCGCT 1338

Db 1081 NNN 1140
 Oy 1339 GCTGCACTGCGCGGTGAGAGCGCGGCAAGAGAGTGGCCAAAGTGGCTGTCAACAA 1398
 Db 1141 NNN 1200
 Oy 1399 TGCCAAAGCCCACTGAGCAACCGTAGGAGCTCCACCCGTTGACATGCGCTGAGAG 1458
 Db 1201 NNN 1260
 Oy 1459 GAGGATGCGGAGTGTCTGTGAGCTCTCTGCGCAAGAGATCATGTCTCAACGCCAAGA 1518
 Db 1261 GAGGATGCGGAGTGTCTGTGAGCTCTCTGCGCAAGAGATCATGTCTCAACGCCAAGA 1320
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 Oy 1639 GCAAGTGGCTTGCAGACAGGCGAGAGAAATATGTGCGCATCTGTCTGCCCGAGGCT 1698
 Db 1441 GCAAGTGGCTTGCAGACAGGCGAGAGAAATATGTGCGCATCTGTCTGCCCGAGGCT 1500
 Oy 1699 GAGCTGAGCTTGCAGAGGAGAGATGCTGTGCTTCCACTGCAATACGTGTGCGAGG 1758
 Db 1501 GAGCTGAGCTTGCAGAGGAGAGATGCTGTGCTTCCACTGCAATACGTGTGCGAGG 1560
 Oy 1759 GCAAGTGGCTTGCAGAGCTTGCAGACAGGCGGAGTGTGAGTGAAGCGCCAGAC 1818
 Db 1561 GCAAGTGGCTTGCAGAGCTTGCAGACAGGCGGAGTGTGAGTGAAGCGCCAGAC 1620
 Oy 1819 GCTGATGAGAGAGAGCGCATTTGACCTGAGCGGCAAGCGGCGGCACTACCGGTGCGCG 1878
 Db 1621 GCTGATGAGAGAGAGCGCATTTGACCTGAGCGGCAAGCGGCGGCACTACCGGTGCGCG 1680
 Oy 1879 CATCTCATGACCTGTGTCTCCGAGCTGACAGTCAAGTGTGCGAGCGCTGCGAGACAGCCCT 1938
 Db 1681 CATCTCATGACCTGTGTCTCCGAGCTGACAGTCAAGTGTGCGAGCGCTGCGAGACAGCCCT 1740
 Oy 1939 GCAAGTGGCGGAGAGCGGCGACACAGAGACTGCCAGGCTGCTCTGCAATCGGCGGCG 1998
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 Oy 1999 TGGCAAGAGGCGGAGACTGACAGCGCTGACAGCGCTGTGCACTGTGCTGCGCGAGCG 2058
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 Oy 2059 ACACTGCGCACTGTCAAGCTGTGTGTGAGAGAGAGCG 2099
 Db 1861 ACACTGCGCACTGTCAAGCTGTGTGTGAGAGAGAGCG 1901

RESULT 4
 AY419492 2173 bp DNA linear GSS 17-DEC-2003
 LOCUS Mus musculus ANKRD3 gene, VIRUTAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY419492
 VERSION AY419492.1 GI:39775449
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 2173)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanendaa,D.M., Civeille,D.R., Lu,F., Murphy,B.,
 Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Snijsky,J.C.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous

TITLE

QY 1998 CTGGCAGAGAGCCCTGACCTTCAGACGCGCTCAACCGCTCTGCACTGCTGCCGCAAG 2057
 DB 1800 CTGGCAGAGAGCCCTGACCTTCAGACGCGCTCAACCGCTCTGCACTGCTGCCGCAAG 1859
 QY 2058 GACACCTGGCCACTGTCAAGCTGCTTTCAGAGAGAAAGCCGATGCTGCGCCGGGAGC 2117
 DB 1860 GACACCTGGCCACTGTCAAGCTGCTTTCAGAGAGAAAGCCGATGCTGCGCCGGGAGC 1919
 QY 2118 CCCTGAACGAGACGCGCGCTGCACTGCTGCCGCAACCGCTCTGCACTGCTGCCGCAAG 2177
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 QY 2178 AGTTGTCAGCGCCGATGTCAATGTCCTGCTTTCAGAGAGAGAGGCTCTGACGCGCTGCAAC 2237
 DB 1980 AGTTGTCAGCGCCGATGTCAATGTCCTGCTTTCAGAGAGAGAGGCTCTGACGCGCTGCAAC 2039
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 DB 2160 GAGGCAAGACCTAG 2173
 RESULT 5
 AK077233 3741 bp mRNA linear HTC 03-APR-2004
 LOCUS AK077233
 DEFINITION Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 RIKEN full-length enriched library, clone:5031407D20
 product:anmyrin repeat domain 3, full insert sequence.
 AK077233
 VERSION AK077233.1 GI:26097247
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 BUKARYOTA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE 20493374
 PUBMED 11042159
 REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Kitesunai, T., Tachio, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishise, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, S.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 JOURNAL sequencing pipeline with 384 multicapillary sequencer
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.

TITLE JOURNAL
 REFERENCE Nature 409, 685-690 (2001)
 AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
 TITLE Group Phase I & II Team.
 JOURNAL Analysis of the mouse transcriptome based on functional annotation
 REFERENCE of 60,770 full-length cDNAs
 AUTHORS Nature 420, 563-573 (2002)
 (bases 1 to 3741)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Furuta, S., Furuta, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/.
 URL: http://fantom.gsc.riken.jp/.
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 Matches 1884; Conservative 0;
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 DEFINITION 5', mRNA Sequence.
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 VERSION BM924233.1 GI:19374612
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 1119)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov

COMMENT Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov> Plate: LLM12807 row: 3 column: 06 High quality sequence stop: 664.

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source

1..1119
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ORIGIN

Query Match 22.0%; Score 849.2; DB 5; Length 1119;
Best Local Similarity 94.0%; Pred. No. 4.5e-199;
Matches 994; Conservative 0; Mismatches 48; Indels 16; Gaps 10;

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QY 128 AAGGTGCGCATGTCATCTGAGGAGCATGCGCTGCGCATAGTCTGCGCCAGCCCGAC 187
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QY 188 GTGCAAGAGAGGAGCGCATGAGCTTTTGGAGAGCCAGAGAGTGAATGAGCCAA 247
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QY 368 CGGTTCGATCATTCACAGAGCGGCGTGGGAGCAATCTTCTGCACTGATGAGCCCG 427
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QY 428 CCACCTCTGCACTGAGACTCAAGCCCGGAGCAATCTGCTGATGCCCATACACATC 487

DB 423 CCATCTCTGACCTGAGACTTCAAGCCCGGAGCAATCTGCTGATGCCACTTACACATC 482

QY 488 AAGATTTCATGTTTGGTCTGCGCAATGTCAGAGCGGCTGTCTCCCATGAGACTCAGC 547

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QY 846 AAG-AAATTACTTGAAGAACCGAGAGCCTGTGTG-AAAGCTGTATGACGAAT-GAAG 902

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RESULT 7
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LOCUS
DEFINITION
UI-CF-FN0-afl-n-24-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
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VERSION
CA312918.1 GI:24531016
KEYWORDS
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 791)
AUTHORS
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
8889548
COMMENT
McCrory Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccrory@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

QY	877	TGAAAGCTGTATGACGAAAGTGAAGAAAGAAACCTGCTCAAGATCTGGACGTGAAGACCCCC	936
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QY	937	GGAGCCCGAGAGCGAGGTGTGCTCGTCGACAGGCTCAAGCGAGCTCTGCGCCCACTTTCGA	996
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QY	997	TAAAGCATACAGCTCTCCGAGCTTCTCTCAAGCTGGACTCTGGAAGTTTCCAGGCTGT	1056
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QY	1296	AGCCGACGAGCGTGAAGCTTGCGCACTGGAACAGCGGTGCAGGCTGTCACCTGGCGGTGG	1355
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QY	1356	AGCCGCGGCAAGAGAGTGTGCGCAAGTGTGCTGCTCAACATATCCAACTCCAACTTGA	1415
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Db	730	GC 731	
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VERSION			
BM981614.1 GI:19604284			
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SOURCE			
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Organism			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
1 (bases 1 to 702)			
Bonaldo,M.F., Lennon,G. and Soares,M.B.			
Normalization and subtraction: two approaches to facilitate gene			
discovery			
Genome Res. 6 (9), 791-806 (1996)			
JOURNAL			
MEDLINE			
PUBMED			
COMMENT			
8889548			
97044477			
Contact: McCreay, PB			
McCreay Lab			
University of Iowa			
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA			
Tel: 319 356 4866			
Fax: 319 356 7171			
Email: paul-mccray@uiowa.edu			
Tissue Procurement: Dr. M. J. Welsh, University of Iowa			
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa			
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa			
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa			
Clone Distribution: Researchers may obtain clones from Research			
Genetics (www.iesgen.com) or from Open BioSystems			

FEATURES		SOURCE	
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ORIGIN			
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Matches	694;	Conservative	0; Mismatches 7; Indels 0; Gaps 0;
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Qy	3215	GTGTGCTGGAGTGAACCAAGCTCTTGGGGGAGAGTGACAGAGAGTGTGTTTTTATCTC	3274
Db	641	GTGTGCTGGAGTGAACCAAGCTCTTGGGGGAGAGTGACAGAGAGTGTGTTTTTATCTC	582
Qy	3275	CACACGCGAGTGTGAAGATTAATTAACATAGTATTACCTAGACATAGACAGTATTACCTAG	3334
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Qy	3335	GTAAATGCACTGTCTACCTGTGACCCCTTCCAGCTCTCATTTTTTGTAGTATTGGGAT	339
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Db	401	GCACCTCAGCAGTGTGGGGGTGAGCCCAAGGGCGGTTCTTGGATGTAAAGATGTGGCCA	342
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Qy	3635	TGATTAAGATTTGATTTAATGTACCATGTATGTTAATGTGAATCTGTGGCGAGTACTT	3694
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QY      3755 GCCTTACCTGTTTGTGTGAGCTGCGTGAAGGAGCAAGAAGTTCATTTGATGTCATTAAGC 3814
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Db      101 GCCTTACCTGTTTGTGTGAGCTGCGTGAAGGAGCAAGAAGTTCATTTGATGTCATTAAGC 42
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ACCESSION      CD630278
VERSION      CD630278.1 GI:40278544
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ORGANISM      Homo sapiens (human)
REFERENCE      1 (bases 1 to 716)
AUTHORS      Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE      Circular rapid amplification of cDNA ends for high-throughput
JOURNAL      extension cloning of partial genes
COMMENT      Genomics 84 (1), 205-210 (2004)
              Contact: Pu GK
              Incyte Genomics, Inc.
              3160 Porter Dr., Palo Alto, CA 94304, USA
              Tel: 6508454102
              Email: gfu@incyte.com.
              Location/Qualifiers
FEATURES
source      1..716
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone_lib="FLP"
              /note="Vector: pDrive Cloning Vector"

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Query Match      17.7%; Score 684.2; DB 6; Length 716;
Best Local Similarity 99.4%; Pred. No. 3.5e-158;
Matches 697; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      1997 GCTGGCAAGAGAGCGGTGACCTCA-GACGGGCTACACCGCTCTGCACTGCGCTGCCGCGAA 2055
      |||
Db      16 GCTGGCAAGAGAGCGGTGACCTCAAGACGAGCTACACCGCTCTGCACTGCGCTGCCGCGAA 75
QY      2056 CGACACCTGCGGCACTGTTCAGCTCTTGTGAGAGAGAAAGCCGATGCTGGCCGCGG 2115
      |||
Db      76 CGACACCTGCGGCACTGTTCAGCTCTTGTGAGAGAGAAAGCCGATGCTGGCCGCGG 135
QY      2116 ACCCTGAAACGAGAGGCGCTGCACTGCTGCCGCCCAACGCGCACTCGAGAGTGTGGA 2175
      |||
Db      136 ACCCTGAAACGAGAGGCGCTGCACTGCTGCCGCCCAACGCGCACTCGAGAGTGTGGA 195
QY      2176 GGAAGTTGGTCAGCGCGCATGATGATGACCTGTTGACGAGCGAGGGGCTCAGCGCGCTGCA 2235
      |||
Db      196 GGAAGTTGGTCAGCGCGCATGATGATGACCTGTTGACGAGCGAGGGGCTCAGCGCGCTGCA 255
QY      2236 CCTGGCCGCCCGGAGCGCGCGAGCAAGAGCGTGAAGTCTGCTCAGGCAATGAGGCGCA 2295
      |||
Db      256 CCTGGCCGCCCGGAGCGCGCGAGCAAGAGCGTGAAGTCTGCTCAGGCAATGAGGCGCA 315
QY      2296 CATCAACTGCGAGAGCTCAAGTTCCAGGCGCGCATGAGCGCGCGCGCCCACTCTCTGG 2355
      |||
Db      316 CATCAACTGCGAGAGCTCAAGTTCCAGGCGCGCATGAGCGCGCGCGCCCACTCTCTGG 375
QY      2356 GCGAAGCAAGACTGAGCTGCTGCGCGAGACCGGGGCTCAAGTGGCGCTTGTGCC 2415

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Db      376 GCGAAGCAAGACTGAGCTGCTGCTGCGAGACCGGGGGTCCACGCGGGGCTTTGTCC 435
      |||
QY      2416 TGTCTGTGTTCTCTGTGAGAGATGAACGATCTCTGCGTGGGCGCCCTGTGTGCTTAACCT 2475
      |||
Db      436 TGTCTGTGTTCTCTGTGAGAGATGAACGATCTCTGCGTGGGCGCCCTGTGTGCTTAACCT 495
QY      2476 AAATGTTAACCAAGCAGAGTGAACATGTGTCATCAGAGGCGGCTGCTGACCGGAG 2535
      |||
Db      496 AAATGTTAACCAAGCAGAGTGAACATGTGTCATCAGAGGCGGCTGCTGACCGGAG 555
QY      2536 TGTCCCTCCAGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2595
      |||
Db      556 TGTCCCTCCAGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 615
QY      2596 CTGCTGTCTGAAGAGGACCGTGGGTCAGAATCATTTGTTGTGCTCTTAATGGTCCCTG 2655
      |||
Db      616 CTGCTGTCTGAAGAGGACCGTGGGTCAGAATCATTTGTTGTGCTCTTAATGGTCCCTG 675
QY      2656 AGCGTGTCTCTCAGTATGAAGCCCGAGCGGTGAAGCAT 2696
      |||
Db      676 AGCGTGTCTCTCAGTATGAAGCCCGAGCGGTGAAGCAT 716

RESULT 11
LOCUS      BM979316/c      705 bp      mRNA      linear      EST 21-FEB-2003
DEFINITION      UI-CF-DUI-adr-o-17-0-UI-81 UI-CF-DUI Homo sapiens cDNA clone
ACCESSION      UI-CF-DUI-adr-o-17-0-UI 3', mRNA sequence.
VERSION      BM979316
KEYWORDS      EST.
SOURCE      Homo sapiens
ORGANISM      Homo sapiens (human)
REFERENCE      1 (bases 1 to 705)
AUTHORS      Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE      Normalization and subtraction: two approaches to facilitate gene
JOURNAL      discovery
MEDLINE      Genome Res. 6 (9), 791-806 (1996)
PUBMED      8889548
COMMENT      Contact: McCray, PB
              McCray Lab
              University of Iowa
              2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
              Tel: 319 356 4866
              Fax: 319 356 7171
              Email: paul-mccray@uiowa.edu
              Tissue Procurement: Dr. M. J. Welsh, University of Iowa
              cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
              cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: Researchers may obtain clones from Research
              Genetics (www.resgen.com) or from Ogen Biosystems
              (www.openbiosystems.com).
              Seq primer: M13 FORWARD
              POLYA=Yes.
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              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="UI-CF-DUI-adr-o-17-0-UI"
              /tissue_type="Primary Lung Epithelial Cells"
              /dev_stage="Adult"
              /lab_host="MDH10B (Life Technologies) (T1 phage resistant)"
              /clone_lib="UI-CF-DUI"
              /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
              modified polylinker; Site 1: Score 1; Site 2: Not 1;
              UI-CF-DUI is a normalized cDNA library containing the
              following tissue(s): Primary Lung Epithelial Cells The

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library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GACTGTAGC.

TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368

TAG LIB=UI-CF-DUI

TAG_SEQ=GACTGTAGC"

ORIGIN

Query Match 17.6%; Score 680.8; DB 5; Length 705;
Best Local Similarity 99.3%; Pred. No. 2,4e-157;
Matches 693; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

3161 TAAAAAATTCCTCCCTTGTAACTCACTGCTGGGAGCTGAGGCGAGCCCTCAGGTCCG 3220
DB TAAAAAATTCCTCCCTTGTAACTCACTGCTGGGAGCTGAGGCGAGCCCTCAGGTCCG 640
3221 TGAAGTGCACCACTCTGGGAGAGAGTGCAGGAGAGGCTGTTTATCTCCACAG 3280
DB TGAAGTGCACCACTCTGGGAGAGAGTGCAGGAGAGGCTGTTTATCTCCACAG 581
3281 CAGTATGAAGATAAATTAATCATAGTATTAATCTAGACATAGACAGTATTAATCTAGTATGAT 3340
DB CAGTATGAAGATAAATTAATCATAGTATTAATCTAGACATAGACAGTATTAATCTAGTATGAT 521
580 CAGTATGAAGATAAATTAATCATAGTATTAATCTAGACATAGACAGTATTAATCTAGTATGAT 521
3341 GCACTGCTCACTGCAACCTCTCCAGCTCATTTTGTAGGTATTTGGATAGGAT 3400
DB GCACTGCTCACTGCAACCTCTCCAGCTCATTTTGTAGGTATTTGGATAGGAT 461
520 GCACTGCTCACTGCAACCTCTCCAGCTCATTTTGTAGGTATTTGGATAGGAT 461
3401 AGTGTGTGGGATAGGGGGAGAGTCTGACCTGCTTGGACAGAGTGCCTCGACCT 3460
DB AGTGTGTGGGATAGGGGGAGAGTCTGACCTGCTTGGACAGAGTGCCTCGACCT 401
460 AGTGTGTGGGATAGGGGGAGAGTCTGACCTGCTTGGACAGAGTGCCTCGACCT 401
3461 CAGCAGTTGGGGGTGTGGCCCGAGGGGGTCTTGGATGTAAGATGGCCATCTAGC 3520
DB CAGCAGTTGGGGGTGTGGCCCGAGGGGGTCTTGGATGTAAGATGGCCATCTAGC 341
400 CAGCAGTTGGGGGTGTGGCCCGAGGGGGTCTTGGATGTAAGATGGCCATCTAGC 341
3521 CTGCTAACTTCACTGCTCACTGTGTCTCCATAGGCTCTTGAATCTGTATTTAGAT 3580
DB CTGCTAACTTCACTGCTCACTGTGTCTCCATAGGCTCTTGAATCTGTATTTAGAT 281
340 CTGCTAACTTCACTGCTCACTGTGTCTCCATAGGCTCTTGAATCTGTATTTAGAT 281
3581 AAGTTTGTGCAAGAGTGAACCTGCTGCAACATGTAACGCTGCTGATATATAG 3640
DB AAGTTTGTGCAAGAGTGAACCTGCTGCAACATGTAACGCTGCTGATATATAG 221
280 AAGTTTGTGCAAGAGTGAACCTGCTGCAACATGTAACGCTGCTGATATATAG 221
3641 AGATTGATTTAATATGACATGATATGTAATCTGTGGGAGAGTATCTTCCAT 3700
DB AGATTGATTTAATATGACATGATATGTAATCTGTGGGAGAGTATCTTCCAT 161
220 AGATTGATTTAATATGACATGATATGTAATCTGTGGGAGAGTATCTTCCAT 161
3701 GGCAGGAATATATCAAGCTGTGAACTGGCTATGTTTAAATGCTCATGTGCTTT 3760
DB GGCAGGAATATATCAAGCTGTGAACTGGCTATGTTTAAATGCTCATGTGCTTT 101
160 GGCAGGAATATATCAAGCTGTGAACTGGCTATGTTTAAATGCTCATGTGCTTT 101
3761 ACTGTTGTGTGACGTGTGAGGAGCAAGAGTCCATTTGATGTAATTAACCAAGTA 3820
DB ACTGTTGTGTGACGTGTGAGGAGCAAGAGTCCATTTGATGTAATTAACCAAGTA 41
100 ACTGTTGTGTGACGTGTGAGGAGCAAGAGTCCATTTGATGTAATTAACCAAGTA 41
3821 CTGCTCACTTTTGTGAATCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3858
DB CTGCTCACTTTTGTGAATCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3

RESULT 12
BI68710 685 bp mRNA linear EST 11-OCT-2001
LOCUS BI68710
DEFINITION 60339042P1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402051 5',
mRNA sequence.

ACCESSION BI68710 GI:16042383
VERSION BI68710.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 685)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at:
<http://image.jnl.gov>
Plate: ULNL2025 row: C column: 12
High quality sequence stop: 680.
location/Qualifiers

FEATURES

source

1..685
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 17.4%; Score 671.4; DB 4; Length 685;
Best Local Similarity 99.6%; Pred. No. 5.1e-155;
Matches 684; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

2610 GGACGGGGGTGAGATCAATTCGTTGCTCTAATGGGCTGAGGCTGCTCTCA 2669
DB 1 GGACGGGGGTGAGATCAATTCGTTGCTCTAATGGGCTGAGGCTGCTCTCA 60
2670 GTGATGAAGCCCGAGGCGGTGAAGATCACTCTCTGAGGCGAGCCACTTGGGTTG 2729
DB 61 GTGATGAAGCCCGAGGCGGTGAAGATCACTCTCTGAGGCGAGCCACTTGGGTTG 120
2730 CTGAGCTCAACAGTCTTGAAGGAGGTGAGGAGAACTGTCTTTTATCTTCAATCAT 2789
DB 121 CTGAGCTCAACAGTCTTGAAGGAGGTGAGGAGAACTGTCTTTTATCTTCAATCAT 180
2790 GAAGGGGCGAGAGGCGCTGCTTAAAGTTCCATGAAATGTTTATTAATAATCTTA 2849
DB 181 GAAGGGGCGAGAGGCGCTGCTTAAAGTTCCATGAAATGTTTATTAATAATCTTA 240
2850 AGAGATGAATACCTTATCAGCTGTGCTGAAACCTGTTAAAAATGTTATTAATGGA 2909
DB 241 AGAGATGAATACCTTATCAGCTGTGCTGAAACCTGTTAAAAATGTTATTAATGGA 300
2910 TAGCTAGTCTTAAATGATGCTGAATGTGGGGTGTGCTTGAAGAAATGTTTATG 2969
DB 301 TAGCTAGTCTTAAATGATGCTGAATGTGGGGTGTGCTTGAAGAAATGTTTATG 360
2970 CAACAGGAAGAAATGTGAGCCAGCTTGGGGGCGTATGTGCGACACTCTTAAC 3029
DB 361 CAACAGGAAGAAATGTGAGCCAGCTTGGGGGCGTATGTGCGACACTCTTAAC 420
3030 CATTCAGCTATTAATCTTGGGTGAGTCTTGTGCAACACACACACAGTGCACATGG 3089
DB 421 CATTCAGCTATTAATCTTGGGTGAGTCTTGTGCAACACACACACAGTGCACATGG 480

QY 3090 TACTAGTCCGCTTGTCTGTGCTTCCCTAAGATGTTTGGCAACTCTAGAGCCACAGGC 3149
DB 481 TACTAGTCCGCTTGTCTGTGCTTCCCTAAGATGTTTGGCAACTCTAGAGCCACAGGC 540
QY 3150 CTAAAGATCATTAATAAAATTTCTCCCTTTGTAACTCAAGTGTGGGAGTGAAGCCAGCC 3209
DB 541 CTAAAGATCATTAATAAAATTTCTCCCTTTGTAACTCAAGTGTGGGAGTGAAGCCAGCC 600
QY 3210 CCTCAGTGTGCTGAGTGCACAGTCTTGGGGAAGAGTGCAGAGAAAGCTGTGTTTTT 3269
DB 601 CCTCAGTGTGCTGAGTGCACAGTCTTGGGGAAGAGTGCAGAGAAAGCTGTG--TTT 658
QY 3270 ATCTCCACACGAGATGATGAAGATAAA 3296
DB 659 ATCTCCACACGAGATGATGAAGATAACA 685

RESULT 13
LOCUS B1868794 665 bp mRNA linear EST 11-OCT-2001
DEFINITION 603391950P1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402052 5',
mRNA sequence.
ACCESSION B1868794
VERSION B1868794.1 GI:16042467
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NIH-MGC http://img.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@db-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNU at:
http://image.llnl.gov
Plate: ILAM1025 row: C column: 13
High quality sequence stop: 663.
Location/Qualifiers

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/issue_type="adenocarcinoma, cell line"
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/clone_1ib="NIH_MGC_90"
/note="Organ: liver; Vector: PCMV-SPORE; Site: 1: Nci;
Site 2: Salt; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN
Query Match 17.2%; Score 665; DB 4; Length 665;
Best Local Similarity 100.0%; Pred. No. 2e-153;
Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2610 GGAACGCTGGGTCGAAATCATTTGCTGCTCTTAATGGAGTGCCTGAGGCTGGTCTCTCA 2669
DB 1 GGAACGCTGGGTCGAAATCATTTGCTGCTCTTAATGGAGTGCCTGAGGCTGGTCTCTCA 60
QY 2670 GTGATGAAGCCCGAGGCGTGAAGCATCTCTCTGAGGCGGACCACTTGGGTTG 2729
DB 61 GTGATGAAGCCCGAGGCGTGAAGCATCTCTCTGAGGCGGACCACTTGGGTTG 120

QY 2730 CTGAGCTCACCACTCTTGAAGGAGTGCAGGGGAAATCTGTTTTTATCTTCATACAT 2789
DB 121 CTGAGCTCACCACTCTTGAAGGAGTGCAGGGGAAATCTGTTTTTATCTTCATACAT 180
QY 2790 GACGGTGGGCGAGAGGCGCTGCTTAAAGTTTCCATGAAATGTTTTATTAATAATCTTA 2849
DB 181 GACGGTGGGCGAGAGGCGCTGCTTAAAGTTTCCATGAAATGTTTTATTAATAATCTTA 240
QY 2850 AGAATGAATATCACTTATCAAGTGTGCTGAAACCTGTAAATAATGTTCAATPAACATTGGA 2909
DB 241 AGAATGAATATCACTTATCAAGTGTGCTGAAACCTGTAAATAATGTTCAATPAACATTGGA 300
QY 2910 TAGTCTAGTCTCTAATGATGCTAGTGTGAGTGTGGCTTTGAAAAACAATGTTTTATG 2969
DB 301 TAGTCTAGTCTCTAATGATGCTAGTGTGAGTGTGGCTTTGAAAAACAATGTTTTATG 360
QY 2970 CAACAAGAACGAATGTGTAGCAGCAGCTTTGGCGGCGTATGTGTGGCCAGCTTTAAC 3029
DB 361 CAACAAGAACGAATGTGTAGCAGCAGCTTTGGCGGCGTATGTGTGGCCAGCTTTAAC 420
QY 3030 CATTCAGTCTAATTAATTGGTGTGAGTCTCTGTGCAACCAACAACAGTGGCCACATGG 3089
DB 421 CATTCAGTCTAATTAATTGGTGTGAGTCTCTGTGCAACCAACAACAGTGGCCACATGG 480
QY 3090 TACTAGTCCGCTTGTCTGTGCTTCCCTAAGATGTTTGGCAACTCTAGAGCCACAGGC 3149
DB 481 TACTAGTCCGCTTGTCTGTGCTTCCCTAAGATGTTTGGCAACTCTAGAGCCACAGGC 540
QY 3150 CTAAAGATCATTAATAAAATTTCTCCCTTTGTAACTCAAGTGTGGGAGTGAAGCCAGCC 3209
DB 541 CTAAAGATCATTAATAAAATTTCTCCCTTTGTAACTCAAGTGTGGGAGTGAAGCCAGCC 600
QY 3210 CCTCAGTGTGCTGAGTGCACAGTCTTGGGGAAGAGTGCAGAGAAAGCTGTGTTTTT 3269
DB 601 CCTCAGTGTGCTGAGTGCACAGTCTTGGGGAAGAGTGCAGAGAAAGCTGTGTTTTT 660
QY 3270 ATCTC 3274
DB 661 ATCTC 665

RESULT 14
LOCUS BG031653 830 bp mRNA linear EST 24-JAN-2001
DEFINITION 603300806P1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4402320 5',
mRNA sequence.
ACCESSION BG031653
VERSION BG031653.1 GI:12422155
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NIH-MGC http://img.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@db-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNU at:
http://image.llnl.gov
Plate: ILAM1010 row: 1 column: 01
High quality sequence stop: 646.
Location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:4402320"
 /tissue_type="mammary adenocarcinoma, cell line"
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 /clone_lib="NIH_MGC_87"
 /note="Organ: breast; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally, oligo-dT primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 16.9%; Score 651.2; DB 4; Length 830;
 Best Local Similarity 93.8%; Pred. No. 5,6e-150;
 Matches 765; Conservative 0; Mismatches 43; Indels 8; Gaps 8;

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1255 CCATGCTGTCGGGACACCAAGCAATGTAAGATCCGACAGCCGACGAGCTGAGACT 1314
1315 GGCACCTGACA-GCGGTGCAAGCTGCTGCACTTGCGGTGAGAGCCGAGCAAGAGAGT 1373
61 GGCACCTGACAAGCGGTGCAAGCTGCTGCACTTGCGGTGAGAGCCGAGCAAGAGAGT 120
1374 GGCACCAAGGTGCTGCTGCAATGCAACCCCACTGAGCAACGCTAGAGGCTCA 1433
121 GGCACCAAGGTGCTGCTGCAATGCAACCCCACTGAGCAACGCTAGAGGCTCA 180
1434 CCCCGTGCACATGAGCGCTGAGAGAGAGGTGCGGGGTGCTGAGAGCTCTGCTGAC 1493
181 CCCCGTGCACATGAGCGCTGAGAGAGAGGTGCGGGGTGCTGAGAGCTCTGCTGAGCG 240
1494 GGAAGATCAGTGTCAAAGCCAAAGATGAGAGCAAGTGAAGAGCTTTCAGAGCC 1553
241 GGAAGATCAGTGTCAAAGCCAAAGATGAGAGCAAGTGAAGAGCTTTCAGAGCC 300
1554 AAGAACGGGATGAGTCTAGACACAGCGCTGCTGAGAGAGAGCTGCTGCTGCTGCTG 1613
301 AAGAACGGGATGAGTCTAGACACAGCGCTGCTGAGAGAGAGCTGCTGCTGCTGCTG 360
1614 TGAATCTTGAAGGGCCGACGCGCATGCAAGTGGCTGCGACGACGAGGAAATATG 1673
361 TGAATCTTGAAGGGCCGACGCGCATGCAAGTGGCTGCGACGAGGAGGAAATATG 420
1674 TGGCATCTGCTGCGCGGAGCGGTGAGAGCTGCAAGGCGCAAGATGCTGCTGCTG 1733
421 TGGCATCTGCTGCGCGGAGCGGTGAGAGCTGCAAGGCGCAAGATGCTGCTGCTG 480
1734 CACTGACCTAAGCTGCTGCGGAGCGCATGCTGCTGCAAGCTGCTGCGCAAGAGC 1793
481 CACTGACCTAAGCTGCTGCGGAGCGCATGCTGCTGCAAGCTGCTGCG-CAAGCAGC 538
1794 CCGGGGTGAGTGAAGCGCCAGACGCTGATGAGAGAGCGCC-ATTGCACTGAGCGCA 1852
539 CCGGGGTGAGTGAAGCGCCAGACGCTGATGAGAGAGCGCCGATGAGACCTGAGCGCA 598
1853 CAGCGGGGACCTAAGCGCGGTGCGCGCATCTGATGAGAGCTGCTGCTGCAAGCTG 1912
599 CAGCGGGGACCTAAGCGCGGTGCGCGCATCTGATGAGAGCTGCTGCTGCAAGCTG 657
1913 -TGCAGCTGCTGCG-CAAGACAGCGCGT-CAAGTGGCGCGGAGAGCGGGGCAACAGAC 1969
658 TTGCATCTGCTGAGACCAAGACACCCCTTATCTGCGGAGAGCGGGGCCAAGAGAC 717
1970 ACTGACAGGCTGCTCTGATCTGAGAGCGGTGAGAGAGAGCGCTGAGCTTCAAGCGCTAC 2029
718 ACTGACAGGCTGCTCTGATCTGAGAGCGGTGAGAGAGAGAGAGAGCGAGCTTCCAGACGGT 777
2030 ACCGCTCTGACCTGAGCTGCGCGCAACGAGACCTG 2065
778 ACCGCTTGGCCCTGCTGAGCGGAAAGCGGACCTG 813

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RESULT 15

BM980861/c
 LOCUS BM980861 657 bp mRNA linear EST 21-FEB-2003
 DEFINITION UI-CF-EN1-ade-1-02-0-UI.61 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-ade-1-02-0-UI 3', mRNA sequence.
 ACCESSION BM980861
 VERSION BM980861.1 GI:19602752
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eultheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1 (bases 1 to 657)
 TITLE Ronaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548

COMMENT
 Contact: McCray, PB

McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@iowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

source

Location/Qualifiers

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 Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-EN1"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-EN1 is a normalized cDNA library containing the
 following tissue(s): Primary Lung Cystic Fibrosis
 Epithelial Cells. The library was constructed according to
 Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was ligated to an EcoR I adaptor, digested with Not
 I, and cloned directionally into pT73-Pac vector. The
 oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is CTGCTCAGCT.
 TAG TISSUE=Human Lung Epithelial Cell lines untreated LPS
 6hr to LPS 24h
 TAG_LIB=UI-CF-EN1
 TAG_SEQ=CTGCTCAGCT"

ORIGIN

Query Match 16.8%; Score 649.6; DB 5; Length 657;
 Best Local Similarity 99.2%; Pred. No. 1.3e-149;
 Matches 652; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 297 CTTCTGAATACTGTTATTAGAAATAGTTTGTGCAAGACGTGACCTGCGTCAACATG 238
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Search completed: September 16, 2005, 06:25:32
 Job time : 11034.7 secs

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RESULT 2

US-09-949-016-1103
Sequence 1103, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1103
LENGTH: 3879
TYPE: DNA
ORGANISM: Human
US-09-949-016-1103

Query Match 98.6%; Score 3804.2; DB 4; Length 3879;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3831; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
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Qy	367	CCGGTTCCGAATTCATCCAGAGACGGCGGTGGGCAATGAATTTCTTCGACTGCATGGACCC	426
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Qy	487	CAAGATTTCTGATTTTGGTCTGGCCAGTGCAGACGGGCTGTCCCATCTGGCATGACCTCAG	546
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Qy	547	CATGATATGGCTGTATTGGCAACATGGCTCACTCCCTCAAGAGCGCATCAGGGAGAAAG	606
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Qy	967	GCTCAAGCGGGCTCTGCGCCCACTTTCGATTAACATACAGCTCTCCGAGCTTCTCTC	1026
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Db	1358	GCGGTGCAAGCTGTGCAAGCTTGGCGGTGAGAGGCGCGGCAAGAGAGTGTGCGCAAGTGGC	1417
Qy	1386	TGTCTGTCAACAAATGCCAACCCCAACTGAGCAACCTGTAGGGGCTTCAACCCCGTTGACCA	1445

Db	1418	TGCTGCTTACAAATGCCAACCCCACTTGAGCAACCGTAAAGGCTCCACCCCGTTGACA	1477
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Db	1958	CACAGACACCCCTGCAAGTGGCGCGCGGAGACGGGGACAACAGACACTGGCACGCTGTCC	2017
QY	1986	TGCATCGGGGCGCTGGCAAGAGGCGCTGACCTTCAGACGGCTACACGGCTGTGACCTGG	2045
Db	2018	TGCATCGGGGCGCTGGCAAGAGGCGCTGACCTTCAGACGGCTACACGGCTGTGACCTGG	2077
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Db	2198	AGGTGTGAGAGAGTTGGTTCAGCGCCGATGTCAATTGACCTGTTTCAGACGAGCAGGGGCTCA	2257
QY	2226	GCGCGCTGCACCTGGCGCGCCCAAGGGCGGGCACGACAGACGTGTGAGACTTGTCTCAGGC	2285
Db	2258	GCGCGCTGCACCTGGCGCGCCCAAGGGCGGGCACGACAGACGTGTGAGACTTGTCTCAGGC	2317
QY	2286	ATGGGGCCCAATCAACCTGCAAGGCGTCAAGTTTCAGGGCGGGCACATGGCCCGCGCA	2345
Db	2318	ATGGGGCCCAATCAACCTGCAAGGCGTCAAGTTTCAGGGCGGGCACATGGCCCGCGCA	2377
QY	2346	CACCTCTCGCGGAGCAAGACCTTAAAGCTGTGCTGTGCGAGACCGGGGGTTCACAGTGGG	2405
Db	2378	CACCTCTCGCGGAGCAAGACCTTAAAGCTGTGCTGTGCGAGACCGGGGGTTCACAGTGGG	2437
QY	2406	GCTCTTGTCTGTCTGTGTTCTCTGTGGGATGGAAGCATCTGTCGTGGGCGCCCTGTG	2465
Db	2438	GCTCTTGTCTGTCTGTGTTCTCTGTGGGATGGAAGCATCTGTCGTGGGCGCCCTGTG	2497
QY	2466	TGGCTTAACTTAATTTAAACCAAGCAGAGTGCATAGTGTGCATCAGGAGCGGCTGTG	2525

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 QY 2586 GATCTTAGGACCTGCTGCTGTAAGGAGCCGTGGTCCAGAAATGATTCGTGGTCTCTTA 2645
 Db 2618 GATCTTAGGACCTGCTGCTGTAAGGAGCCGTGGTCCAGAAATGATTCGTGGTCTCTTA 2677
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 Db 2738 CCTGAGGCGAGCCACTTGGGTTGCTGAGCTCACAGTCTTGGAGGAGTGCAGGGGAA 2797
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 Db 2798 ACTGTGTTTTTATCTTCAATACATGACGTGGGAGAGAGGCGTGTCTTAAGTTCCAT 2857
 QY 2826 GGAATGTTTTTATCTTCAATACATGAGATGAAATACCTTATCAGCTGTGTTGAAACCT 2885
 Db 2858 GGAATGTTTTTATCTTCAATACATGAGATGAAATACCTTATCAGCTGTGTTGAAACCT 2917
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 QY 2946 TGGCTTTGAAACAAATGTTTATGACCAAGAAAGAAAGTGTAGAGCCAGCTTTGGCGG 3005
 Db 2978 TGGCTTTGAAACAAATGTTTATGACCAAGAAAGAAAGTGTAGAGCCAGCTTTGGCGG 3037
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 Db 3098 AACCAACACACGCTGCCACATGATCTAGCTGCGGTTCTGCTTCCCTAAGATGT 3157
 QY 3126 TTTGGCACTCTAGAGCCACAGGCTTAAGATCTTAAATATTCCTCTTGTATACCTC 3185
 Db 3158 TTTGGCACTCTAGAGCCACAGGCTTAAGATCTTAAATATTCCTCTTGTATACCTC 3217
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 Db 3218 AGTGTGGGAGCTGAGGCGAGCCCTCAGGTGCTGAGTGCACAGTCTTGGGAGAA 3277
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 Db 3278 GGTGACAGAGAACTGTGTTTTTATCTCCACAGAGTATGAAATTAATCAATAGT 3337
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 Db 3338 ATTAACCTAGACATAGACAGTATTAACCTAGTATGACCTGCTCACTGCAACCTTCCCA 3397
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QY 3606 CGTGCAAAATGTAACCGTGGCTGTGTATGATGAGATTGATATTAATGATACCATGTAT 3665
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 Db 3758 ACTGCTATGTTTATTAATGCTCATTTGGCTTTTACCTGTGTGTGAGCTGCGTGAAGGA 3817
 QY 3786 CAAGAAGTTCATTTGATGATGATTAAGCAAAAGTACTGCTTCTTTTGAATCTGAA 3845
 Db 3818 CAAGAAGTTCATTTGATGATGATTAAGCAAAAGTACTGCTTCTTTTGAATCTGAA 3877
 QY 3846 AA 3847
 Db 3878 AA 3879
 RESULT 3
 US-09-949-016-5205
 ; Sequence 5205, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5205
 ; LENGTH: 3868
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-5205
 Query Match 97.9%; Score 3777.4; DB 4; Length 3868;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 3818; Conservative 0; Mismatches 11; Indels 4; Gaps 3;
 QY 7 GTCCGCGCGATGAGAGGCGGAGCGGAGACCCCATAGGCGCTGCGGCTGCTGCGACCTT 66
 Db 39 GACGTGCGCGATGAGAGGCGGAGCGGAGACCCCATAGGCGCTGCGGCTGCGACCTT 98
 QY 67 CGACGCGGCGAGTTCACGCGGCTGGAGAGAGTGGGCTCGGGCGGCTTCGAGCAGTGT 126
 Db 99 CGACGCGGCGAGTTCACGCGGCTGGAGAGAGTGGGCTCGGGCGGCTTCGAGCAGTGT 158
 QY 127 CAAGGTGCGCATGTCACCTGGAAGACCTGTGCTGCTCAATAGTCTCGCCAGCCTTGA 186
 Db 159 CAAGGTGCGCATGTCACCTGGAAGACCTGTGCTGCTCAATAGTCTCGCCAGCCTTGA 218
 QY 187 CGTGCACGACAGGAGCGCATGAGCTTTTGGAAAGACCAAGAAAGATGAGATGGCCAA 246
 Db 219 CGTGCACGACAGGAGCGCATGAGCTTTTGGAAAGACCAAGAAAGATGAGATGGCCAA 278
 QY 247 GTTTGGCTACATCCGCGGTGTATGGCATGCGCGCAACCTGTCCGCTGTGATGGA 306
 Db 279 GTTTGGCTACATCCGCGGTGTATGGCATGCGCGCAACCTGTCCGCTGTGATGGA 338
 QY 307 GTACATGAGAGCGGCTCCCTGGAAGCTGTGCTTCGAGCCATTGCAATGGATCT 366

Db 339 GTACATGAGAGACGGGCTCCCTGGAAAAGCTGTGGGCTCGAGGCCATTGGGATCT 398
Qy 367 CCGGTTCCGAAATCATATCCAGAGACGGCGGTGGGCAATGAATCTTCTGCACTGATGGCCCC 426
Db 399 CCGGTTCCGCAATCATCCAGAGACGGCGGTGGGCAATGAATCTTCTGCACTGATGGCCCC 458
Qy 427 GCCACTCCGCAACCTGGACCTTCAAGCCCGGCAATCTCGCTGGATATGCGCACTACAGT 486
Db 459 GCCACTCCGCAACCTGGACCTTCAAGCCCGGCAATCTCGCTGGATATGCGCACTACAGT 518
Qy 487 CAAGATTTCTGATTTTGGTCTGGCCAAAGTGCACACGGGCTGTCTCCATCGCATGACCTGAG 546
Db 519 CAAGATTTCTGATTTTGGTCTGGCCAAAGTGCACACGGGCTGTCTCCATCGCATGACCTGAG 578
Qy 547 CATGATGGCTGTGTTGGCAATGCTTACCTCTCTCCAGAGCCCATTCAGGAGAAAG 606
Db 579 CATGATGGCTGTGTTGGCAATGCTTACCTCTCTCCAGAGCCCATTCAGGAGAAAG 638
Qy 607 CCGGCTCTTCCAGACCAAGCAAGATGTATACAGCTTTGGATCCGATCTGGGGGGTGTCT 666
Db 639 CCGGCTCTTCCAGACCAAGCAAGATGTATACAGCTTTGGATCTGGGGGGTGTCT 698
Qy 667 CACACAGAAAGACCGTTTGCAGATGAGAAACATCTGCAATCATATGTTGAAGTGTGT 726
Db 699 CACACAGAAAGACCGTTTGCAGATGAGAAACATCTGCAATCATATGTTGAAGTGTGT 758
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Db 1898 ACCGCTGAGCCCGCATCTCATGACCTGTGCTTCCAGAGTGTCAAGCTGTGACT 1957
Qy 1926 CACAGACACCCCTGCAAGTGGCCGCGAGAGAGGGGCAACAGAGACTGGCAGGCTGTCC 1985
Db 1958 CACAGACACCCCTGCAAGTGGCCGCGAGAGAGGGGCAACAGAGACTGGCAGGCTGTCC 2017
Qy 1986 TGCATTCGGGGGCTGGAGAGAGGCGGTGACCTGAGACGGCTAACCGCTGTGACCTTG 2045
Db 2018 TGCATTCGGGGGCTGGAGAGAGGCGGTGACCTGAGACGGCTAACCGCTGTGACCTTG 2077
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QY 2586 GATCTAGGCACTGCTGCTGAGAGGGAACGTTGGGTCAAGATCATTTCCGTGTGCTCTTA 2645
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DB 2798 ACTGATTTTTTATCTTCATATCATGACGGTGGGCAAGAGGCGCTGCTTAAAGTTTCCAT 2857
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DB 2858 GGAATTTGTTTTTAAATAATCTTAAAGATGAATACCTTATCAGCTGTTGCTGAACCT 2917
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DB 3098 AACCAACACACAGTGGCCACATGCTATGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTG 3157
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DB 3216 AGTGTCTGGGACCTGAGCGAGCCCTCAGTCTGCTGAGTGCACCAAGTCTTGGGGAGA 3275
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DB 3276 GGTGCAAGAAAGCTGTGTTTTTATCTCAACGAGATGAGTAAGTAAATTAACATAGT 3335
QY 3306 ATTACCTTAACATPAGCAGTATTAATCTAGTAGATGACATGCTGCACTGCACTTCCCA 3365
DB 3336 ATTACCTTAACATPAGCAGTATTAATCTAGTAGATGACATGCTGCACTGCACTTCCCA 3395
QY 3366 GCTCTCATTTTTTTTATGATGATTTGGGATAGGGATAGTGTGGGGATAGGGGGAGTG 3425
DB 3396 GCTCTCATTTTTTTTATGATGATTTGGGATAGGGATAGTGTGGGGATAGGGGGAGTG 3455
QY 3426 TTTCTGACCTGCTTTGACAGCTGCTCCGCACTGACAGATTTGGGGGTGTGGCCCCAAG 3485
DB 3456 TTTCTGACCTGCTTTGACAGCTGCTCCGCACTGACAGATTTGGGGGTGTGGCCCCAAG 3515
QY 3486 GGGGTTCTTGAATGTAAGATGAGCTGACCTGCTGTAACCTTCACTGCTCACTGTGT 3545
DB 3516 GGGGTTCTTGAATGTAAGATGAGCTGACCTGCTGTAACCTTCACTGCTCACTGTGT 3575
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QY 3606 CCGTCAAAATGATCCGTGCTGTATATGATAGATTTGAATTAATGTAACATGATAT 3665

DB 3636 CGTGCAAAACATGATCCGTGGCTGTATATGATGATGATGATGATGATGATGATGATGAT 3695
QY 3666 GTTATATGATATCTGTGGGAGAGATTAATTTCCATGCGCAGAGAAATATCCAGCTTGAA 3725
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DB 3756 ACTGCTATGTTTTTATATATGCTCATTTGCTCTTATCTGTTGTGAGCTGCGTAGGGA 3815
QY 3786 CAAGAAGTTCCATTTGATGATGATPAAAGCAAAAGTACTTGCCTACTTTTGA 3838
DB 3816 CAAGAAGTTCCATTTGATGATGATPAAAGCAAAAGTACTTGCCTACTTTTGA 3868

RESULT 4
US-09-799-451-905
; Sequence 905, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feijian
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799, 451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 905
; LENGTH: 3981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (2496)
US-09-799-451-905

Query Match 94.4%; Score 3643; DB 4; Length 3981;
Best Local Similarity 96.1%; Pred. No. 0; Indels 146; Gaps 3;
Matches 3825; Conservative 0; Mismatches 11;

QY 17 ATGAGGCGCAGCGGCGGAGCCCATGAGGCGCTGCTGCGCACCTTGCACGCGGAGC 76
DB 1 ATGAGGCGCAGCGGCGGAGCCCATGAGGCGCTGCTGCGCACCTTGCACGCGGAGC 60
QY 77 GAGTTACAGGGCTGAGAGAGGTGGGCTCGGCGGCTTGGGCAAGTGTACAGGTGGC 136
DB 61 GAGTTACAGGGCTGAGAGAGGTGGGCTCGGCGGCTTGGGCAAGTGTACAGGTGGC 120
QY 137 CATGTCCATGGAAGACCTGGCTGGCCATCAAGTGTGCGCCAGCTGCAAGTGTGAGC 196
DB 121 CATGTCCATGGAAGACCTGGCTGGCCATCAAGTGTGCGCCAGCTGCAAGTGTGAGC 180
QY 197 AGGAGCCCATGAGCTTTTGAAGAGCAAGAGATGAGATGAGCCAGTTTGTGCTAC 256

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Db	241	ATCTGCCTGTGTATAGCATCTGCCTGCAGACCTGTGGCTGTGATCAATGAGTACATGAG	300
Oy	317	ACGGGCTCTCTGGAAGAAAGCTGTGGCTTTCCGAGCCATTGGCATTTCTCCGGTTCCGA	376
Db	301	ACGGGCTCTCTGGAAGAAAGCTGTGGCTTTCCGAGCCATTGGCATTTCTCCGGTTCCGA	360
Oy	377	ATCATCCAGAGACGGCGGTGGAGCATGAATCTTCCGCACTGACATGAGCCCGCCACTCTCG	436
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Db	421	CACCTGGAACCTCAAGCCCGCGAGACATCTCTGTGATGAGCCCATACAGTCAGAAATTTCT	480
Oy	497	GATTTTGGTCTGGCCCAATGCGACGGGCTGTCCCATCTGCAATGACTTCAAGATGAGTGGC	556
Db	481	GATTTTGGTCTGGCCCAATGCGACGGGCTGTCCCATCTGCAATGACTTCAAGATGAGTGGC	540
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Oy	617	GACACCAAGCAGATGTATACAGCTTTTGCATTCGATCTGAGGGCGTGTCAACAGAG	676
Db	601	GACACCAAGCAGATGTATACAGCTTTTGCATTCGATCTGAGGGCGTGTCAACAGAG	660
Oy	677	AAAGCGTTTGCAGATGAGAGAAACATCTGCAATCATGTGAAAGTGTGAAAGGGCCAC	736
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Oy	737	CGCCCCGAGCTCGCGCCCGGTGTGAGAGACCCGGCCGGCGGCGTGAAGCACTGATATACG	796
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Oy	893	GAAAGTGAAGAAACGTCTCATATGATCTGAGCGTGAAGACCCGCCCGAGCCAGAGCGAG	952
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Oy	1013	TCCGAGCTTCTCTCAAGCTGGAACCTGGAAGTTTCCAGAGGCTGTGAGAGGCCCGAGAG	1072
Db	1141	TCCGAGCTTCTCTCAAGCTGGAACCTTGAAGTTTCCAGAGGCTGTGAGAGGCCCGAGAG	1200
Oy	1073	CTCAAGCCGAGCTCTCTGAGTCAAGCTGCCATGTCGCGCAGTGGAGAAAGGCTCTCG	1132
Db	1201	CTCAAGCCGAGCTCTCTGAGTCAAGCTGCCATGTCGCGCAGTGGAGAAAGGCTCTCG	1260
Oy	1133	GGGGTGTCTCGGTGAGATCGGCTTTCTTTCAGAGATCATCTGTGGCTGTCTTTGAG	1192
Db	1261	GGGGTGTCTCGGTGAGATCGGCTTTCTTTCAGAGATCATCTGTGGCTGTCTTTGAG	1320

QY	1193	CGGGACCTTTCACACAGCGATCTTGATACAAAGA	CGTCCAGAGAAGAA	CGTTGTGGA	1252
Db	1321	CGGGACCTTTCACACAGCGATCTTGATACAAAGA	CGTCCAGAGAAGAA	CGTTGTGGA	1379
QY	1253	TGCGATGCTGTCC	-GGGACACACAGCAACGTAGTAATCTTGAGCGCGAGAGCTGTGGA		1311
Db	1380	TGCGATGCTGTCC	GGGGAGACACAGCAACGTAGTAATCTTGAGCGCGAGAGCTGTGGA		1439
QY	1312	CTTGCGACCTGAGCAGCGGTGCGACCTTGTCACCTTGACCTGACCGGTGAGGCTCGGGCAAGAGA			1371
Db	1440	CCTGCGACCTGAGCAGCGGTGCGACCTTGTCACCTTGACCGGTGAGGCTCGGGCAAGAGA			1499
QY	1372	GTGGCGCAAGTGGCTGCTCAACATGCGAACCCCA	CGTGGCAACGCTAGGGCTC		1431
Db	1500	GTGGCGCAAGTGGCTGCTCAACATGCGAACCCCA	CGTGGCAACGCTAGGGCTC		1559
QY	1432	CACCCCGTTCACATGCGCGCTGAGAGAGAGGTGCGGGGTGT	CGTGGAGCTCTTGCTGCG		1491
Db	1560	CACCCCGTTCACATGCGCGCTGAGAGAGAGGTGCGGGGTGT	CGTGGAGCTCTTGCTGCG		1619
QY	1492	ACGGAAGATCAGTGTCAA	CGCCAAAGATTAGAGACCAAGTGGACAGCCCTTCCA	CTTTGCAAC	1551
Db	1620	GCGGAAGATCAGTGTCAA	CGCCAAAGATTAGAGACCAAGTGGACAGCCCTTCCA	CTTTGCAAC	1679
QY	1552	CCAGAACGGGGATGATGCTTAGCACACGGGCTCTGTTGAGAGAGAACGCTCGGTCAACGA			1611
Db	1680	CCAGAACGGGGATGATGCTTAGCACACGGGCTCTGTTGAGAGAGAACGCTCGGTCAACGA			1739
QY	1612	GATGACCTTTAGGGGCGGAGCGCCCATGTCACGTGAGCTTGCCAGCA	CGGGCAGAGAAATAT		1671
Db	1740	GATGACCTTTAGGGGCGGAGCGCCCATGTCACGTGAGCTTGCCAGCA	CGGGCAGAGAAATAT		1799
QY	1672	CGTGCGCATCTCGTGGCGCGAGGCGGTGGA	CGTAGCGCTGACGAGGCAAGATGCTGAGCT		1731
Db	1800	CGTGCGCATCTCGTGGCGCGAGGCGGTGGA	CGTAGCGCTGACGAGGCAAGATGCTGAGCT		1859
QY	1732	GCACATGCATCAGCGCTGCTTGAGCAGGGCAC	CTGCGCATGCTGCAAGCTGCTGGCCAAAGA		1791
Db	1860	GCACATGCATCAGCGCTGCTTGAGCAGGGCAC	CTGCGCATGCTGCAAGCTGCTGGCCAAAGA		1919
QY	1792	GCCTGGGCTGATGTGAA	CGCGCCAGAGCGTGGATGGAGAGACGCGCATTTGCACTGGGCGC		1851
Db	1920	GCCTGGGCTGATGTGAA	CGCGCCAGAGCGTGGATGGAGAGACGCGCATTTGCACTGGGCGC		1979
QY	1852	ACAGCGCGGAGACTACCGCTGAGCGCGCATCTATGCA	CGCTGTGCTTCCAGCTCAACGT		1911
Db	1980	ACAGCGCGGAGACTACCGCGCTGAGCGCGCATCTATGCA	CGCTGTGCTTCCAGCTCAACGT		2039
QY	1912	CTGCAAGCTGTGGACAGACACCCCTTGAC	CTGACCGCGGAGACCGGGCACACGAGCAC		1971
Db	2040	CTGCAAGCTGTGGACAGACACCCCTTGAC	CTGACCGCGGAGACCGGGCACACGAGCAC		2099
QY	1972	TGCGACGGCTGCTCCGTCATCGGGGCGCTGGCAAGAGAGCGTGA	CTTCAAGCGCTACAC		2031
Db	2100	TGCGACGGCTGCTCCGTCATCGGGGCGCTGGCAAGAGAGCGTGA	CTTCAAGCGCTACAC		2159
QY	2032	CGCTCTGCACTTGCTGCGCGCAACGAGCAC	CTGCGCACTGTCAAGCTGTTGTGAGGA		2091
Db	2160	CGCTCTGCACTTGCTGCGCGCGCAACGAGCAC	CTGCGCACTGTCAAGCTGTTGTGAGGA		2219
QY	2092	GAAAGCCGATGTGCTGCGCGCGGGAGACCCCTTAA	CCAGACGGCGCTGCACTGGGCTGGCGC		2151
Db	2220	GAAAGCCGATGTGCTGCGCGCGGGAGACCCCTTAA	CCAGACGGCGCTGCACTGGGCTGGCGC		2279
QY	2152	CCA	CGGAGCTGAGAGGATGTGATGACGCGCGCATGTCAATTTGACTGTTTGA		2211
Db	2280	CCA	CGGAGCTGAGAGGATGTGATGACGCGCGCATGTCAATTTGACTGTTTGA		2339
QY	2212	CGAGCAGGGCTC	ACGCGGCTTGACCTTGCGCCCAAGGCGCGGACCGACAGACAGCGGTGGA		2271
Db	2340	CGAGCAGGGCTC	ACGCGGCTTGACCTTGCGCCCAAGGCGCGGACCGACAGACAGCGGTGGA		2399

QY	1330	TGCCAGCTTGCTGCACTCGGCGGTGGAGAGCGCGCAAGAGAGTGGCCAACTGCTGCT	1389
Db	27214	TGCCAGCTTGCTGCACTCGGCGGTGGAGAGCGCGCAAGAGAGTGGCCAACTGCTGCT	27273
QY	1390	GCTCAACAAATGCCAAACCCCAACCTGAGCAACCTGATGGGGCTCCACCCCGTTGCAATGAC	1449
Db	27274	GCTCAACAAATGCCAAACCCCAACCTGAGCAACCTGATGGGGCTCCACCCCGTTGCAATGAC	27333
QY	1450	CGTGGAGAGAGAGGGTGCAGGAGTGTCTGTAGAGCTCTCTGGACAAGAAATCACTGTCAA	1509
Db	27334	CGTGGAGAGAGAGGGTGCAGGAGTGTCTGTAGAGCTCTCTGGAGAAATCACTGTCAA	27393
QY	1510	CGCCAAGATAGAGCCATGTGACAAGCCCTTCACTTTGACACCCAGACCGAGATGATC	1569
Db	27394	CGCCAAGATAGAGCCATGTGACAAGCCCTTCACTTTGACACCGAGATGATC	27453
QY	1570	TAGCAACAAGGCGGTGTGGAGAAAGACGCTCGGTCAAGAGGTGACCTTGAAGGGCGG	1629
Db	27454	TAGCAACAAGGCGGTGTGGAGAAAGACGCTCGGTCAAGAGGTGACCTTGAAGGGCGG	27513
QY	1630	GACGCCATGACAGCTGAGCTTCCACACAACGAGCAAGAAATATCGTGGCATCTCTGTGAG	1689
Db	27514	GACGCCATGACAGCTGAGCTTCCACACAACGAGCAAGAAATATCGTGGCATCTCTGTGAG	27573
QY	1690	CCGAGCGCTGACGTAGCTTGCACAGGCAAGATATCGTGTGCACTGCACTACCTGCG	1749
Db	27574	CCGAGCGCTGACGTAGCTTGCACAGGCAAGATATCGTGTGCACTGCACTACCTGCG	27633
QY	1750	CTGGAGAGGGCCACTCGGCCATCTGTCAAGCTGTGGCCAAACGCGGGGGTGTAGTGTAA	1809
Db	27634	CTGGAGAGGGCCACTCGGCCATCTGTCAAGCTGTGGCCAAACGCGGGGGTGTAGTGTAA	27693
QY	1810	CGCCCAAGAGCTGAGTGGAGAGAGCCATTGCACTTGGCGCACAGCGCGAGCACTAACG	1869
Db	27694	CGCCCAAGAGCTGAGTGGAGAGAGCCATTGCACTTGGCGCACAGCGCGAGCACTAACG	27753
QY	1870	CGTGGCGCGCATCTCTCATGACCTTGTGCTCGACGTCAACGTGTGACAGCTTGGCAACA	1929
Db	27754	CGTGGCGCGCATCTCTCATGACCTTGTGCTCGACGTCAACGTGTGACAGCTTGGCAACA	27813
QY	1930	GACACCCCTGACAGTGTGGCGGGGAGAGAGGCAACAGACATGCGCAAGGTGTCTCTGCA	1989
Db	27814	GACACCCCTGACAGTGTGGCGGGGAGAGAGGCAACAGACATGCGCAAGGTGTCTCTGCA	27873
QY	1990	TGCGGGCGCTGGCAAGAGGCGGTGACCTTGAACGGCTAACACGCTTGTGCACTTGGCTGC	2049
Db	27874	TGCGGGCGCTGGCAAGAGGCGGTGACCTTGAACGGCTAACACGCTTGTGCACTTGGCTGC	27933
QY	2050	CCGCAACGAGCAACTGTGCACCTGTCAAGCTTGTGTGAGAGAAAGGCGAGTGTGTGC	2109
Db	27934	CCGCAACGAGCAACTGTGCACCTGTCAAGCTTGTGTGAGAGAAAGGCGAGTGTGTGC	27993
QY	2110	CCGGGGAACCCCTGAAACAGAGGCGGTGCACCTGTGGCGGCCACAGGAGACCTGGAGGT	2169
Db	27994	CCGGGGAACCCCTGAAACAGAGGCGGTGCACCTGTGGCGGCCACAGGAGACCTGGAGGT	28053
QY	2170	GGTGGAGAGATTGTGTCAAGCGCCATGTCAATTGAACCTTGTGACAGAGAGGGCTCAGAGC	2229
Db	28054	GGTGGAGAGATTGTGTCAAGCGCCATGTCAATTGAACCTTGTGACAGAGAGGGCTCAGAGC	28113
QY	2230	GCTGCACTTGAGCGCGCCAGGGCGGCAACGACAGAGGATGAGATCTTGTCAAGGATGG	2289
Db	28114	GCTGCACTTGAGCGCGCCAGGGCGGCAACGACAGAGGATGAGATCTTGTCAAGGATGG	28173
QY	2290	GGCCCAATCAACTGTGAGAGCTTCAAGTTCAAGGGGGGCAATGAGCCCGGCGCAACT	2349
Db	28174	GGCCCAATCAACTGTGAGAGCTTCAAGTTCAAGGGGGGCAATGAGCCCGGCGCAACT	28233
QY	2350	CGTGGAGAGAGCAAGCACTTATGCTGTGGCGCTGAGAGACCGAGGGGTCAAGTGGGGCTC	2409
Db	28234	CGTGGAGAGAGCAAGCACTTATGCTGTGGCGCTGAGAGACCGAGGGGTCAAGTGGGGCTC	28293
QY	2410	TTGTCTGTCTGTGTGTTCTCTGTGGGAGTGAAGATCTGCTGAGGGGCCCGGTGTGAGC	2469

Db	28294	TTGTCCTGCTCTGTTCTCTGCGGGATGAAAGATCTCGCTGGGGCCCGTTGGC	28355
Qy	2470	TTACCTTAAAGTTTAAACAAGAGGAGCATGGTGCATCAGAGAGCGGCTGCTGTA	2529
Db	28354	TTTACTTAAATTTTATACCAACAGAGGAGCATGGTGCATCAGAGAGCGGCTGCTGTA	28411
Qy	2530	CCGAGAGTGTCCCTCCAGGTGAAGCTGGCTCAGGTGCATGCTCCGCTCATCATGATC	2589
Db	28414	CCGAGAGTGTCCCTCCAGGTGAAGCTGGCTCAGGTGCATGCTCCGCTCATCATGATC	28472
Qy	2530	TAGGCACCTGTGTCTGAAGGAGCCGTGGGTCAAGTCAATTTGGTGTGCTCTAATGGG	2649
Db	28474	TAGGCACCTGTGTCTGAAGGAGCCGTGGGTCAAGTCAATTTGGTGTGCTCTAATGGG	28533
Qy	2650	TCGCTGAGGCTGTGTCTCAGTATGAAGCCCAAGCGTGAAGATCCACTCTCTCTG	2709
Db	28534	TCGCTGAGGCTGTGTCTCAGTATGAAGCCCAAGCGTGAAGATCCACTCTCTCTG	28599
Qy	2710	AGCGGAGCCACTTGGGTTGCTGGAGCTCAACAGTCTTGAGGAGGTGCAGGGGAACTG	2769
Db	28594	AGCGGAGCCACTTGGGTTGCTGGAGCTCAACAGTCTTGAGGAGGTGCAGGGGAACTG	28655
Qy	2770	TGTTTTTATCTTATACATGACGTGGGAGAGAGCCCTGTCTTAAAGTTTCCATGGA	2829
Db	28654	TGTTTTTATCTTATACATGACGTGGGAGAGAGCCCTGTCTTAAAGTTTCCATGGA	28711
Qy	2830	TTGTTTTATAAATATCTTAAAGATGAATACCTTACAGCTGTGCTTGAACCTGTGA	2889
Db	28714	TTGTTTTATAAATATCTTAAAGATGAATACCTTACAGCTGTGCTTGAACCTGTGA	28777
Qy	2890	AAAATGTTCAATACATTTGATAGTACTAGTCTTAAATGATGCTTAAGTACTGAGTTGGC	2949
Db	28774	AAAATGTTCAATACATTTGATAGTACTAGTCTTAAATGATGCTTAAGTACTGAGTTGGC	28833
Qy	2950	TTTGGAAAAATGTTTTATATGCAACAAGAAAGATGTATGACACCACTTTGGGGGGCGT	3009
Db	28834	TTTGGAAAAATGTTTTATATGCAACAAGAAAGATGTATGACACCACTTTGGGGGGCGT	28893
Qy	3010	ATGTGTGGCCAGCTCTTAAACATTCAGAGCTAATTTACTTGGGTGAGTCTTGTGGAACCC	3069
Db	28894	ATGTGTGGCCAGCTCTTAAACATTCAGAGCTAATTTACTTGGGTGAGTCTTGTGGAACCC	28955
Qy	3070	ACACACACGTGCCACATGGTACTAGCTGCGTTCGTTTCGTTGCTTAAGATGTTTTG	3129
Db	28954	ACACACACGTGCCACATGGTACTAGCTGCGTTCGTTTCGTTGCTTAAGATGTTTTG	29011
Qy	3130	GCAACTCTAAGGCCACACGGCTAAGAGTCATTTAAAAATTTCTCCCTTTGTAACCTCAGTC	3189
Db	29014	GCAACTCTAAGGCCACACGGCTAAGAGTCATTTAAAAATTTCTCCCTTTGTAACCTCAGTC	29077
Qy	3180	CTGGGGACTGAGGGAGAGCCCGCTCAGGTCCTGGAAGTGCACACAGTCTTGGGGAAGAGTTC	3249
Db	29072	CTGGGGACTGAGGGAGAGCCCGCTCAGGTCCTGGAAGTGCACACAGTCTTGGGGAAGAGTTC	29133
Qy	3250	CAGAGAAAGCTGTGTTTTTATCTCAACACAGATGAAGATPAAATTCATATGATATTA	3309
Db	29132	CAGAGAAAGCTGTGTTTTTATCTCAACACAGATGAAGATPAAATTCATATGATATTA	29191
Qy	3310	CTTACAGCATAGACAGTATTTACCTTAGTGAATGCACTGCTCACTGCAACCTTCCAGCTTC	3369
Db	29192	CTTACAGCATAGACAGTATTTACCTTAGTGAATGCACTGCTCACTGCAACCTTCCAGCTTC	29251
Qy	3370	TCATTTTTGTAGGTGATTTGGGATAGAGATAGTGTGGGTATAGGGGGAGAGTGTTC	3429
Db	29252	TCATTTTTGTAGGTGATTTGGGATAGAGATAGTGTGGGTATAGGGGGAGAGTGTTC	29311
Qy	3430	TGACCTGCTTTGCAGACGTGCTCCGACCTCAGACATTTGGGGTGTGCCCCAGGAGCGG	3489
Db	29312	TGACCTGCTTTGCAGACGTGCTCCGACCTCAGACATTTGGGGTGTGCCCCAGGAGCGG	29377
Qy	3490	TTCTTGGATGTAAGATGTGGCCATCTAGCTTGTACTTCACTGTCACTGTGTGCCA	3549

Db	28474	TAAGCACTGCTGCTCTAAGAGGACCGTGGGTCAAGATTCATTTCCTGTGCTCTTAATGGG	28533
Qy	2650	TCGCTGAAGGCTGCTCTCTCACTGATGATGAAGCCCAAGCGTGGAGATCCACTCTCTCTG	2709
Db	28534	TCGCTGAAGCGTGGTCTCTCTCACTGATGATGAAGCCCAAGCGTGGAGATCCACTCTCTCTG	28593
Qy	2710	AGGCGAGCCACCTTGGGTTGCTGGAGCTCAACAGCTTGAAGGGAAGGTGCAAGGGGAAAC	2769
Db	28594	AGGCGAGCCACCTTGGGTTGCTGGAGCTCAACAGCTTGAAGGGAAGGTGCAAGGGGAAAC	28653
Qy	2770	TGTTTTTATCTTCATACATGACGCTGGGAGAGAGGCGCTGTCTTAAAGTTTCAATGAA	2829
Db	28654	TGTTTTTATCTTCATACATGACGCTGGGAGAGAGGCGCTGTCTTAAAGTTTCAATGAA	28713
Qy	2830	TTGTTTTATMAAATATCTTAAGAGATGAATACCTTATCAGCTGTGCTTGAACCTGTTA	2889
Db	28714	TTGTTTTATMAAATATCTTAAGAGATGAATACCTTATCAGCTGTGCTTGAACCTGTTA	28773
Qy	2880	AAAAATGTTTCAATACATTTGGATAGCTTAGTCTCTTAATGATGGCTAAGTAGTGGGTTGGC	2949
Db	28774	AAAAATGTTTCAATACATTTGGATAGCTTAGTCTCTTAATGATGGCTAAGTAGTGGGTTGGC	28833
Qy	2950	TTTGAAGAACATGTTTATATGCAACAGAGAAAGATGCTAGCAGCCAGCTTTGGCGGGCGCT	3009
Db	28834	TTTGAAGAACATGTTTATATGCAACAGAGAAAGATGCTAGCAGCCAGCTTTGGCGGGCGCT	28893
Qy	3010	ATGCTGTGGCCAGCTCTTAAACCATTCACAGTCTATTTACTTGGGATGAGTCTTGTGGACAA	3069
Db	28894	ATGCTGTGGCCAGCTCTTAAACCATTCACAGTCTATTTACTTGGGATGAGTCTTGTGGACAA	28953
Qy	3070	AACAACACGTGGCCCACTGGTATCTAGCTGCCGTTCCGTTTCTCGTGGCTTAAGATGTTTG	3129
Db	28954	AACAACACGTGGCCCACTGGTATCTAGCTGCCGTTCCGTTTCTCGTGGCTTAAGATGTTTG	29013
Qy	3130	GCAACTCTAGAGGACACAGGCGCTAAGAGCTAATAAAAAATCTCCCTTGTGAACCTGAGTG	3189
Db	29014	GCAACTCTAGAGGACACAGGCGCTAAGAGCTAATAAAAAATCTCCCTTGTGAACCTGAGTG	29071
Qy	3190	CTGGGGACTGAGGGAGAGGCCCTTCAAGGTGCTGTGAGTGACCAAGTCTTGGGGAAGAAGTG	3249
Db	29072	CTGGGGACTGAGGGAGAGGCCCTTCAAGGTGCTGTGAGTGACCAAGTCTTGGGGAAGAAGTG	29133
Qy	3250	CAGAGAGAGCTGTGTTTTTATCTTCCACACGCACTATGAAGATTAATTAATCATATGATTA	3309
Db	29132	CAGAGAGAGCTGTGTTTTTATCTTCCACACGCACTATGAAGATTAATTAATCATATGATTA	29191
Qy	3310	CCTAGACATTAACAGTATTAACCTAAGGATGATGACCTGCTCAACCTGCAACCTTCCAGCTG	3369
Db	29192	CCTAGACATTAACAGTATTAACCTAAGGATGATGACCTGCTCAACCTGCAACCTTCCAGCTG	29251
Qy	3370	TCAATTTTGTAGGTGATTTTGGATATAGGATATGCTTTTGGGATATGGGAGAGTGTTC	3429
Db	29252	TCAATTTTGTAGGTGATTTTGGATATAGGATATGCTTTTGGGATATGGGAGAGTGTTC	29311
Qy	3430	TGACCTGCTTTGACAGACGTGCTCCGACCTCAGACATTTTGGGATGTGGCCCAAGGCGG	3489
Db	29312	TGACCTGCTTTGACAGACGTGCTCCGACCTCAGACATTTTGGGATGTGGCCCAAGGCGG	29371
Qy	3490	TTCTTGGATGTAAGAAAGATGGGCGCATCTAGCTGTGTAATTTCACTGTCACTGTGTCCCA	3549
Db	29372	TTCTTGGATGTAAGAAAGATGGGCGCATCTAGCTGTGTAATTTCACTGTCACTGTGTCCCA	29431
Qy	3550	TAGGGTGCCTTCTGAATCTGTTATTTAGAAATTAAGTTTGTGACAAAGTGAACCTGCTG	3609
Db	29432	TAGGGTGCCTTCTGAATCTGTTATTTAGAAATTAAGTTTGTGACAAAGTGAACCTGCTG	29491
Qy	3610	CAAAATGATACCTGTGGCCCTGTGATATGATAGAGATTGATATTAATGATCAATGATATGTA	3669
Db	29492	CAAAATGATACCTGTGGCCCTGTGATATGATAGAGATTGATATTAATGATCAATGATATGTA	29551
Qy	3670	ATGTGAATCTGTGGGACAGAGATCTTTTTCATGTGACAGAAATATTCAAAGCTGTGAAAC	3729
Db	29552	ATGTGAATCTGTGGGACAGAGATCTTTTTCATGTGACAGAAATATTCAAAGCTGTGAAAC	29611

Qy	3730	GCATGTTTAAATATGCTCATTTGCTCTTACTGTGTGTGTGAGCTCGGTGAGGAGCAAG	3789
Db	29612	GCTATGTTTAAATATGCTCATTTGCTCTTACTGTGTGTGTGAGCTCGGTGAGGAGCAAG	29657
Qy	3790	AAGTTCATTTGAGTGCATATTAAGCAAGACTTGCCTACTTTTGTGANCTG	3842
Db	29672	AAGTTCATTTGAGTGCATATTAAGCAAGACTTGCCTACTTTTGTGAGCTG	29724

RESULT 7
US-09-781-882-3
; Sequence 3, Application US/09781882
; Patent No. 6630335
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 14171 Protein Kinase, a No. 6630335el Human
; TITLE OF INVENTION: Protein Kinase and Uses Thereof
; FILE REFERENCE: 035800-209014(5800-6
; CURRENT APPLICATION NUMBER: US/09/781,882
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: U.S. 60/182,096
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: H. sapiens
US-09-781-882-3

Query Match	61.0%; Score 2355; DB 4; Length 2355;
Beet Local Similarity	100.0%; Pred. No. 0;
Matches 2355; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

Qy	17	ATGAGAGGCGACGCGCGGAGCCCAATGCGGCTCTGCGCTGCTGCGACCTTGACGCGGCG	76
Db	1	ATGAGAGGCGACGCGCGGAGCCCAATGCGGCTCTGCGCTGCTGCGACCTTGACGCGGCG	60
Qy	77	GAGTTCAAGGGCTGGGAGAAAGGTGGGCTCGGGCGGCTTCCGGGAGGTGTACAAGTGGCG	136
Db	61	GAGTTCAAGGGCTGGGAGAAAGGTGGGCTCGGGCGGCTTCCGGGAGGTGTACAAGTGGCG	120
Qy	137	CATGTCACCTGGAAGACTGTGGCTGGCCATCAAGTGTGCTGCCACGCTTGCAGTGCAGC	196
Db	121	CATGTCACCTGGAAGACTGTGGCTGGCCATCAAGTGTGCTGCCACGCTTGCAGTGCAGC	180
Qy	197	AAGGAGCGCATGAGACTTTTGGAAAGACCAGAAAGATGAGATGGCCAGTTTGGCTAC	256
Db	181	AAGGAGCGCATGAGACTTTTGGAAAGACCAGAAAGATGAGATGGCCAGTTTGGCTAC	240
Qy	237	ATCCGCTCTGTGTATGAGATATGCGCGGAGACTGTGGGCTGGTGTATGAGATACATGGAG	316
Db	241	ATCCGCTCTGTGTATGAGATATGCGCGGAGACTGTGGGCTGGTGTATGAGATACATGGAG	300
Qy	317	ACGGGCTCCCTGGAAAGACTGTGGCTTGGAGCCATTGGCCATTTGCGGTTCCGA	376
Db	301	ACGGGCTCCCTGGAAAGACTGTGGCTTGGAGCCATTGGCCATTTGCGGTTCCGA	360
Qy	377	ATCATCCACGAGACGGCGGTGGGCAATGAACTTCTGCACTGCAATGGCCCGGCACTCTG	436
Db	361	ATCATCCACGAGACGGCGGTGGGCAATGAACTTCTGCACTGCAATGGCCCGGCACTCTG	420
Qy	437	CACCTGGGACTCAAGCCCGCGAATCATCTGGTGGATGGCCACTACAGTCAAGATTCT	496
Db	421	CACCTGGGACTCAAGCCCGCGAATCATCTGGTGGATGGCCACTACAGTCAAGATTCT	480
Qy	497	GATTTTGGTCTGGCCAGTGCACGGGCTGTCCACTTGCATGACTTACAGATGGATGGC	556
Db	481	GATTTTGGTCTGGCCAGTGCACGGGCTGTCCACTTGCATGACTTACAGATGGATGGC	540
Qy	557	CTGTTTGGGCAATGCGCTACTCTCCTTCAAGAGGCGATCAGGAGAAAGCGGCTCTTC	616

Db 541 CTGTTGGGCAATGCGCTACCTCCCTCCAGAGCGCATCAGAGGAGAAGACCGGCTTTC 600
QY 617 GACACCAAGCAGATGTATACAGCTTTGGATGTCATCTGGGGGTGCTCAACAAGAG 676
Db 601 GACACCAAGCAGATGTATACAGCTTTGGATGTCATCTGGGGGTGCTCAACAAGAG 660
QY 677 AAGCGTTTGGCAGATGAGAAGAACATCCCTGCAATCAATGATGAGTGTGAAGGGCCAC 736
Db 661 AAGCGTTTGGCAGATGAGAAGAACATCCCTGCAATCAATGATGAGTGTGAAGGGCCAC 720
QY 737 GCGCCCGAGCTGCGCGCGGTGTCAGAGCCGCGCGCGCTGACGCCACTGATACGC 796
Db 721 GCGCCCGAGCTGCGCGCGGTGTCAGAGCCGCGCGCGCTGACGCCACTGATACGC 780
QY 797 CTATGTCAGCGGTGTCGAGGGGGGATCCGAGTTAGGCCCACTTCCAGAAATTAAT 856
Db 781 CTATGTCAGCGGTGTCGAGGGGGGATCCGAGTTAGGCCCACTTCCAGAAATTAAT 840
QY 857 TCTGAAACCGAGAGACTGTGTGTAAGAAAGCTGATGACGAAGTGAAGAAATCTGCTATGAT 916
Db 841 TCTGAAACCGAGAGACTGTGTGTAAGAAAGCTGATGACGAAGTGAAGAAATCTGCTATGAT 900
QY 917 CTGGAAGTGAAGAGCCCGCGAGCCAGAGCGAGGTGCTGTCAGAGCTTCTCAGAGCTGAC 976
Db 901 CTGGAAGTGAAGAGCCCGCGAGCCAGAGCGAGGTGCTGTCAGAGCTTCTCAGAGCTGAC 960
QY 977 GCGCTGCGCCCACTTTCATTAACGATCAAGCTCTCCAGCTTCTCAGAGCTGAC 1036
Db 961 GCGCTGCGCCCACTTTCATTAACGATCAAGCTCTCCAGCTTCTCAGAGCTGAC 1020
QY 1037 TCTGAGTTTCCAGAGCTTCCAGAGGCTCCAGAGAGCTCAAGCTGCTCTGATGTC 1096
Db 1021 TCTGAGTTTCCAGAGCTTCCAGAGGCTCCAGAGAGCTCAAGCTGCTCTGATGTC 1080
QY 1097 AAGCTGCAATCGTCCGCGAGTGGGAAAGAGCTCTCGGGGGTGTCTCGGTGACCTCCGC 1156
Db 1081 AAGCTGCAATCGTCCGCGAGTGGGAAAGAGCTCTCGGGGGTGTCTCGGTGACCTCCGC 1140
QY 1157 TTTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGAACTTTCACACGATCTG 1216
Db 1141 TTTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGAACTTTCACACGATCTG 1200
QY 1217 GGTACCAAGAGCTGCAAGAAAGAGCTTGTGATGCTGTCCTGGGACACACAC 1276
Db 1201 GGTACCAAGAGCTGCAAGAAAGAGCTTGTGATGCTGTCCTGGGACACACAC 1260
QY 1277 AAACTGATGAAGTCTCTGAGCGCGAGAGCTGGAATCTGGAAGCGGTGAC 1336
Db 1261 AAACTGATGAAGTCTCTGAGCGCGAGAGCTGGAATCTGGAAGCGGTGAC 1320
QY 1337 CTGCTGCACTGCGGTGAGAGCGCGGCAAGAGAGTGCCTCAAGTGTGCTCTCAAC 1396
Db 1321 CTGCTGCACTGCGGTGAGAGCGCGGCAAGAGAGTGTGCTCTCAAGTGTGCTCTCAAC 1380
QY 1397 AATGCAACCCCAACTGAGCAACCTGAGGGCTTCCACCCCTGTGCAATGCGGTGAG 1456
Db 1381 AATGCAACCCCAACTGAGCAACCTGAGGGCTTCCACCCCTGTGCAATGCGGTGAG 1440
QY 1457 AAGAGGTCGCGGGTGTGTCAGCTCTGTCGGCAAGAAATGAGTCAACCGCCAG 1516
Db 1441 AAGAGGTCGCGGGTGTGTCAGCTCTGTCGGCAAGAAATGAGTCAACCGCCAG 1500
QY 1517 GATGAGACCAAGTGAAGAGCTTCACTTTCAGAGCCAGAGCGGGATGAGTTCACACA 1576
Db 1501 GATGAGACCAAGTGAAGAGCTTCACTTTCAGAGCCAGAGCGGGATGAGTTCACACA 1560
QY 1577 GCGCTGCTGTTGAGAGAAAGCGCTGCTGATACAGAGTGAAGCTTTGAGGGCCGAGCC 1636
Db 1561 GCGCTGCTGTTGAGAGAAAGCGCTGCTGATACAGAGTGAAGCTTTGAGGGCCGAGCC 1620
QY 1637 ATGCAAGTGGCTGCGAGAGCGGGCAGAGATATGTCGTCGATCTCTGCTGCGCCAGAG 1696
Db 1621 ATGCAAGTGGCTGCGAGAGCGGGCAGAGATATGTCGTCGATCTCTGCTGCGCCAGAG 1680

QY 1697 GTGAGCGTGAAGCTGAGGGCAAGATGCTGAGCTGACCTGACCTAGCTGCTGAG 1756
Db 1681 GTGAGCGTGAAGCTGAGGGCAAGATGCTGAGCTGACCTGACCTAGCTGCTGAG 1740
QY 1757 GGCACCTGCGCCATGTCACAGCTGTCGCGCAAGAGCGGGGGTGAAGTGAAGCGCCAG 1816
Db 1741 GGCACCTGCGCCATGTCACAGCTGTCGCGCAAGAGCGGGGGTGAAGTGAAGCGCCAG 1800
QY 1817 ACGCTGATGAGAGAGCGCCATTGCACTGAGCGCAAGCGCGGCACTTACCGTGGCC 1876
Db 1801 ACGCTGATGAGAGAGCGCCATTGCACTGAGCGCAAGCGCGGCACTTACCGTGGCC 1860
QY 1877 GCGATCCCTATGACCTGTGCTCCGAGGTCAAGCTGTCAGAGCTGTCGCAACAAGCC 1936
Db 1861 GCGATCCCTATGACCTGTGCTCCGAGGTCAAGCTGTCAGAGCTGTCGCAACAAGCC 1920
QY 1937 CTGCACTGAGCGCGAGAGCGGGCACAAGCACTGCGCAGCTGCTTCTGATGAGGC 1996
Db 1921 CTGCACTGAGCGCGAGAGCGGGCACAAGCACTGCGCAGCTGCTTCTGATGAGGC 1980
QY 1997 GCTGCAAGAGAGCGCGTGAATCTCAAGCGCTTACACCGCTTTCAGCTGCGCGAG 2056
Db 1981 GCTGCAAGAGAGCGCGTGAATCTCAAGCGCTTACACCGCTTTCAGCTGCGCGAG 2040
QY 2057 GGAACCTGCGCACTGTCAAGCTGCTTGTGAGGAGAGCGAATGTCGAGCGCGGGA 2116
Db 2041 GGAACCTGCGCACTGTCAAGCTGCTTGTGAGGAGAGCGAATGTCGAGCGCGGGA 2100
QY 2117 CCCCTGAACAGAGCGCGCTGCACTGAGCTGCGCGCAAGGACCTGAGAGTGTGAG 2176
Db 2101 CCCCTGAACAGAGCGCGCTGCACTGAGCTGCGCGCAAGGACCTGAGAGTGTGAG 2160
QY 2177 GAGTGTGAGCGCGGATGTCATGATCTGTTCAAGAGAGAGGCTCAAGCGCTGAC 2236
Db 2161 GAGTGTGAGCGCGGATGTCATGATCTGTTCAAGAGAGAGGCTCAAGCGCTGAC 2220
QY 2237 CTGCGCGCGAGAGCGCGGCAAGCAAGAGTGAAGCTGCTGAGGATGAGGCGCCAC 2296
Db 2221 CTGCGCGCGAGAGCGCGGCAAGCAAGAGTGAAGCTGCTGAGGATGAGGCGCCAC 2280
QY 2297 ATCAACTGAGAGCTCAAGTTCCAGGGCGGCAATGAGCGCGCGCACTCTGCGG 2356
Db 2281 ATCAACTGAGAGCTCAAGTTCCAGGGCGGCAATGAGCGCGCGCACTCTGCGG 2340
QY 2357 CGAGCAAGACTAG 2371
Db 2341 CGAGCAAGACTAG 2355

RESULT 8
US-09-188-930-257
; Sequence 257, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Ormest, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 257
; LENGTH: 3516
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-257

Query Match	45.6%	Score 1760.8	DB 3	Length 3516
Best Local Similarity	83.7%	Pred. No. 0		
Matches 2044	Conservative 0	Mismatches 387	Indels 11	Gaps 4
QY	18	TGAGAGGGGAGCGGGGAGCCCATGGGGCCCTGGGGCGCTGCGGAGCACTTCGACGCGGGCG	77	
Db	5	TGAGAGGGGAGAGGCGGGGCGGGGCGGTGGGCTCTGGGGCTCTGGGACCTTCGACGCGGGCG	64	
QY	78	AGTTCA CGGGCTGGAGAGAGGTGGGCTCGGGCGGGCTTGGGGCAGGTGTACAGAGTGGCGC	137	
Db	65	AATTGGCAGGCTGGAGAGAGGTGGGCTCGGGCGGGCTTGGGGCAGGTGTACAGAGTGGCGC	124	
QY	138	ATGTCCACTGGAAAGCTGGCGCTGACATCAAGTGTCCGCCAGCTGGACGTGCACACA	197	
Db	125	ATGTGCATGGAAAGACGTGGCGCTGGATCAAGTGTCCGCCAGCTGGACGTGCACACA	184	
QY	198	GGGAGCGCATGGAGCTTTTGGAGAAAGCCAGAAAGATGAGATGGGCCAAGTTTGCGTACA	257	
Db	185	GGGAGCGAATGGAGCTCCCTGGAGGAAGCTTAAGAAATGGAATGGGCCAAGTTCCGATACA	244	
QY	258	TCCTGCTGTGTATGGCAATCTGCGCGCAACCTGTGGCGCTGGTCAATGAGTACATGAGAGA	317	
Db	245	TTCTACCTGTGTACGGCAATGCCAGAAACCTGTGGCTGGTGTCAATGAGTACATGAGAGA	304	
QY	318	CGGGCTCCCTGGAAAAAGCTGTGGCTTGGAGGCCATTGCCATGGAGATCTCCGGTTCCGAA	377	
Db	305	CAGGCTCCCTGGAGAAAGCTGTGGCGCTCGACAGCCATTGCTTGGGGAACCTGGCGCTTCCGA	364	
QY	378	TCATCCAGAGAGCGGGCGGTGGGCAATGAACTTCCTGCACTGGATGGGCCCGGCACTCCGCG	437	
Db	365	TCGTCAAGAGACACCGGGGCGATGAACTTCCTGCAATGGACATGCTCCGCGCACTGCTGCG	424	
QY	438	ACCTGGAACCTCAAGGCCCGCGCAACATCTGTCTGATGGCCACATCCACACTCAAGATTTCTG	497	
Db	425	ACCTGACACTGAAGCCAGAGCAACATCTGTCTGATGGCCACATCCACACTCAAGATTTCTG	484	
QY	498	ATTTTGTGTGGCCAAAGTGCAACGGGCTGTGCCACTGCGATGACTCAAGATGATGGCC	557	
Db	485	ACTTTGGGCTGGCCAAAGTGCAATGCAATGCTCCACTCAAGACTCAAGATGATGGCC	544	
QY	558	TGTTTGGCAATGGCCCTTACCTCCCTCCAGAGCGCATAGGGAGAAAGCGGCGCTCTTCG	617	
Db	545	TGTTTGGCAATGGCCCTTACCTCCCTCCAGAGCGCAATCGTAGAAAGCGGCGCTTGTTCG	604	
QY	618	ACACCAAGCAGATGTATACAGCTTTCGATCTGGGGGCGTGTCAACAGAGA	677	
Db	605	ACACCAACATATATATACAGCTTTCGATCTGGGGGCGTGTCAACAGAGA	664	
QY	678	AGCCGTTTGCAGATGAGAAAGACATCTGCACATCATGTGTAAGGTGTGAAAGGCGCAC	737	
Db	665	AGCCATTTTGCAGATGAGAAAGACATCTGCACATCATGTGTAAGGTGTGAAAGGCGCAC	724	
QY	728	GGCCCGGAGCTGGCGGCGCGGTGTGCAAGAGCCCGGCGCGCTGCGAGCCACCTGATACGCC	797	
Db	725	GGCCAGAGCTGGCACCCCATCTGCACAAACCCCGGCGCGGTGTGCAAGAGCGCTGATACGCC	784	
QY	798	TCATGCAAGGCTGTGGCAGGGGGAATCCGAGGTTAAGGCCACTTCCAAAGAAATTAATTCTT	857	
Db	785	TCATGCAAGGCTGTGGCAGGGGGAATCCGAGGTTAAGGCCACTTCCAAAGAAATTAATTCTT	844	
QY	858	CTGAACCCGAGGACCTGTGTGTAAAAAGCTGTAGTACGAAGTGAAGAACTGTCTCATGTATC	917	
Db	845	CTGAACCCGAGGACCTTTTGTGTGAAGGCTGTAGTGAAGAGGTGAAGAACTGTGTCTCATGTATC	904	
QY	918	TGAGCGTGAAGAGCCCGCGAGCCGAGAGCGGAGGTGTGCTG-----CGAGGCTCA	971	
Db	905	CAGGCGAGAGAAAGCTCTTAGAGTCCAGAGGTGAAGGCCAGGCCAGTCTTCACGCCCTCA	964	
QY	972	AGCGGGCCCTTCGCCCGACCTTCGATTAACGATTAAGGCTTCGAGGCTTCCTCAAGC	1031	
Db	965	AGCGGGCCCTTCCTCCCGCTTCGATTAACGATTCGATTCGAGGCTTCCTCAAGC	1024	
QY	1032	TGGAACCTTGAAATTTCCAGGCTGTGCGAGGCGCCGAGGAGCTCAAGCGCAGCTCTCTCG	1091	

Db	1025	TGACCTCTGGGATCTCCCAAGCTTTTAAAGCCCCGAAGCTCAGCCGAAGTTCTCTG	1084
Qy	1092	AGTCGAAGCTGCCATCGTCGCGCAGTGGGAAGAGCTCTCGGGGTGTCCTCGGTGACT	1151
Db	1085	AATCAGAGCTCCATCGCTCCAGCAGTGGCAAGAGGCTCTCGGGGGTGTCCTCAGTGA	1144
Qy	1152	CCGCTTCTCTCTTCAGAGATCACTGTCCGTCTCTTTAGCGGGAACTTTCAACACGC	1211
Db	1145	CAGCTTTTCTCTCAGAGAGATCGCTGTCATCTGTCTTTTGAAGCGGGAAGCTTCAACAG	1204
Qy	1212	ATCTGGGATACCAAGAGCGTCAGAGAAGAGCTTGATGTGCATCGTGC -CGGAC	1270
Db	1205	ACCTGGGCCCAAC -AGACATTCAGAGAAGAGCTTAGTGATGCCATCATATCAGGGAC	1263
Qy	1271	ACCAAGAACTGATGAAGATCTTCGACGCGCAGGACGTGACCTGGACCTGGAACAGCG	1330
Db	1264	ACCAAGAGGCTGATGAGAGATCTTACAGCCCAAGATGTGACCTTGTTATAGACAGAG	1323
Qy	1331	GCCAGCTCTGTCACCTTGGCGGTGAGAGCGCGGCAAGAGATGTCGCAAGTGGCTCTG	1380
Db	1324	GCCAGCTCTGTCACCTTGGCTGTGAGAGCGGCAAGAGAGTGTGTCAAGTGGCTCTG	1383
Qy	1331	CTCAACATGTCACACCCCAACCTTGAAGAACCTGTAGGGGCTCACCCCGTTGACATGG	1450
Db	1384	CTTAAACAATGCAACCCCAACCTTGAACCAACAGAGAGGCTCTTACACATGCAATG	1443
Qy	1451	GTGAGAGAGAGGTGTGCGGGGTGTGTGTGAGAGCTCTGTGTGCAACGGAATCAGTGA	1510
Db	1444	GTGAGAGCGGAAGGAGACGTGGAATTTGTGAGGTATCTGTGAGCGCGGAAGACAG	1503
Qy	1511	GCCAGAGATGAGAACAGATGACAGCCCTCACTTTGACGCCCAAGACGGGAATGATCT	1570
Db	1504	GCCAAAGATGAGAACAGATGACAGCCCTGCACTTTGACGCCCAAGATGGAAGAGCC	1563
Qy	1571	AGCAACAAGGCTGTGTGGAAGAAGAAGCGCTCGGTCAACAGAGGTGACTTTGAGGG	1630
Db	1564	AGCAACAAGGCTGTGTGGAAGAAGAAGCTTCTTCAATGAGGTGACTTTGAGGGCG	1623
Qy	1631	ACGCCATGACAGTGGCCCTGACAGCAGGGCAGAGATATCTGCGCATCTGCTCGC	1690
Db	1624	ACACCCATGACATGTAGCCTGTGCACACAGACAGAGAACATTGTGCCACCTGTCTCG	1683
Qy	1691	CGAGCGGTGACGTGAAGCTTGCAGGGCAGAGATCTGTGCTGCCATGCACTACGTGCC	1750
Db	1684	CTGTGTGTGATGTGGGCTGTGCAGGAAGATCTGTGTTGCTGTGCACTTAGTGTGCC	1743
Qy	1751	TGCGAGGGCCACCTGTCCATGTCAAGCTGTGGCCAAAGACCGGGGTGAGTGTAA	1810
Db	1744	TGCGAGGGCCACCTTCCATTGTTAAGTGTGTACCAAGCAGCTGTGGGTGAGTGTAA	1803
Qy	1811	GCCCAAGCGCTGAGTGGAGAGACGCCATTGACCTGGCCGCAACAGCGCGGCACTACGC	1870
Db	1804	GCCCAAGACATGACGGGAGAGACCCCTGCACTGTGTGCTGCAGAGGGGCAATTACGT	1863
Qy	1871	GTGGCCCGCATCTCATGACCTGTGTCTCGAGCTCAACGTCTGACGCTGTGCAAG	1930
Db	1864	GTGGCTTGCAATTCATTGACCTGTGTCTGTATGTAACTGTCAAGGCTTACAGGCAAG	1923
Qy	1931	ACAACCTTGACAGTGGCCGCGGAGACGGGGCAACAGACATGCGCAGGCTGTCTGTAT	1990
Db	1924	ACAACCTTGACAGTGTGCTGCAAGACCTGGAACACTGTATCTGCAAGGCTTACTTGTAT	1983
Qy	1991	CGGGCGGTGCAAGAGAGCGGTACCTCAACGGGCTCAACGGCTGACCTTGGCTGGC	2050
Db	1984	CGTGTGTGTGCAAGAGAGGCTTTTGAACCTCAAGGCTTATGTGCTTGGACCTTGGAC	2043
Qy	2051	CGCAACGACACCTGGCCACTGTCAAGCTGTGTGAGAGAGAGCGCATGTCTGGC	2110
Db	2044	CAGAAATGACACCTGGCTATCTGTCAAGTGTCTTAAAGAGAGAGGCGTATGTATGGCT	2103
Qy	2111	CGGGAGCCCTGAAACAGAGCGCGCTGCACTGTGTGCGGCCACGGGCACTCGAAGTGT	2170

Db 127 ATGTGCACTGGAAAGACGTGGCTCCGCGATCAAGTGTCCGCCAGTTGTGACCTTCAGAGCA 186
Qy 198 GGGAGCCGATGAGAGCTTTTGGAGAAGGCCAAGAGATGAGATGGCCAAATTTGCTACA 257
Db 187 GGGAAAGATGAGAGCTTCTGGAGGAAGCTTAAAGATGAGATGGCCAAATTTGCTACA 246
Qy 258 TCTGCTGCTGATGATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317
Db 247 TTTCACTGTGTGATCGGCAATATGCGAGAACTGTGGCTGTGTCAATGAGATGAGAGA 306
Qy 318 CGGGCTCTCCGGAAAGCTGCTGCTGAGGCCATTGGCAATGGAGTCTCGGTTCCGA 377
Db 307 CAGGCTCTCCGGAGAGCTGCTGCTGAGGCCATTGGCAATGGAGTCTCGGCTTTCCGA 366
Qy 378 TCATCAAGAGAGCGGCGTGGGATGAATCTTCTGCTCATGCAATGGCCCGCATCTGTC 437
Db 367 TCGTCAAGAGAGCGGCGTGGGATGAATCTTCTGCTCATGCAATGGCCCGCATCTGTC 426
Qy 438 ACCTGGAACCTCAAGCCCGGAGAACATCCCTGCTGAGATGCCCATCAAGTCAAGATTTCTG 497
Db 427 ACTTGAACCTTGAAGCGAGAGAACATCTGCTGAGATGCCCATCAAGTCAAGATTTCTG 486
Qy 498 ATTTTGTCTGGCCAAAGTGAACCGGCTGTCCCACTGCGATGACCTCAGCATGATGAGCC 557
Db 487 ACTTTGGGCTGGCCAAAGTGAACCGGCTGTCCCACTGCGATGACCTCAGCATGATGAGCC 546
Qy 558 TGTTTGGCAATATGCGCTTACTCTCCAGAGCGCATGAGGAGAAAGCGGCTCTTTCG 617
Db 547 TGTTTGGTAAATCCCTTAACTCTCCAGAGCGAATTTGAGAGAGAGCGCTTGTTCG 606
Qy 618 ACAACCAAGCAGATGATTAACAGCTTTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 677
Db 607 ACAACCAAGCAGATGATTAACAGCTTTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 666
Qy 678 AGCCGTTTGCAGATGAGAAAGCATCTGCAATGATGATGATGATGATGATGATGATGATG 737
Db 667 AGCCATTTGCAATGATTAAGAAAGCATCTGCAATGATGATGATGATGATGATGATGATG 726
Qy 738 GCCCGAGCTGCGCCGCTGTGCAAGAGCCCGCGCGCGCTGCAAGCCATCTGATAGCC 797
Db 727 GCCCAGAGCTGCAACCCATCTGCAAGAGCCCGCGCGCGCTGTGCTCAGAGCTGATAGGA 786
Qy 798 TCATCAAGCGGCTGCGAGAGGGGATCCGCGAGTTAGGCCCATCTTCAAGAAATTAATCT 857
Db 787 TAATCAAGCGGCTGCGAGAGCCCAAGAGTGGGCGCATCTTCAAGAAATTAATCT 846
Qy 858 CTGAACCGAGAGACCTGTGTGAAGAAAGCTGATGACGAAGTGAAGAAAGCTGCTCATGATC 917
Db 847 CTGAACCGAGAGACCTTTGTGTGAAGAAAGCTGATGAGAGTGAAGAAAGCTGCTCATGAGC 906
Qy 918 TGAAGCTGAAAAAGCCCGGAGCCCAAGAGCGAGAGTGTGCTG-----GAGGCTCA 971
Db 907 CAGGCGAGAAAAAGCTCTCTAGAGTCCAGAGTGAAGAGCCCAAGTCTTCAAGCCCTCA 966
Qy 972 AGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1031
Db 967 AGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1026
Qy 1032 TGAAGCTGAGATTTCCAGAGCTGTGAGAGGCCCGAGAGAGCTCAGCGCGAGCTCTCTG 1091
Db 1027 TGAAGCTGAGATTTCCAGAGCTCTTGAAGGCCCGAGAGAGCTCAGCGAGATTTCTCTG 1086
Qy 1092 AGTCAAGCTGCAATGCTGCGGAGTGGGAGAGAGCTCTCGGAGGCTGCTCTGCTGAGT 1151
Db 1087 AATGCAAGCTCCCATGCTGCAAGAGTGGCAAGAGCTCTCGGAGGCTGCTCTGAGTGAAGT 1146
Qy 1152 CGGCTCTCTCTTCCAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1211
Db 1147 CAGGCTTTTCTTCCAGAGAGATGCTGTCACTGCTTTTGAAGCGGAGATTTCAAGAGG 1206
Qy 1212 ATCTGGGTACCAAGAGCTTCAAGAGAGAGCTTGTGATGCAATGCTGTC-CGGAGC 1270

Db 1207 ACTGAGGCCCCAC-AGACATTCAGAAAGAGCTAGTGAATGATCATATACAGGGAC 1265
Qy 1271 ACCAGCAATCTGATGAAGATCTGCAAGCCCGAGAGCTGGAATCTGGAATCTGGAAGGGT 1330
Db 1266 ACCAGCAGGCTGATGAAGATCTTACAGCCCGAGAGTGAATCTGATGATGAGAGT 1325
Qy 1331 GCCAGCTGCTGCACTGAGGCTGAGAGCGGCGCAAGAGATGAGCGCAAGTGGCTGCTG 1390
Db 1326 GCCAGCTGCTGCACTGAGGCTGAGAGCGGCGCAAGAGATGAGCGCAAGTGGCTGCTG 1385
Qy 1391 CTCAAGATGCAACCCCAACTGAGCAACCTGAGGAGCTTCAACCCGTTGACATAGCC 1450
Db 1386 CTTAACATGCAACCCCAACTGAGCAACCTGAGGAGCTTCAACCACTGATATAGCT 1445
Qy 1451 GTGAGAGAGAGGCTGAGGCTGCTGAGATCTCTGCTGCAAGAGATCAAGTCAAC 1510
Db 1446 GTGAGAGAGAGGAGCTGGAATTTGAGATCTGCTGAGCCGGAAGACCAAGTCAAT 1505
Qy 1511 GCCAAGATGAGAGCAAGTGAACAGCCCTCACTTTCAGCCCGAGAGAGGATGAGTCT 1570
Db 1506 GCCAAGATGAGAGCAAGTGAACAGCCCTGCTGCACTTTCAGCCCGAGAGAGGAGCC 1565
Qy 1571 AGCAGAGCTGCTGTTGAGAGAGAGCGCTCGGTCAACGAGTGAATTTGAGAGGCTGG 1630
Db 1566 AGCAGAGCTGCTGTTGAGAGAGAGCGCTTCTGTCAATGAGTGAAGCTTGAAGGCGGA 1625
Qy 1631 ACGCCATGCAACCTGAGCTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1690
Db 1626 ACACCAAGTGAATGAGCTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1685
Qy 1691 CGAGGCTGAGAGTGAAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1750
Db 1686 CGTGTGTGATGATGAGGCTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1745
Qy 1751 TGGCAGGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1779
Db 1746 TGGCAGGCGCACTTCCCATGTAAGCT 1774

RESULT 12
US-09-188-930-66
; Sequence 66, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strechan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011C1
; CURRENT APPLICATION NUMBER: US/09/188, 930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 1888
; TYPE: DNA
; ORGANISM: mouse
; FEATURES:
; NAME/KEY: unsure
; NAME/KEY: (1690)
; NAME/KEY: unsure
; LOCATION: (1755) ... (1755)
; NAME/KEY: unsure
; LOCATION: (1864) ... (1864)
; US-09-188-930-66

Query Match 33.3%; Score 1284; DB 3; Length 1888;
Best Local Similarity 83.1%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 298; Indels 21; Gaps 9;


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Sequence 39629, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 39629
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-39629

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Query Match	15.6%	Score 600.6	DB 4	Length 601	
Best Local Similarity	99.8%	Pred. No. 7,2e-147			
Matches	600	Conservative	1	Mismatches	0
				Indels	0
				Gaps	0
QY	2047	TCCTCGCAACGGAACACTGGGCCACTGTCAAGCTGCTTGTCCAGAGAAAGCCCAATGTGCT	2106		
Db	601	TGCCCCGCAACGGAACACTGGGCCACTGTCAAGCTGCTTGTCCAGAGAAAGGCCCAATGTGCT	542		
QY	2107	GGCCCCGGGGAACCCCTGAACCAAGAGGGGCTGACCTGCTGCGGCCACGGGACCTGGGA	2166		
Db	541	GGCCCCGGGGAACCCCTGAACCAAGAGGGGCTGACCTGCTGCGGCCACGGGACCTGGGA	482		
QY	2167	GATGTGAGAGAGTTGTGTCAAGCGCCGATGTCAATTGACTGTTCAGCAAGACAGGGCTCAG	2228		
Db	481	GATGTGAGAGAGTTGTGTCAAGCGCCGATGTCAATTGACTGTTCAGCAAGACAGGGCTCAG	422		
QY	2227	CGCGCTGCACTGTGCGCGCCCAAGGCTCGGGAACGCAACAGCGGTGAGAACTTGTCTCAAGCA	2286		
Db	421	CGCGCTGCACTGTGCGCGCCCAAGGCTCGGGAACGCAACAGCGGTGAGAACTTGTCTCAAGCA	362		
QY	2287	TGGGGCCCAATCAACTGCAAGAGCTCAAGTTCCAGGGGCGGCATGGCCCGCCGAC	2346		
Db	361	TGGGGCCCAATCAACTGCAAGAGCTCAAGTTCCAGGGGCGGCATGGCCCGCCGAC	302		
QY	2347	ACTCTTGGCGGCAAGCAAGCCTAGCTGGCTGCTGCGGAAGCCGGGAGTTCACGTGGGG	2406		
Db	301	ACTCTTGGCGGCAAGCAAGCCTAGCTGGCTGCTGCGGAAGCCGGGAGTTCACGTGGGG	242		
QY	2407	CTCTTGTCTGTCTGTGTGTCTCTGTGGGATGAAACATCTGTGTTGGGGCCCGTGT	2466		
Db	241	CTCTTGTCTGTCTGTGTGTCTCTGTGGGATGAAACATCTGTGTTGGGGCCCGTGT	182		
QY	2467	GGCTTACCTAAATGTTAAACAAAGCAGAGGTGACATGTGTCCATCAGAGAGCGGCTGTGC	2528		
Db	181	GGCTTACCTAAATGTTAAACAAAGCAGAGGTGACATGTGTCCATCAGAGAGCGGCTGTGC	122		
QY	2527	TGACCGGAGGTGTCCTCCCTCCAGGTGAAGCTGCTCAGGTGCACATGCCGCTTCATCATCG	2586		
Db	121	TGACCGGAGGTGTCCTCCCTCCAGGTGAAGCTGCTCAGGTGCACATGCCGCTTCATCATCG	62		
QY	2587	ATCTTAGGCACTGTGTGTGAAGGGAACGTTGGTTCAGAAATCATTTGGTGTGCTTAAT	2646		
Db	61	ATCTTAGGCACTGTGTGTGAAGGGAACGTTGGTTCAGAAATCATTTGGTGTGCTTAAT	2		
QY	2647	G 2647			
Db	1	G 1			
RESULT	15				

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US-09-949-016-181232/c
; Sequence 181232, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181232
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-181232

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Query Match	15.6%	Score 600.6;	DB 4;	Length 601;
Best Local Similarity	99.8%	Pred. No. 7,2e-147;		
Matches 600;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2047	TCGCCGACCGAGCACTTGCCACTGTGCATGACTGTGTGTGAGAGAGAAAGCCCATATGTCCT		2106
DB	601	TGCCCGCAACGGAACCTTGCGCACTGTCAAGCTGCTTGTGAGAGAGAAAGGCCCATATGTCCT		542
QY	2107	GGCCCGGGGAAACCCCTGAAACGAGACGGGCGTCGACCTTGCTGCCGCCCACTCTCGA		2166
DB	541	GGCCCGGGGAAACCCCTGAAACGAGACGGGCGTCGACCTTGCTGCCGCCCACTCTCGA		482
QY	2167	GGTGTGAGAGAGTTGTGTCAAGCGCCATGTTCATTGACTTGTTCGACGACAGGGGCTCAG		2226
DB	481	GGTGTGAGAGAGTTGTGTCAAGCGCCATGTTCATTGACTTGTTCGACGACAGGGGCTCAG		422
QY	2227	CGCCCTGCACCTGGCCCCCGGACGGGCGGGCAACGACAGCGGTGAGACTCTGTCTCAGGCA		2286
DB	421	CGCGCTGCACCTGGCGCCCCGAGGGCGGACGACGACAGCGGTGAGACTCTGTCTCAGGCA		362
QY	2287	TGGGGCCCACTCAACTGTCAGAGCCCTCAAGTTTCAGAGGGCGGCGCAGTSCCCCGCGCAC		2346
DB	361	TGGGGCCCACTCAACTGTCAGAGCCCTCAAGTTTCAGAGGGCGGCGCAGTSCCCCGCGCAC		302
QY	2347	ACTCTGCGGCGGAAAGCAAGACTTACTGTGCTGCTGTGGGAGACCGGGGGTTCAGTGTGGG		2406
DB	301	ACTCTGCGGCGGAAAGCAAGACTTACTGTGCTGCTGTGGGAGACCGGGGGTTCAGTGTGGG		242
QY	2407	CTCTTGTCTGTCCCTGAGTTCCTGTGTGGGAGTGAAGATCTGTGCGGGCCCCGTGTGT		2466
DB	241	CTCTTGTCTGTCCCTGAGTTCCTGTGTGGGAGTGAAGATCTGTGCGGGCCCCGTGTGT		182
QY	2467	GCGTTACTTAATGTATTAACAGAGAGAGTGAACGTGTGCCATCAGAGAGCGGCTGTC		2526
DB	181	GCGTTACTTAATGTATTAACAGAGAGAGTGAACGTGTGCCATCAGAGAGCGGCTGTC		122
QY	2527	TGACCGGAGTTCCTCCACAGTGAACCTGTGCTCAGGTGACACATGCCCGCTCATCATACG		2586
DB	121	TGACCGGAGTTCCTCCACAGTGAACCTGTGCTCAGGTGACACATGCCCGCTCATCATACG		62
QY	2587	ATCTAGGCACTGTGCTGTGAAGGAGCCGTGGATCAGAAATCAATTTGTGTGCTCTTAAT		2646
DB	61	ATCTAGGCACTGTGCTGTGAAGGAGCCGTGGATCAGAAATCAATTTGTGTGCTCTTAAT		2
QY	2647	G 2647		
DB	1	G 1		

Search completed: September 16, 2005, 07:15:47
Job time : 1884.6 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 16, 2005, 01:22:53 ; Search time 8751.61 Seconds
(without alignments)
2938.605 Million cell updates/sec

Title: US-10-658-904-1

Perfect score: 3860
Sequence: 1 ccacgcgtccgcgcgcgtatg.....tgaaaaaaaaaaagg 3860

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7389322 seqs, 333128559 residues

Total number of hits satisfying chosen parameters: 14778644

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3859	100.0	3860	US-10-658-904-1	Sequence 1, Appli
2	3836	99.4	3860	US-10-354-358-37	Sequence 37, Appli
3	3804.2	98.6	3879	US-10-172-118-1840	Sequence 1840, Ap
4	3804.2	98.6	3879	US-10-342-887-1840	Sequence 1840, Ap
5	3804.2	98.6	3879	US-10-648-593-16	Sequence 16, Appli
6	3794.8	98.3	3890	US-10-923-035-23	Sequence 23, Appli
7	3643	94.4	3981	US-10-302-172-905	Sequence 905, Appli

8	2606.4	67.5	2691	US-10-172-118-324	Sequence 324, App
9	2606.4	67.5	2691	US-10-342-887-324	Sequence 324, App
10	2355	61.0	2355	US-10-658-904-3	Sequence 3, Appli
11	2327.2	60.3	2355	US-10-128-174-15	Sequence 15, Appli
12	2327.2	60.3	2355	US-10-128-174-16	Sequence 16, Appli
13	2327.2	60.3	2355	US-10-128-174-18	Sequence 18, Appli
14	2327.2	60.3	2355	US-10-128-174-19	Sequence 19, Appli
15	2325.6	60.2	2355	US-10-128-174-1	Sequence 1, Appli
16	2324	60.2	2355	US-10-128-174-14	Sequence 14, Appli
17	2324	60.2	2355	US-10-128-174-17	Sequence 17, Appli
18	2324	60.2	2355	US-10-128-174-20	Sequence 20, Appli
19	2324	60.2	2355	US-10-128-174-21	Sequence 21, Appli
20	2324	60.2	2355	US-10-128-174-22	Sequence 22, Appli
21	2324	60.2	2355	US-10-128-174-23	Sequence 23, Appli
22	2322.4	60.2	2355	US-10-164-080-6	Sequence 6, Appli
23	2322.4	60.2	2355	US-10-258-951-31	Sequence 31, Appli
24	2322.4	60.2	2355	US-10-866-050A-257	Sequence 257, App
25	1760.8	45.6	3516	US-10-866-050A-257	Sequence 257, App
26	1760.8	45.6	3516	US-10-152-661-257	Sequence 257, App
27	1746.4	45.2	2370	US-10-164-080-1	Sequence 1, Appli
28	1744.8	45.2	2370	US-10-399-327-1	Sequence 1, Appli
29	1310.2	33.9	1774	US-10-128-174-11	Sequence 11, Appli
30	1310.2	33.9	1774	US-10-866-050A-403	Sequence 403, App
31	1284	33.3	1888	US-10-152-661-403	Sequence 403, App
32	1284	33.3	1888	US-10-866-050A-66	Sequence 66, Appli
33	1181.8	30.6	2356	US-10-152-661-66	Sequence 66, Appli
34	1130	29.3	1203	US-10-146-473-19	Sequence 19, Appli
35	461.4	12.0	535	US-10-029-386-25382	Sequence 25382, A
36	415.2	10.8	420	US-10-240-425-883	Sequence 883, App
37	375	9.7	449	US-10-276-774-159	Sequence 159, App
38	375	9.7	449	US-09-880-107-3584	Sequence 3584, Ap
39	375	9.7	449	US-09-967-768A-202	Sequence 202, App
40	357	9.2	361	US-10-843-641A-6347	Sequence 6347, Ap
41	357	9.2	361	US-09-920-300A-184	Sequence 184, App
42	357	9.2	361	US-10-033-528-184	Sequence 184, App
43	357	9.2	361	US-10-039-526-184	Sequence 184, App
44	295.8	7.7	594	US-10-961-527-184	Sequence 184, App
45	292.4	7.6	2696	US-10-029-386-889	Sequence 889, App
				US-10-128-174-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-658-904-1
; Sequence 1, Application US/10658904
; Publication No. US20040048305A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: Protein Kinase, A No. US20040048305A1 Human
; TITLE OF INVENTION: Protein Kinase and Uses Thereof
; FILE REFERENCE: MP100-0101RCPIM
; CURRENT APPLICATION NUMBER: US/10/658,904
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 09/781,882
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/182,096
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (17)...(2371)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (1)...(3860)
; OTHER INFORMATION: n = A,T,C or G

US-10-658-904-1

Query Match 100.0%; Score 3859; DB 18; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CACCTTCGACCGCGGCGAGTTCCACGCGCTGGAGAGGTGGCTGGCGCGCTTGGGCA 120
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QY 181 CCTGCACGTCCGACGACGAGGAGCGCATGGAGCTTTTGAAGAGCCAAAGATGAGAT 240
DB 181 CCTGCACGTCCGACGACGAGGAGCGCATGGAGCTTTTGAAGAGCCAAAGATGAGAT 240
QY 241 GGCCTCAAGTTTCGCTACATCTGCTGTGTATGGCATCTGCCGGAACCTGTGCGCTG 300
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QY 301 CATGAGATACATGAGAGCGGCGCTCCCTGGAAGAGCTGCTGGCTTGGAGCCATTGGCATT 360
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DB 361 GGAATCCGCGTTCCGAATCATCCAGAGACGCGGCGGATGAACCTTCCTGCACTGCAT 420
QY 421 GGCCTCCGCGCATCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 480
DB 421 GGCCTCCGCGCATCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 480
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DB 481 CCAAGTCAAGATTTCTGATTTTGTGTGGCCAAAGTGCACACGCGCTGTCCCATCTGCATT 540
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DB 721 GGTGTGAAGGCGCACCGCGCCGAGCTGCGCGCTGTGTCAGAGCCCGCGCGCGCTG 780
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QY 841 CTTTCCAGAAATTTACTTCTGAAAACGAGAGCTGTGTGAAAAGCTGTGATGAGAAAGTGA 900
DB 841 CTTTCCAGAAATTTACTTCTGAAAACGAGAGCTGTGTGAAAAGCTGTGATGAGAAAGTGA 900
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DB 1141 CTGGTGAATCTCCGCTTTCTTCTTCCAGAGATCATCTGTGCTGTCTTTTGAAGCGGAAAC 1200
QY 1201 TTYCAACGAGATTTGGGTACCAAGAGCTCCAGAGAGAAAGCTTGGATTCATTCG 1260
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QY 1321 GGAAGAGGTGCGAGCTGCTGCACTGGCGGTGAGAGCGGCGCAAGAGTGGCCCA 1380
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QY 1381 GTGGCTGCTGCTCAACAATGCGCAACCCCAACTGAGGACCGTGAAGGAGCTTCAACCGGTT 1440
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DB 1741 CTAAGCTGCGTGGCAGGAGCGACCTGCCCATGCTCAAGCTGTGGCCTGAAGCAGCGGAGT 1800
QY 1801 GAGTGTGAACGCCCAAGACGCTGATGAGAGGAGCCCATATGCACTGGCGCGCACAGCGGG 1860
DB 1801 GAGTGTGAACGCCCAAGACGCTGATGAGAGGAGCCCATATGCACTGGCGCGCACAGCGGG 1860
QY 1861 GCACTACCGCGTGGCGCGCATCTCATGACCTGTGTCTCCAGCTCAACGCTGCAAGCTT 1920
DB 1861 GCACTACCGCGTGGCGCGCATCTCATGACCTGTGTCTCCAGCTCAACGCTGCAAGCTT 1920
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QY 1981 GCTCTGATGATGGGCGCTGGCAAGAGCGGTGACCTCAGACGAGCTACACCGCTGTGCA 2040
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DB 2581 TGAATGATGAG 2640
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DB 2641 CCTTAATGAG 2700
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DB 2761 GGGAGAGCTGTGTTTATCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
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DB 2821 TGCATGAGATGTTTATTAATAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
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DB 2881 AACCTGTAAATGTTTATTAATAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
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DB 2941 GGGGTTGGCTTTGAG 3000
QY 3001 GGGGAGAGATGTTGAG 3060
DB 3001 GGGGAGAGATGTTGAG 3060
QY 3061 TGAAG 3120
DB 3061 TGAAG 3120
QY 3121 GATGTTTGGAG 3180
DB 3121 GATGTTTGGAG 3180
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DB 3181 AACTGAGTGTGAG 3240
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DB 3241 GAG 3300
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DB 3301 ATGATGATGAG 3360
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DB 3361 TCCAGAGCTCATTTTGTGAG 3420
QY 3421 GAGTGTGAG 3480
DB 3421 GAGTGTGAG 3480
QY 3481 CAG 3540
DB 3481 CAG 3540
QY 3541 TGTGTGAG 3600
DB 3541 TGTGTGAG 3600
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DB 3601 CCTGTGAG 3660
QY 3661 TGTATGATGAG 3720
DB 3661 TGTATGATGAG 3720
QY 3721 TTTGAG 3780
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QY 3781 AGGAG 3840
DB 3781 AGGAG 3840
QY 3841 TGAAG 3860
DB 3841 TGAAG 3860

RESULT 2
US-10-354-358-37
; Sequence 37, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Tsai, Feng-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 48663, 8897, 1682, 17667, 9225,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MP102-020P1R000000
; CURRENT APPLICATION NUMBER: US/10/354.358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600

PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/364,517
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/382,995
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/388,853
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,395
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq For Windows Version 4.0
SEQ ID NO: 37
LENGTH: 3860
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (17) ... (2371)
US-10-358-37

Query Match 99.4%; Score 3836; DB 16; Length 3860;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 2; Gaps 2;
Matches 3858; Conservative 0;

QY 1 CCACGCTCCGCGCGATGAGGCGAGCGCGGAGCCCATGAGGCTTGCGCTGCTCG 60
DB 1 CCAAGCTCCGCGCGATGAGGCGAGCGCGGAGCCCATGAGGCTTGCGCTGCTCG 60
QY 61 CACCTTCCACGCGGCGAGTTTCA CGGCGTGGAGAGGTGGCTGGCGGCTTGGGCA 120
DB 61 CACCTTCCACGCGGCGAGTTTCA CGGCGTGGAGAGGTGGCTGGCGGCTTGGGCA 120
QY 121 GGTGACAAAGGTGCGCATCTGCTGCTGTATGAGCATCTGCGCGCAATGCTGCCAG 180
DB 121 GGTGACAAAGGTGCGCATCTGCTGCTGTATGAGCATCTGCGCGCAATGCTGCCAG 180
QY 181 CTTGCACTGACGACGACGAGGAGCGATGAGCTTTGGAAGAGCCAAAGATGAGAT 240
DB 181 CTTGCACTGACGACGACGAGGAGCGATGAGCTTTGGAAGAGCCAAAGATGAGAT 240
QY 241 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 CATGAGATGACATGAGAGGCGCTCCCTGGAAGAGCTTGAGGCTTGAGGCAATGCA 360
DB 301 CATGAGATGACATGAGAGGCGCTCCCTGGAAGAGCTTGAGGCTTGAGGCAATGCA 360
QY 361 GGAATCCGCTTCCGATTCATCCAGAGAGCGGCTGAGGCAATGCTTCTGCACTGAT 420
DB 361 GGAATCCGCTTCCGATTCATCCAGAGAGCGGCTGAGGCAATGCTTCTGCACTGAT 420
QY 421 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 GGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 CCAAGTCAAGATTTCTGATTTTGTCTGCGCAAGTGCAGCGGCTGCTCCATCTGCA 540
DB 481 CCAAGTCAAGATTTCTGATTTTGTCTGCGCAAGTGCAGCGGCTGCTCCATCTGCA 540
QY 541 CTTGAGATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 CTTGAGATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

DB 541 CTTGAGATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GAAAGCGGCTCTTCCACACCAAGCAGATGATTAAGCTTTGCGATTCGATCTGGG 660
DB 601 GAAAGCGGCTCTTCCACACCAAGCAGATGATTAAGCTTTGCGATTCGATCTGGG 660
QY 661 CGTCTCAACAGAGAGCGTTTGGAGATGAGAGAAATCTGCAATCATATGTTGAA 720
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DB 721 GGTGTGAAGGCGCACCGCCCGAGCTGCGCGCTGTGCAAGAGCCGCGCGCTG 780
QY 781 CAGGCACTGATAGCGCTTCAATGAGCGGCTGCGAGGAGATCCGAGATTAGCCAC 840
DB 781 CAGGCACTGATAGCGCTTCAATGAGCGGCTGCGAGGAGATCCGAGATTAGCCAC 840
QY 841 CTTCCAGAAATTAATCTTCTGAAACCGAGACCTGTGAAAGCTGATGACGAATGAA 900
DB 841 CTTCCAGAAATTAATCTTCTGAAACCGAGACCTGTGAAAGCTGATGACGAATGAA 900
QY 901 AGAAATGCTCATGATCTGACGTAAGAAAGCCCCCGAGCCGAGAGCGATGTGCC 960
DB 901 AGAAATGCTCATGATCTGACGTAAGAAAGCCCCCGAGCCGAGAGCGATGTGCC 960
QY 961 TGCAGGCTCAAGGCGGCTCTGCGCCCGACCTTGATTAAGCACTGACGCTTCCGAGCT 1020
DB 961 TGCAGGCTCAAGGCGGCTCTGCGCCCGACCTTGATTAAGCACTGACGCTTCCGAGCT 1020
QY 1021 TCTCTCAGCTGAGCTCTGAGATTTCCAGAGCTGCGAGGCGCCCGAGAGACTCAACCG 1080
DB 1021 TCTCTCAGCTGAGCTCTGAGATTTCCAGAGCTGCGAGGCGCCCGAGAGACTCAACCG 1080
QY 1081 CAGCTCTCTGAGTCCAAAGCTGCGCATGCTCGGAGTGGAGAGAGCTCTCGGGGTGTC 1140
DB 1081 CAGCTCTCTGAGTCCAAAGCTGCGCATGCTCGGAGTGGAGAGAGCTCTCGGGGTGTC 1140
QY 1141 CTGCTGAGACTCGGCTCTCTTCCAGAGATCACTGCTGCTGCTTGAAGGAGAAC 1200
DB 1141 CTGCTGAGACTCGGCTCTCTTCCAGAGATCACTGCTGCTGCTTGAAGGAGAAC 1200
QY 1201 TTCAACAGCGATCTGGGTACCAAGAGCTCCAGAGAGAACTTGTGATCCATCG 1260
DB 1201 TTCAACAGCGATCTGGGTACCAAGAGCTCCAGAGAGAACTTGTGATCCATCG 1260
QY 1261 TGTCTC-GGACACCAAGCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1319
DB 1261 TGTCTC-GGACACCAAGCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1319
QY 1320 TGGACAGGCTGCGAGCTGCTGCACTGCGCGTGGAGGCGGCGCAAGAGAGTGGCCA 1379
DB 1320 TGGACAGGCTGCGAGCTGCTGCACTGCGCGTGGAGGCGGCGCAAGAGAGTGGCCA 1379
QY 1380 AGTGGCTGCTGCTCAACATGCAATGCCAACCCCAACTGAGCAACCTGAGGCGCTCA 1439
DB 1380 AGTGGCTGCTGCTCAACATGCAATGCCAACCCCAACTGAGCAACCTGAGGCGCTCA 1439
QY 1440 TGCATATGCGCTGAGAGAGGAGTGGCGGCTGTCTGAGAGCTCTCTGCTGCAAGAA 1499
DB 1440 TGCATATGCGCTGAGAGAGGAGTGGCGGCTGTCTGAGAGCTCTCTGCTGCAAGAA 1499
QY 1500 TCAATGTCACAGGCAAGATGAGAGACAGTGAAGAGCTTCTGAGGCGCCAGAG 1559
DB 1500 TCAATGTCACAGGCAAGATGAGAGACAGTGAAGAGCTTCTGAGGCGCCAGAG 1559
QY 1560 GGGATGAGTCTGAGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1619
DB 1560 GGGATGAGTCTGAGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1619
QY 1620 TTGAGGCGCGGACCGCCATGCACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1679
DB 1620 TTGAGGCGCGGACCGCCATGCACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1679

QY	1660	TCCTGCTGCGCCGAGGCGCTGGAACGTGAAGCCTGACGGGCAAGGAAATGCCCTGGCTGCACTGCG	1739
Db	1680	TCCTGCTGCGCGCGAAGGCGGTGGAACGTGAACCTGACGGGCAAGGAAATGCCCTGGCTGCACTGCG	1739
QY	1740	ACTAAGCTGCGCTGGGACGAGGCAACCTGGCCCATCGTCAAGCTCTGGCCAAAGCAGCGGGGG	1799
Db	1740	ACTAAGCTGCGCTGGGACGAGGCAACCTGGCCCATCGTCAAGCTCTGGCCAAAGCAGCGGGGG	1799
QY	1800	TGAAGTGAACGCGCCGACGCTGGATGGAGAGAGCGCCATTGCACTTGGCCGCAACGCGCG	1859
Db	1800	TGAAGTGAACGCGCCGACGCTGGATGGAGAGAGCGCCATTGCACTTGGCCGCAACGCGCG	1859
QY	1860	GGCACTACCGGGTGGCGCGGCATCCATCGACCTGTGTCCGAGCGTCAACGTCTGGACGC	1919
Db	1860	GGCACTACCGGGTGGCGCGGCATCCATCGACCTGTGTCCGAGCGTCAACGTCTGGACGC	1919
QY	1920	TGCTTGGCAACAACAACCCCTGCAACGTAGCGCGGAGACGAGGCAACGAGCACTGCCAAGC	1979
Db	1920	TGCTTGGCAACAACAACCCCTGCAACGTAGCGCGGAGACGAGGCAACGAGCACTGCCAAGC	1979
QY	1980	TGCTCTGTCGATTCGGGGGCGCTGGCAAGAGAGCGCTTGAACCTCAAGCGGCTCAACCGCTGCG	2039
Db	1980	TGCTCTGTCGATTCGGGGGCGCTGGCAAGAGAGCGCTTGAACCTCAAGCGGCTCAACCGCTGCG	2039
QY	2040	ACCTGGCTGCGCGGCAACGAGCAACCTGGGCAACTGTCAAGCTCTGTTGAGAGAGAGGCG	2099
Db	2040	ACCTGGCTGCGCGGCAACGAGCAACCTGGGCAACTGTCAAGCTCTGTTGAGAGAGAGGCG	2099
QY	2100	ATGTGCTGAGCCCGGGAGACCCCTTGAACAAGACGGCGCTGCACTTGGCTGCGCCCAACGGGC	2159
Db	2100	ATGTGCTGAGCCCGGGAGACCCCTTGAACAAGACGGCGCTGCACTTGGCTGCGCCCAACGGGC	2159
QY	2160	ACTGGGAGTGTGTGAAGAGATTGTGCAAGCGGAGATGTCAATTTGACCTGTTGACAGAGCAGG	2219
Db	2160	ACTGGGAGTGTGTGAAGAGATTGTGCAAGCGGAGATGTCAATTTGACCTGTTGACAGAGCAGG	2219
QY	2220	GGCTGAGGCGCGCTGCAACCTGGCGCGCCAGAGCGCGGCAACGCAACAACGCTGGAACCTTGC	2279
Db	2220	GGCTGAGGCGCGCTGCAACCTGGCGCGCGCCAGAGCGCGGCAACGCAACAACGCTGGAACCTTGC	2279
QY	2280	TCAGGCAATGGGGGCCCAATCAACCTTGCAGAGCCTTAAGTTCAAGGGCGGCCCATATGGCCCCG	2339
Db	2280	TCAGGCAATGGGGGCCCAATCAACCTTGCAGAGCCTTAAGTTCAAGGGCGGCCCATATGGCCCCG	2339
QY	2340	CGGCAACACTCCTTGGCGGAGAACAGACCTTAGCTGGCTCGCGGACAGCGGGGGGTCCA	2399
Db	2340	CGGCAACACTCCTTGGCGGAGAACAGACCTTAGCTGGCTCGCGGACAGCGGGGGGTCCA	2399
QY	2400	CGTGGGGGCTCTTGTCTGTCTGTGTTCCTCGTGGGGAATGAACGATCTTGCCTGGGGCC	2459
Db	2400	CGTGGGGGCTCTTGTCTGTCTGTGTTCCTCGTGGGGAATGAACGATCTTGCCTGGGGCC	2459
QY	2460	CGGTGTGCGCTTAACTTAATGTTAACAAAGCAAGAGTGAACATATGGGCAATCAGAGGGGG	2519
Db	2460	CGGTGTGCGCTTAACTTAATGTTAACAAAGCAAGAGTGAACATATGGGCAATCAGAGGGGG	2519
QY	2520	CTGCTGCTGAACGAGAGTGTCCCTCAAGGTGAAGCTGGCTCAGGTGCAATGCCCGCTCC	2579
Db	2520	CTGCTGCTGAACGAGAGTGTCCCTCAAGGTGAAGCTGGCTCAGGTGCAATGCCCGCTCC	2579
QY	2580	ATCATTCGATCTTAGGCACTGTCTGTCTGAAGGGGACGCTGGGCTCAGAAATCATTTTCGTTTGGC	2639
Db	2580	ATCATTCGATCTTAGGCACTGTCTGTCTGAAGGGGACGCTGGGCTCAGAAATCATTTTCGTTTGGC	2639
QY	2640	TCCTTAATGGGTGGCTGAGGCTGGTCTCTCAAGTGAAGAGCCCAAGCGCTGGAAGCATCA	2699
Db	2640	TCCTTAATGGGTGGCTGAGGCTGGTCTCTCAAGTGAAGAGCCCAAGCGCTGGAAGCATCA	2699
QY	2700	CTCTCTCTGAGGCGAAGCACTTGGGTTTGTGAAGCTCAACAATCTTTGAGGAGAGTGA	2755
Db	2700	CTCTCTCTGAGGCGAAGCACTTGGGTTTGTGAAGCTCAACAATCTTTGAGGAGAGTGA	2755

QY	2760	GGGGAAACTGTGTTTTTTTATCTTCAATACATGACGTGGGCAAGAGGCGTGTCTTAAGT	281.3
Db	2760	GGGGAAACTGTGTTTTTTTATCTTCAATACATGACGTGGGCAAGAGGCGTGTCTTAAGT	281.9
QY	2820	TTCCATGGAATGTGTTTTTAATAAATCTGTAAGAGATGAATPACTTATCAGCTGTGCTTG	287.9
Db	2820	TTCCATGGAATGTGTTTTTAATAAATCTGTAAGAGATGAATPACTTATCAGCTGTGCTTG	287.9
QY	2880	AAACTGTGTAATAAATGTTCATATACATTTGAGATGCTAGTCTCTAAATGATGGCTAAGTAG	293.9
Db	2880	AAACTGTGTAATAAATGTTCATATACATTTGAGATGCTAGTCTCTAAATGATGGCTAAGTAG	293.9
QY	2940	TGGGTTGAGCTTGTGAAAACAATGTTTTATGCAACAAGAACGAATGGTAGACGCACTT	299.9
Db	2940	TGGGTTGAGCTTGTGAAAACAATGTTTTATGCAACAAGAACGAATGGTAGACGCACTT	299.9
QY	3000	TGCGGGGGGTATGTCGTGGCCAGCTCTTAACCATTCAGTCAATTAAGTTGGGTAGTCCCTT	305.9
Db	3000	TGCGGGGGGTATGTCGTGGCCAGCTCTTAACCATTCAGTCAATTAAGTTGGGTAGTCCCTT	305.9
QY	3060	GTGGACAACCAACAACAGCTGCCACATGTGACTAGCTGCCGTTCTGTTCTCGTTGCTCA	311.9
Db	3060	GTGGACAACCAACAACAGCTGCCACATGTGACTAGCTGCCGTTCTGTTCTCGTTGCTCA	311.9
QY	3120	AGATGTTTTGGCACTCTAGAGCCAAGGCGCTTAAGAGTCATTAATAAAATTCCTCCTTGT	317.9
Db	3120	AGATGTTTTGGCACTCTAGAGCCAAGGCGCTTAAGAGTCATTAATAAAATTCCTCCTTGT	317.9
QY	3180	AACCTCATGCTGTGGGGAATGAGGGAGGCCCTCAGAGCGGTGAGAGTCAACAGCTTTGG	323.9
Db	3180	AACCTCATGCTGTGGGGAATGAGGGAGGCCCTCAGAGCGGTGAGAGTCAACAGCTTTGG	323.9
QY	3240	GGAAGAGGTGCAAGAGAGCTGTGTTTTTATCTCCAACGCAAGTATGAAATAAATTA	329.9
Db	3240	GGAAGAGGTGCAAGAGAGCTGTGTTTTTATCTCCAACGCAAGTATGAAATAAATTA	329.9
QY	3300	CATAGTAATTAACCTAGACATPAGACAGATTAACCTAGTAGATGCACTGCTCACCTGACCC	335.9
Db	3300	CATAGTAATTAACCTAGACATPAGACAGATTAACCTAGTAGATGCACTGCTCACCTGACCC	335.9
QY	3360	TTCCAGCTCTCATTTTTTGTATAGTGATTTTGGGATAGGGAATGAGTTTGGGGATGAGG	341.9
Db	3360	TTCCAGCTCTCATTTTTTGTATAGTGATTTTGGGATAGGGAATGAGTTTGGGGATGAGG	341.9
QY	3420	GGAAGTTTCTGACCTGCTTTGACAGACGTGCTCCGACCTCAGCAGTTTGGGGTGTGGC	347.9
Db	3420	GGAAGTTTCTGACCTGCTTTGACAGACGTGCTCCGACCTCAGCAGTTTGGGGTGTGGC	347.9
QY	3480	CCCAAGGCGGTTCTTGAGTGTAAAGATGTGGCCATCTAGCTGTGAACCTTCACTGTCAAC	353.9
Db	3480	CCCAAGGCGGTTCTTGAGTGTAAAGATGTGGCCATCTAGCTGTGAACCTTCACTGTCAAC	353.9
QY	3540	CTGTGTCCCATAGGGTGCTTCTGAAATCTGTATTTAGAAATAGTTTGTTCAGAAACGTG	359.9
Db	3540	CTGTGTCCCATAGGGTGCTTCTGAAATCTGTATTTAGAAATAGTTTGTTCAGAAACGTG	359.9
QY	3600	ACCCGCGGTGCAAAACATGATCCGTGGCCCTGGATATGATAGAGATGTATATTAATGTAAC	365.9
Db	3600	ACCCGCGGTGCAAAACATGATCCGTGGCCCTGGATATGATAGAGATGTATATTAATGTAAC	365.9
QY	3660	ATGTAATGTAATGTGAATCTGTGGCAGAGATACTTTTCATGGCAGAAATATCAACACT	371.9
Db	3660	ATGTAATGTAATGTGAATCTGTGGCAGAGATACTTTTCATGGCAGAAATATCAACACT	371.9
QY	3720	GTTGAAACTGCGCTATGTTTTTAATATAGCTCATGTGCTCTTAACGTGTGTGAGACTGGGT	377.9
Db	3720	GTTGAAACTGCGCTATGTTTTTAATATAGCTCATGTGCTCTTAACGTGTGTGAGACTGGGT	377.9
QY	3780	GAGGAGCAAGAAATGTCATTTGATGTCAATTAAGCAAGATGCTTGCTCACTTTTGTGAAG	383.9
Db	3780	GAGGAGCAAGAAATGTCATTTGATGTCAATTAAGCAAGATGCTTGCTCACTTTTGTGAAG	383.9
QY	3840	CTGAAAAAAAAAAAAAAAAAGC 3860	

Db 3840 CTGAAAAAAAAAAAAAG 3860

RESULT 3
US-10-172-118-1840
; Sequence 1840, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT FILING DATE: 2002-06-14
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1840
; LENGTH: 3879
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_020639
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1840

Query Match 98.6%; Score 3804.2; DB 17; Length 3879;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3831; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY 7 GTCGCGCGCGATGAGGCGGAGCGGCGGAGCCCATGAGGCGCTGCGGCGGACCTT 66
Db 39 GACGTCGCGGATGAGGCGGAGCGGCGGAGCCCATGAGGCGCTGCGGCGGACCTT 98
QY 67 CGACGCGGCGGAGTTTCAACGCGGCTGAGAGAGGTGGGCTTGGGCGGCTTGGGCAAGTGT 126
Db 99 CGACGCGGCGGAGTTTCAACGCGGCTGAGAGAGGTGGGCTTGGGCGGCTTGGGCAAGTGT 158
QY 127 CAAGGTGCGGCGGATGTCATGAGAGAGCTGCGGCTGAGAGAGCTTGGGCGGCTTGGGCAAGTGT 186
Db 159 CAAGGTGCGGCGGATGTCATGAGAGAGCTGCGGCTGAGAGAGCTTGGGCGGCTTGGGCAAGTGT 218
QY 187 CGTCGACGACGAGGAGCGGATGAGCTTTTGAAGAAGGCAAGAAGATGAGATGAGCA 246
Db 219 CGTCGACGACGAGGAGCGGATGAGCTTTTGAAGAAGGCAAGAAGATGAGATGAGCA 278
QY 247 GTTTCGCTACATCTGCTGCTGTGTATGCACTGCGCGGAACCTGTGCGGCTGTGATGGA 306
Db 279 GTTTCGCTACATCTGCTGCTGTGTATGCACTGCGCGGAACCTGTGCGGCTGTGATGGA 338
QY 307 GTACATGAGAGAGGCGCTCCTTGGAAAAAGCTGCTGCTTGGAGCGCATTTGGCATTTGGATCT 366
Db 339 GTACATGAGAGAGGCGCTCCTTGGAAAAAGCTGCTGCTTGGAGCGCATTTGGCATTTGGATCT 398
QY 367 CGGCTTCCGAATCATTCACAGAGCGGCGGTGGGCAATGAACTTCTGCACTGATGAGCC 426
Db 399 CGGCTTCCGAATCATTCACAGAGCGGCGGTGGGCAATGAACTTCTGCACTGATGAGCC 458
QY 427 GCGACTCTTGCACTTGACCTCAAGCCCGCAATCTCTGCTGATGAGCCATGACCTCAAG 486
Db 459 GCGACTCTTGCACTTGACCTCAAGCCCGCAATCTCTGCTGATGAGCCATGACCTCAAG 518
QY 487 CAAGATTTTGAATTTTGTGCTGCGGCAAGTGCACCGGCGTCTCCACTGCGATGACCTCAAG 546
Db 519 CAAGATTTTGAATTTTGTGCTGCGGCAAGTGCACCGGCGTCTCCACTGCGATGACCTCAAG 578

QY 547 CATGATGCGCTGTTGGCAAAATGCGCTTACTCTCCCTGACAGCGCATGAGAGAG 606
Db 579 CATGATGCGCTGTTGGCAAAATGCGCTTACTCTCCCTGACAGCGCATGAGAGAG 638
QY 607 CCGGCTCTTGCAACCAAGCAAGATGATACAGCTTTGGCATGCTGAGGCGTGTCT 666
Db 639 CCGGCTCTTGCAACCAAGCAAGATGATACAGCTTTGGCATGCTGAGGCGTGTCT 698
QY 667 CACAGAGAGAGCGGTTTGCAGATGAGAGAAATCATCTGCACTATGAGTGAAGTGT 726
Db 699 CACAGAGAGAGCGGTTTGCAGATGAGAGAAATCATCTGCACTATGAGTGAAGTGT 758
QY 727 GAAAGGCGCACCGCCCGAGCTCCCGCGTGTGAGAGCCCGCGCGCGCTTGACCA 786
Db 759 GAAAGGCGCACCGCCCGAGCTCCCGCGTGTGAGAGCCCGCGCGCGCTTGACCA 818
QY 787 CCGATACGCTCATGACGCGGTCTGCGAGGAGATCCCGAGATTAGGCCCACTTCCA 846
Db 819 CCGATACGCTCATGACGCGGTCTGCGAGGAGATCCCGAGATTAGGCCCACTTCCA 878
QY 847 AGAAATTACTTTGAAAACCGAGACCTGTGAAAAGCTGATGACGAAGTGAAGAAG 906
Db 879 AGAAATTACTTTGAAAACCGAGACCTGTGAAAAGCTGATGACGAAGTGAAGAAG 938
QY 907 TGCTCATGATCTGACGCTGAAAAGCCCGCGAGCCCGAGAGCGAGGTGTCTGCGAG 966
Db 939 TGCTCATGATCTGACGCTGAAAAGCCCGCGAGCCCGAGAGCGAGGTGTCTGCGAG 998
QY 967 GCTCAAGCGGCGCTCTGCGCCCACTTGTATATGATACAGCTTCTCCAGCTTCTCTC 1026
Db 999 GCTCAAGCGGCGCTCTGCGCCCACTTGTATATGATACAGCTTCTCCAGCTTCTCTC 1058
QY 1027 ACAGTGGACCTGAGGTTTCCAGGCTGTGCGAGGCGCGCGAGAGCTACGCGCAGCTC 1086
Db 1059 ACAGTGGACCTGAGGTTTCCAGGCTGTGCGAGGCGCGCGAGAGCTACGCGCAGCTC 1118
QY 1087 CTCTGATGCTCAAGCTGACATCTGCGAGAGTGGAGAGAGCTCTCGGAGGTGTCTCGGT 1146
Db 1119 CTCTGATGCTCAAGCTGACATCTGCGAGAGTGGAGAGAGCTCTCGGAGGTGTCTCGGT 1178
QY 1147 GGAATCGGCTTCTCTTCCAGAGATCACTGTGCTGTCTTTTGAAGGGAACCTTCAAC 1206
Db 1179 GGAATCGGCTTCTCTTCCAGAGATCACTGTGCTGTCTTTTGAAGGGAACCTTCAAC 1238
QY 1207 CAGGATGCGGATCAACAAGCTGCAAGAGAAAGCTTGTGATGCCATGCTGTCC- 1265
Db 1239 CAGGATGCGGATCAACAAGCTGCAAGAGAAAGCTTGTGATGCCATGCTGTCC- 1297
QY 1266 GGAACAACCAAGAACTGATGAATCTTGAAGCGCGAGAGAGTGTGACTGTGACA 1325
Db 1298 GGAACAACCAAGAACTGATGAATCTTGAAGCGCGAGAGAGTGTGACTGTGACA 1357
QY 1326 GCGGTGCAAGCTGCTGCACTGCGCGGTGAGAGCGCGGCAAGAGATGCGGCAAGTGC 1385
Db 1358 GCGGTGCAAGCTGCTGCACTGCGCGGTGAGAGCGCGGCAAGAGATGCGGCAAGTGC 1417
QY 1386 TGCTGCTCAACATGTCACAAACCCCAACCTGAGCAACCGTAAAGGCGCTTCAACCCGTTGACA 1445
Db 1418 TGCTGCTCAACATGTCACAAACCCCAACCTGAGCAACCGTAAAGGCGCTTCAACCCGTTGACA 1477
QY 1446 TGCGCTGAGAGAGAGGTGCGGAGTGTCTGTGAGCTTCTGCTGCAACGGAAGTCAAGT 1505
Db 1478 TGCGCTGAGAGAGAGGTGCGGAGTGTCTGTGAGCTTCTGCTGCAACGGAAGTCAAGT 1537
QY 1506 TGAACGCCAAGATGAGAGCAAGTGAACAGCTTCTCACTTTGCAAGCCCAAGACGGGATG 1565
Db 1538 TGAACGCCAAGATGAGAGCAAGTGAACAGCTTCTCACTTTGCAAGCCCAAGACGGGATG 1597
QY 1566 AGTCTAGACAAGCGGTGCTGTTGAGAGAAAGCGCTGCTGCAAGAGGTGAGCTTTGAGG 1625
Db 1598 AGTCTAGACAAGCGGTGCTGTTGAGAGAAAGCGCTGCTGCAAGAGGTGAGCTTTGAGG 1657
QY 1626 GCGGAGCGCCCATGACAGTGTGCTGCGAGCAAGGAGAGAGATATGCTGTGCACTCTGC 1685

Db	1658	GCCGCGACGCCCATGCACTGAGCGCTGACAGACCGGCGAGGAATATCTGCGCATCTCG	1717
Qy	1686	TGCGCCGAGGGGTGAGAGCTGAGCGCTGACAGGCGAAGATGACTGCGCTGCGCATCTGCACTACG	1745
Db	1718	TGCGCCGAGGGGTGAGAGCTGAGCGCTGAGAGGCGAAGATGACTGCGCTGCGCATCTGCACTACG	1777
Qy	1746	CTGCGCTGGCAGAGGCGCACCTGCGCATCTGTCAGACGTCTGAGCGCAAGCACCGCGGGGTGAGTG	1805
Db	1778	CTGCGCTGGCAGAGGCGCACCTGCGCATCTGTCAGACGTCTGAGCGCGCAAGCACCGGGGTGAGTG	1837
Qy	1806	TGAACGCCGACAGCGCTGAGTGGAGAGACGCCATTGCACTTGGCCCGCACACCGCGGGGCACT	1865
Db	1838	TGAACGCCGACAGCGCTGAGTGGAGAGACGCCATTGCACTTGGCCCGCACACCGCGGGGCACT	1897
Qy	1866	AACCGCGTGGCCCGGAGTCCTCACTGCAACGTGCTCCGACGTCACACGTCTGAGCGCTGCGG	1925
Db	1898	AACCGCGTGGCCCGGAGTCCTCACTGCAACGTGCTCCGACGTCACACGTCTGAGCGCTGCGG	1957
Qy	1926	CACAGACACCCCTGTCACGTGAGCGCGCGGAGACGGGGGACACAGAGCATTCGACGCTGCTCC	1985
Db	1958	CACAGACACCCCTGTCACGTGAGCGCGCGGAGACGGGGGACACAGAGCATTCGACGCTGCTCC	2017
Qy	1986	TGCATTGCGGGGCGCTGGCAGAGAGGCGGTGACCTTCAGACGCTACACCGCTCTGCACTTGG	2045
Db	2018	TGCATTGCGGGGCGCTGGCAGAGAGGCGGTGACCTTCAGACGCTACACCGCTCTGCACTTGG	2077
Qy	2046	CTGCGCCGCGACAGGACACTTGGCGCATCTGTCAGACGTGCTTTCAGAGAGAGAGCGAGTGGC	2105
Db	2078	CTGCGCCGCGACAGGACACTTGGCGCATCTGTCAGACGTGCTTTCAGAGAGAGAGCGAGTGGC	2137
Qy	2106	TGGCCCGGGGAGCCCTTGACACAGACGGGCGCTGACCTTGGCTGGCCGACCGGCACTTCGG	2165
Db	2138	TGGCCCGGGGAGCCCTTGACACAGACGGGCGCTGACCTTGGCTGGCCGACCGGCACTTCGG	2197
Qy	2166	AGGTGATGAGAGAGTTGATGACAGCGCGGATGTCATTGACCTGTTCGACGAGCAGGGGCTCA	2225
Db	2198	AGGTGATGAGAGAGTTGATGACAGCGCGGATGTCATTGACCTGTTCGACGAGCAGGGGCTCA	2257
Qy	2226	GCGCGCTGCACTTGGCGCGGCCGACGGGCGCGGACCGACAGAGGTGAGAGACTTGGTCAGAGC	2285
Db	2258	GCGCGCTGCACTTGGCGCGGCCGACGGGCGCGGACCGACAGAGGTGAGAGACTTGGTCAGAGC	2317
Qy	2286	ATGGGAGCCACATCAACCTGCGAGAGCCTCAAGTTTCAGGAGGAGGACATGGCCCGCCGCGCA	2345
Db	2318	ATGGGAGCCACATCAACCTGCGAGAGCCTCAAGTTTCAGGAGGAGGACATGGCCCGCCGCGCA	2377
Qy	2346	CACTCCTGCGCGGAGCAAGACCTTACCTGCTGCTGCGAGACCGGAGGATCCAGTGGG	2405
Db	2378	CACTCCTGCGCGGAGCAAGACCTTACCTGCTGCTGCGAGACCGGAGGATCCAGTGGG	2437
Qy	2406	GCTCTTGTGTCCTGTCTGTGTGTCCTGTGTGGGAGTGAAGAGTCTGCGTGGGGGCCCGTTG	2465
Db	2438	GCTCTTGTGTCCTGTCTGTGTGTCCTGTGTGGGAGTGAAGAGTCTGCGTGGGGGCCCGTTG	2497
Qy	2466	TGGCTTACCTAAATGTTAACAGAGGAGAGTGAACATGTGTCATCAAGAGCGGCTGCTG	2525
Db	2498	TGGCTTACCTAAATGTTAACAGAGGAGAGTGAACATGTGTCATCAAGAGCGGCTGCTG	2557
Qy	2526	CTGACCGGAGTGTCCCTTCAGAGTGAAGCTGACTGAGGTGACATGCGCGCTCATCATC	2585
Db	2558	CTGACCGGAGTGTCCCTTCAGAGTGAAGCTGACTGAGGTGACATGCGCGCTCATCATC	2617
Qy	2586	GATTTAGGACCTGCTGTCTTGAAGAGGACGCTGGGTCAAAATCATTTGCTTGTGCTCCAA	2645
Db	2618	GATTTAGGACCTGCTGTCTTGAAGAGGACGCTGGGTCAAAATCATTTGCTTGTGCTCCAA	2677
Qy	2646	TGGGTGCTGAGGCTGCTCTCAAGATGAAGAGCCACAGGCGTGGAACTACACTCTCT	2705
Db	2678	TGGGTGCTGAGGCTGCTCTCTCAAGATGAAGAGCCACAGGCGTGGAACTACACTCTCT	2737
Qy	2706	CTGAGGCGAGCCACTTGGGTTGCTGAGACTCACCAAGCTTGAAGGAGGTGCAAGGGGA	2765

Db	2738	CTGAGGCGAGCCACTCTGGGTCCTGAGCTACCAAGTCTTGAGGAGGTGCAGGGGAA	2797
Qy	2766	ACTGTGTTTTTATCTTCAATACATGACGGTGGGCAAGAGGCGCTGTCTTAAAGTTTCAT	2825
Db	2798	ACTGTGTTTTTATCTTCAATATATGACGGTGGGCAAGAGGCGCTGTCTTAAAGTTTCAT	2857
Qy	2826	GGAATGTTTTTATATAATATCTTAAAGATGAATTAACCTTATCAAGCTGTGCTTGAACCT	2885
Db	2858	GGAATGTTTTTATATAATATCTTAAAGATGAATTAACCTTATCAAGCTGTGCTTGAACCT	2917
Qy	2886	GTTAAAAATGTTCAATACATTGATGATCTAGTCTCTAAATGATGGCTAAATGATGGGGT	2945
Db	2918	GTTAAAAATGTTCAATACATTGATGATCTAGTCTCTAAATGATGGCTAAATGATGGGGT	2977
Qy	2946	TGGCTTTGAAAAACATGTTTTTATGCAACAGAAACGATGGTAGACACAGCTTGGGGG	3005
Db	2978	TGGCTTTGAAAAACATGTTTTTATGCAACAGAAACGATGGTAGACACAGCTTGGGGG	3037
Qy	3006	GCGTATGTGTGGCCAGCTCTTAAACATTCAGTCTATTACTGGGTGATAGTCTGTGGAC	3065
Db	3038	GCGTATGTGTGGCCAGCTCTTAAACATTCAGTCTATTACTGGGTGATAGTCTGTGGAC	3097
Qy	3066	AAACCAACAACGAGCCCAATGGATACAGTGTGCGTGTCTTCGTGTGCTTAAGAATGT	3125
Db	3098	AAACCAACAACGAGCCCAATGGATACAGTGTGCGTGTCTTCGTGTGCTTAAGAATGT	3157
Qy	3126	TTTGGCAACTCTAAGACCAACAGGCTTAAGAGTCAATTAATAAATTCCTCTTTGTACCTC	3185
Db	3158	TTTGGCAACTCTAAGACCAACAGGCTTAAGAGTCAATTAATAAATTCCTCTTTGTACCTC	3217
Qy	3186	AGTGTGTGGGACCTGAGGGAGACCCCCCTCAAGTCCCTGTGAGTGCACACGCTTGGGGAGA	3245
Db	3218	AGTGTGTGGGACCTGAGGGAGACCCCCCTCAAGTCCCTGTGAGTGCACACGCTTGGGGAGA	3277
Qy	3246	GGTGACAGAGAAGCGTGTGTATCTCCACACGACAGTATGAAGATTAATACATAGT	3305
Db	3278	GGTGACAGAGAAGCGTGTGTATCTCCACACGACAGTATGAAGATTAATACATAGT	3337
Qy	3306	ATTACCTTAGACATAGACAGATTAACCTAAGTAGATGCACTGCTCACCTGCACCTTCCCA	3365
Db	3338	ATTACCTTAGACATAGACAGATTAACCTAAGTAGATGCACTGCTCACCTGCACCTTCCCA	3397
Qy	3366	GCTCTCATTTTTTGTTAGGTGATTTGGGATTAAGGATAGGTGTTGGGGGATGAGGGGAGTG	3425
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RESULT 4
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; Sequence 1840, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Limeley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1840
; LENGTH: 3879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1840

Query Match      98.6%; Score 3804.2; DB 18; Length 3879;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3831; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
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 QY 2586 GATCTAGGCACTGTGCTGTAAGAGACGCTGGGCTCAAGATCAATTTGTTGCTCTTA 2645
 DB 2618 GATCTAGGCACTGTGCTGTAAGAGACGCTGGGCTCAAGATCAATTTGTTGCTCTTA 2677
 QY 2646 TGGGTGCTGAGGCTGTGCTCTCAAGTGAAGAGCCCAAGGCTGGAAGCACTCTCT 2705
 DB 2678 TGGGTGCTGAGGCTGTGCTCTCAAGTGAAGAGCCCAAGGCTGGAAGCACTCTCT 2737
 QY 2706 CCGAGGCGAGCACTGGGTTGCTGAGCTCAAGAGTCTTGAAGGAGGTGAGGAGAA 2765
 DB 2738 CCGAGGCGAGCACTGGGTTGCTGAGCTCAAGAGTCTTGAAGGAGGTGAGGAGAA 2797
 QY 2766 ACTGTGTTTTTATCTTCAATACAGAGGTGGCAAGAGGCTGTCTTAAAGTTTCAAT 2825
 DB 2798 ACTGTGTTTTTATCTTCAATACAGAGGTGGCAAGAGGCTGTCTTAAAGTTTCAAT 2857

QY 2826 GGAATGTTTTTATTAATAATCTTAAGAGATGAATACCTTATCAGCTGTGCTGAACCT 2885
 DB 2858 GGAATGTTTTTATTAATAATCTTAAGAGATGAATACCTTATCAGCTGTGCTGAACCT 2917
 QY 2886 GTTAAATGTTCAATTAATGATAGTCTGCTTAATGATGAGTGAAGTGGGCT 2945
 DB 2918 GTTAAATGTTCAATTAATGATAGTCTGCTTAATGATGAGTGAAGTGGGCT 2977
 QY 2946 TGGCTTGAATAATGTTTATGCAACAAAGAAAGAAAGTGTACAGCACTTGGCGG 3005
 DB 2978 TGGCTTGAATAATGTTTATGCAACAAAGAAAGAAAGTGTACAGCACTTGGCGG 3037
 QY 3006 GCGATGTTGGCCAGCTCTTAACATTCAGTCTAATTACTTGGGAGTGGTGGAC 3065
 DB 3038 GCGATGTTGGCCAGCTCTTAACATTCAGTCTAATTACTTGGGAGTGGTGGAC 3097
 QY 3066 AACCAACACAGTGGCCACATGATAGTGTGCTGCTGCTGCTGCTGAAGTGT 3125
 DB 3098 AACCAACACAGTGGCCACATGATAGTGTGCTGCTGCTGCTGCTGAAGTGT 3157
 QY 3126 TTTGGCACTTAAGAGCAAGGCTTAAGATCAATTAATAATCTCCCTTGTAACTC 3185
 DB 3158 TTTGGCACTTAAGAGCAAGGCTTAAGATCAATTAATAATCTCCCTTGTAACTC 3215
 QY 3186 AGTGTGGGAGCTGAGGAGCGCCCTCAGGCTGCTGAGTGAACAGTCTTGGGAGAA 3245
 DB 3216 AGTGTGGGAGCTGAGGAGCGCCCTCAGGCTGCTGAGTGAACAGTCTTGGGAGAA 3275
 QY 3246 GGTGCAAGAGAGCTGTGTTTTTATCTCAACAGCAGATGAAGATTAATTAATAGT 3305
 DB 3276 GGTGCAAGAGAGCTGTGTTTTTATCTCAACAGCAGATGAAGATTAATTAATAGT 3335
 QY 3306 ATTACTGAACATTAAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3365
 DB 3336 ATTACTGAACATTAAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3395
 QY 3366 GCTCTCAATTTTGTAGGATTTGGAGTGAAGTGTGGGATGAGGAGGAGT 3425
 DB 3396 GCTCTCAATTTTGTAGGATTTGGAGTGAAGTGTGGGATGAGGAGGAGT 3455
 QY 3426 TTTCTGACCTGCTTGAAGAGCTGCTCGCACTCAGCAGTGTGGGATGAGGAGG 3485
 DB 3456 TTTCTGACCTGCTTGAAGAGCTGCTCGCACTCAGCAGTGTGGGATGAGGAGG 3515
 QY 3486 GCGGTTCTTGAATGAAGAGTGGGCACTAGGCTGTGAATCTTCACTGTGCT 3545
 DB 3516 GCGGTTCTTGAATGAAGAGTGGGCACTAGGCTGTGAATCTTCACTGTGCT 3575
 QY 3546 CCCATAGGAGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3605
 DB 3576 CCCATAGGAGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3635
 QY 3606 CGTGAACATGTACCGTGGCTGTATATGATAGATGAATTAATTAATTAATTAAT 3665
 DB 3636 CGTGAACATGTACCGTGGCTGTATATGATAGATGAATTAATTAATTAATTAAT 3695
 QY 3666 GTTAAATGGAATCTGTGGGAGAGATCTTTCATGAGAGAAATATCAAGCTGTGA 3725
 DB 3696 GTTAAATGGAATCTGTGGGAGAGATCTTTCATGAGAGAAATATCAAGCTGTGA 3755
 QY 3726 ACTGCTAATGTTTAAATGCTCATGAGCTTAACTGTTGTGAGCTGAGTGAAGGA 3785
 DB 3756 ACTGCTAATGTTTAAATGCTCATGAGCTTAACTGTTGTGAGCTGAGTGAAGGA 3815
 QY 3786 CAAGAAGTTCAATTTGATGTCAATTAAGCAAGTCTTGTGCTTATTTGAAGCTGAAA 3845
 DB 3816 CAAGAAGTTCAATTTGATGTCAATTAAGCAAGTCTTGTGCTTATTTGAAGCTGAAA 3875
 QY 3846 AAAAAAAAAA 3858
 DB 3876 AAAAAAAAAA 3888


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RESULT 7
US-10-302-172-905
; Sequence 905, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids an
; FILE REFERENCE: 803.1CNCp
; CURRENT APPLICATION NUMBER: US/10/302.172
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pc_fl_genes Version 2.0
; LENGTH: 3981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2496)
US-10-302-172-905

Query Match      94.4%; Score 3643; DB 16; Length 3981;
Beet Local Similarity 96.1%; Pred. No. 0;
Matches 3825; Conservative 0; Mismatches 11; Indels 146; Gaps 3;

QY      17  ATGAGAGGCGACGCGCGGAGCCCATGAGCCCTGCGCTGCGACGACCTTCGACGCGGAGC 76
DB      1  ATGAGAGGCGACGCGCGGAGCCCATGAGCCCTGCGCTGCGACGACCTTCGACGCGGAGC 60

QY      77  GAGTTCAAGCGGCTGGAGAGAGGTGGCTTGGCGCGCTTGGGCAAGTGTACAAAGTGGGC 136
DB      61  GAGTTCAAGCGGCTGGAGAGAGGTGGCTTGGCGCGCTTGGGCAAGTGTACAAAGTGGGC 120

QY      137  CATGTCACATGGAAGCCTGGCTGGCATCAAGTCTGGCCGACGCTGACGCTGACGAC 196
DB      121  CATGTCACATGGAAGCCTGGCTGGCATCAAGTCTGGCCGACGCTGACGCTGACGAC 180

QY      197  AGGAGCGCATGAGCTTTTGGAGAGCCAGAGAGATGAGATGAGCCAAAGTTTGGCTAC 256
DB      181  AGGAGCGCATGAGCTTTTGGAGAGCCAGAGAGATGAGATGAGCCAAAGTTTGGCTAC 240

QY      257  ATCTGCTGTGTATGGCATCTGCGCGCAACCTGTGCGCTGTGATGAGATGATGAG 316
DB      241  ATCTGCTGTGTATGGCATCTGCGCGCAACCTGTGCGCTGTGATGAGATGATGAG 300

QY      317  AGGCGCTCCCTGGAAAAGCTGTGGCTTGGAGGCAATGAGGATCTCCGTTCCGA 376
DB      301  AGGCGCTCCCTGGAAAAGCTGTGGCTTGGAGGCAATGAGGATCTCCGTTCCGA 360

QY      377  ATCATTCACAGACGCGCGTGGCATGAACTTCTGCACTGATGAGCCCGCACTCTG 436
DB      361  ATCATTCACAGACGCGCGTGGCATGAACTTCTGCACTGATGAGCCCGCACTCTG 420

QY      437  CACCTGACCTCAAGCCCGGAAACATCTGCTGATGCCCACTACCACTCAAGATTTC 496
DB      421  CACCTGACCTCAAGCCCGGAAACATCTGCTGATGCCCACTACCACTCAAGATTTC 480

QY      497  GATTTTGTGTGGCCAAAGTGAACGCGGCTGTCCCACTGATGAGCCCTGAGATGAG 556
DB      481  GATTTTGTGTGGCCAAAGTGAACGCGGCTGTCCCACTGATGAGCCCTGAGATGAG 540

QY      557  CTGTTTGGACAACTGCTTACCTCCCTCAAGAGCGATGAGGAGAGAGCGGCTTTC 616
DB      541  CTGTTTGGACAACTGCTTACCTCCCTCAAGAGCGATGAGGAGAGAGCGGCTTTC 600
    
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QY      617  GACACCAAGACCAATGATACAGCTTTGGATGCTATCTGGGCGGTGCTCACAGAG 676
DB      601  GACACCAAGACCAATGATACAGCTTTGGATGCTATCTGGGCGGTGCTCACAGAG 660

QY      677  AAGCGTTTGCAGATGAGAGAAACATCTTGCACATCAATGATGAGTGAAGTGAAGGCGCAC 736
DB      661  AAGCGTTTGCAGATGAGAGAAACATCTTGCACATCAATGATGAGTGAAGTGAAGGCGCAC 720

QY      737  CGCCCCGAGCTGCCCGGCTGTGACAGAGCCCGGCGGCTTGGACACCTGATGCGC 796
DB      721  CGCCCCGAGCTGCCCGGCTGTGACAGAGCCCGGCGGCTTGGACACCTGATGCGC 780

QY      797  CTGATGAGGCGGTGTGGCAAGGCGGATCCGAGATTAGGCCCACTTC----- 844
DB      781  CTGATGAGGCGGTGTGGCAAGGCGGATCCGAGATTAGGCCCACTTC----- 840

QY      845  ----- 844
DB      841  CTGAAATGGGAGACTATCCCGCAAGTGTGGCAAGCTGTGCTCCCTGTGATGGCAGGTGG 900

QY      845  ----- 844
DB      901  CGCTCCCCCGGAGAGGCTTCCGCTTGAATCTGAATCATATCCAGTGAATGTCCC 960

QY      845  -----CAAGAAATTACTTTCTGAAAACGAGAGACCTGTGTGAAAAGCTGATGAC 892
DB      961  CTTTCTTCCCAACAAGAAATTACTTTCTGAAAACGAGAGACCTGTGTGAAAAGCTGATGAC 1020

QY      893  GAAGTGAAGAGAACTGTCTATGATCTGGAAGTGAAGAGCCCGGAGCCCAAGAGCGAG 952
DB      1021  GAAGTGAAGAGAACTGTCTATGATCTGGAAGTGAAGAGCCCGGAGCCCAAGAGCGAG 1080

QY      953  GTGTGCTGTGGAGGCTCAAGCGGCGCTTGGCCCGCACTTTCGATTAACGCTAAGCTC 1012
DB      1081  GTGTGCTGTGGAGGCTCAAGCGGCGCTTGGCCCGCACTTTCGATTAACGCTAAGCTC 1140

QY      1013  TCCGAGCTTCTCTACAGCTGGAATCTGAGATTTCCAGAGCTGTGAGAGGCGCCGAGAG 1072
DB      1141  TCCGAGCTTCTCTACAGCTGGAATCTGAGATTTCCAGAGCTGTGAGAGGCGCCGAGAG 1200

QY      1073  CTCAGCGCAGCTCTCTGATCTCAAGCTGCAATGTCCTGGCAGTGGAGAGAGGCTCTCG 1132
DB      1201  CTCAGCGCAGCTCTCTGATCTCAAGCTGCAATGTCCTGGCAGTGGAGAGAGGCTCTCG 1260

QY      1133  GGGGTGTCTGTGTGAGATCTCGGCTTCTTCCAGAGAGATCACTGTGTGCTCTTGGAG 1192
DB      1261  GGGGTGTCTGTGTGAGATCTCGGCTTCTTCCAGAGAGATCACTGTGTGCTCTTGGAG 1320

QY      1193  CGGGAACCTTCAACCAAGCATCTGAGTACCAAGAGCTGCAGAGAGAGAGCTTGTGA 1252
DB      1321  CGGGAACCTTCAACCAAGCATCTGAGTACCAAGAGCTGCAGAGAGAGAGCTTGTGA 1379

QY      1253  TGCATCTGTTC- GGGACACAGCAAACTGATGAAGATCTGACGCGCAGAGCTTGA 1311
DB      1380  TGCATCTGTTC- GGGAGACACAGCAAACTGATGAAGATCTGACGCGCAGAGCTTGA 1439

QY      1312  CTTGCACTGGAACAGCGGTGCAAGCTGTGCACTTGGCGGTGGAAGCCCGGCAAGGGA 1371
DB      1440  CTTGCACTGGAACAGCGGTGCAAGCTGTGCACTTGGCGGTGGAAGCCCGGCAAGGGA 1499

QY      1372  GTGGCCCAAGTGGGTGCTGCTCAACATGCAACCCCACTGAGCAACCTGAGGGGCTC 1431
DB      1500  GTGGCCCAAGTGGGTGCTGCTCAACATGCAACCCCACTGAGCAACCTGAGGGGCTC 1559

QY      1432  CACCCGTTTGCACATGCGCGTGAAGAGAGGAGTGGAGTGTGAGCTTCTGTGGC 1491
DB      1560  CACCCGTTTGCACATGCGCGTGAAGAGAGGAGTGGAGTGTGAGCTTCTGTGGC 1619

QY      1492  ACGGAAGATCAAGTGTCAACGCGCAAGATGAGAGCAAGTGTGACACCTTCCACTTGTGAGC 1551
DB      1620  ACGGAAGATCAAGTGTCAACGCGCAAGATGAGAGCAAGTGTGACACCTTCCACTTGTGAGC 1679
    
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1552 CCAGAACGGGGATGATGCTCTAGACACACGGCTGCTGTTGGAGAGAAACGCTCGGTCAAGCA 1611
1680 CCAGAACGGGGACGAGTCTAGACACACGGCTGCTGTTGGAGAGAAACGCTCGGTCAAGCA 1739
1612 GGTGGAATTGAGGGCCGGAAGCCATGACAGTGGCCTGCGACGACCGGGACAGAGAAATAT 1671
1740 GGTGGAATTGAGGGCCGGAAGCCATGACAGTGGCCTGCGACGACCGGGACAGAGAAATAT 1799
1672 GGTGGAATTGAGGGCCGGAAGCCATGACAGTGGCCTGCGACGACCGGGACAGAGAAATAT 1731
1800 GGTGGAATTGAGGGCCGGAAGCCATGACAGTGGCCTGCGACGACCGGGACAGAGAAATAT 1859
1732 GGTGGAATTGAGGGCCGGAAGCCATGACAGTGGCCTGCGACGACCGGGACAGAGAAATAT 1791
1860 GGTGGAATTGAGGGCCGGAAGCCATGACAGTGGCCTGCGACGACCGGGACAGAGAAATAT 1919
1792 GGTGGAATTGAGGGCCGGAAGCCATGACAGTGGCCTGCGACGACCGGGACAGAGAAATAT 1851
1920 GGTGGAATTGAGGGCCGGAAGCCATGACAGTGGCCTGCGACGACCGGGACAGAGAAATAT 1979
1852 ACAGCGCGGGACCTACCGCGTGGCCCGCATCTCTACATCGACCTGTGCTCCGACGTCAAGT 1911
1980 ACAGCGCGGGACCTACCGCGTGGCCCGCATCTCTACATCGACCTGTGCTCCGACGTCAAGT 2039
1912 CTGCAAGCTCTGCGACACAGACACCCCTGCACTGTGCGCGGAGAGACGGGGACACACAGAC 1971
2040 CTGCAAGCTCTGCGACACAGACACCCCTGCACTGTGCGCGGAGAGACGGGGACACACAGAC 2099
1972 TGCCAGGGCTGCTCCGACATCGGGGGGCTGGACAGAGAGGGCGGAGACCTGACAGCGGTACAC 2031
2100 TGCCAGGGCTGCTCCGACATCGGGGGGCTGGACAGAGAGGGCGGAGACCTGACAGCGGTACAC 2159
2032 CGCTCTGACCTGCTGCGACCGGACCGGACACCTGCGCACTGTACAGCTGCTTGTGAGGA 2091
2160 CGCTCTGACCTGCTGCGACCGGACCGGACACCTGCGCACTGTACAGCTGCTTGTGAGGA 2219
2092 GAAAGCCGATGTGCTGCGACCGGACCGGACACCTGCGCACTGTACAGCTGCTTGTGAGGA 2151
2220 GAAAGCCGATGTGCTGCGACCGGACCGGACACCTGCGCACTGTACAGCTGCTTGTGAGGA 2279
2152 CCAACGGGACCTGCGAGGTGTGAGAGAGTGTGACAGCGCGGATGATGACCTGTTGCA 2211
2280 CCAACGGGACCTGCGAGGTGTGAGAGAGTGTGACAGCGCGGATGATGACCTGTTGCA 2339
2212 CCAACGGGACCTGCGAGGTGTGAGAGAGTGTGACAGCGCGGATGATGACCTGTTGCA 2271
2340 CCAACGGGACCTGCGAGGTGTGAGAGAGTGTGACAGCGCGGATGATGACCTGTTGCA 2399
2272 GACTGTGCTCAGGACATGAGGACCTGACATCTGACAGAGCTGACAGTGTGACAGGACCTG 2331
2400 GACTGTGCTCAGGACATGAGGACCTGACATCTGACAGAGCTGACAGTGTGACAGGACCTG 2459
2332 TGAGCCCGGCGGACACCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2391
2460 TGAGCCCGGCGGACACCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2519
2392 GGGGATCAGAGTGGGCTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2451
2520 GGGGATCAGAGTGGGCTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2579
2452 GGGGATCAGAGTGGGCTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2511
2580 GGGGATCAGAGTGGGCTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2639
2512 GGGGATCAGAGTGGGCTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2571
2640 GGGGATCAGAGTGGGCTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2699
2572 CCGGCTCAGATCATCTAGAGACCTGCTGTCTAGAGAGACCTGCTGTCTAGATCATCTT 2631
2700 CCGGCTCAGATCATCTAGAGACCTGCTGTCTAGAGAGACCTGCTGTCTAGATCATCTT 2759
2632 CCGGCTCAGATCATCTAGAGACCTGCTGTCTAGAGAGACCTGCTGTCTAGATCATCTT 2691

2760 GGTGTGCTCTAATGAGGTGCTGAGGCTGGTCTCTAGATGATGAAGCCCAAGGCTGGA 2819
2692 AGCATCACTCTCTCTGAGGCGAGCACTTGGGTTGCTGAGACTCAACGATCTTAAAG 2751
2820 AGCATCACTCTCTCTGAGGCGAGCACTTGGGTTGCTGAGACTCAACGATCTTAAAG 2879
2752 GAGGTGAGAGGAGAACTGTGTTTATCTTCAATACATGACGGGAGAGAGAGGCTGT 2811
2880 GAGGTGAGAGGAGAACTGTGTTTATCTTCAATACATGACGGGAGAGAGAGGCTGT 2939
2812 CTTAAAGTTTCAATGAGATGTTTATTAATATCTTAAAGATGATTAATCTTAAAGCT 2871
2940 CTTAAAGTTTCAATGAGATGTTTATTAATATCTTAAAGATGATTAATCTTAAAGCT 2999
2872 GTTCTTGAACCTGTTAAATGTTCAATTAATGATGATGATGATGATGATGATGATGATGATGAT 2931
3000 GTTCTTGAACCTGTTAAATGTTCAATTAATGATGATGATGATGATGATGATGATGATGATGAT 3059
2932 CTTAAAGTTTCAATGAGATGTTTATTAATATCTTAAAGATGATTAATCTTAAAGCT 2991
3060 CTTAAAGTTTCAATGAGATGTTTATTAATATCTTAAAGATGATTAATCTTAAAGCT 3119
2992 GCGAGCTTGGGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3051
3120 GCGAGCTTGGGGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3179
3052 GAGTCTTGTGAGAC 3111
3180 GAGTCTTGTGAGAC 3239
3112 GTTGTCTTAAGATGTTTGTGAGCACTTGAAGCAGAGGCTTAAGATGATTAAGATGATTAAGAT 3171
3240 GTTGTCTTAAGATGTTTGTGAGCACTTGAAGCAGAGGCTTAAGATGATTAAGATGATTAAGAT 3299
3172 CCGTTTGAACCTCAGTCTGAGGAGCTGAGGAGCGAGCCCTCAAGTCTGAGAGTGAAC 3231
3300 CCGTTTGAACCTCAGTCTGAGGAGCTGAGGAGCGAGCCCTCAAGTCTGAGAGTGAAC 3359
3232 AGTCTTGGGAGAGAGTGTGAG 3291
3360 AGTCTTGGGAGAGAGTGTGAG 3419
3292 TAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3351
3420 TAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3479
3352 CTGCAACCTTCCAGCTCTCAATTTTGTAGAGATTTGGAGATAGGAGATAGGATTTTGGG 3411
3480 CTGCAACCTTCCAGCTCTCAATTTTGTAGAGATTTGGAGATAGGAGATAGGATTTTGGG 3539
3412 GTATGAGGAGAGATTTTGTACCTGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3471
3540 GTATGAGGAGAGATTTTGTACCTGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3599
3472 GGTGTGAGGAG 3531
3600 GGTGTGAGGAG 3659
3532 ACTGTCACTGTGTCCATGAGGAGCTTGTGAGATGATGATGATGATGATGATGATGATGATGAT 3591
3660 ACTGTCACTGTGTCCATGAGGAGCTTGTGAGATGATGATGATGATGATGATGATGATGATGAT 3719
3592 AGAAGTGAACCTGCTGAGCAATGATACCTGCTGATGATGATGATGATGATGATGATGATGAT 3651
3720 AGAAGTGAACCTGCTGAGCAATGATACCTGCTGATGATGATGATGATGATGATGATGATGAT 3779
3652 AATGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3711
3780 AATGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3839
3712 TCCAAGCTTGTGAACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3771

Db 3840 TCCAAGCTGTGAAACGTGGCTATGTTTAAATATGCTCATTTGCTTTACTGTGTG 3899
Qy 3772 GACTCCGTGAGGAGCAAGAAGTTCCATTTGATGTCAATAAGCAAGTACTTCTACTT 3831
Db 3900 GACTGCCGTGAGGAGCAAGAAGTTCCATTTGATGTCAATAAGCAAGTACTTCTACTT 3959
Qy 3832 TTTTGAANCTGAAAAAAAAAAAA 3853
Db 3960 TTTTGAANCTGAAAAAAAAAAAA 3981

RESULT 8
US-10-172-118-324
; Sequence 324, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Lineley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 324
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATON INFORMATION:
; DATABASE ACCESSION NUMBER: AL137448
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-324

Query Match 67.5%; Score 2606.4; DB 17; Length 2691;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2635; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

Qy 1211 GATCTGGGTACCAAGAGCTGCAGAAAGCTGTGATGTGACATGTGTCC-GGGA 1269
Db 36 GATCTGGGTACCAAGAGCTGCAGAAAGCTGTGATGTGACATGTGTCCGGGA 94
Qy 1270 CACCAAGCAAACTGATGAAGATCTGCAAGCCGAGAGAGCTGGAAGCTGGAAGAGCGG 1329
Db 95 CACCAAGCAAACTGATGAAGATCTGCAAGCCGAGAGAGCTGGAAGCTGGAAGAGCGG 154
Qy 1330 TCCCAAGCTGTGCACTGCGGTGAGAGCCGGGCAAGAGAGTGGCCAAAGTGGCTGT 1389
Db 155 TCCCAAGCTGTGCACTGCGGTGAGAGCCGGGCAAGAGAGTGGCCAAAGTGGCTGT 214
Qy 1390 GGTCAACAATGCAACCCCAACCTGAGCAACGTTAGGGGCTCACCCGTTGCAATGGC 1449
Db 215 GGTCAACAATGCAACCCCAACCTGAGCAACGTTAGGGGCTCACCCGTTGCAATGGC 274
Qy 1450 CTGGAAGAGAGGTGCGGGGTGTGCTGAGAGCTCTGCTGGAAGAGATCAAGTCA 1509
Db 275 CTGGAAGAGAGGTGCGGGGTGTGCTGAGAGCTCTGCTGGAAGAGATCAAGTCA 334
Qy 1510 CGCCAAAGATGAGAGCAAGTGAAGAGCCCTTCACTTTGAGCCCAAGAACGGGATGAGTC 1569
Db 335 CGCCAAAGATGAGAGCAAGTGAAGAGCCCTTCACTTTGAGCCCAAGAACGGGATGAGTC 394
Qy 1570 TAGCAACAGGCTGTGTTGGAAGAAGAGCCCTCGGTCAAAGAGAGTGAATTTGAAGGCGG 1629
Db 395 TAGCAACAGGCTGTGTTGGAAGAAGAGCCCTCGGTCAAAGAGAGTGAATTTGAAGGCGG 454
Qy 1630 GAGGCCAATGCAAGTGGCTGTGCAGAGCGGGCAGAGAGATATCGTGGCATCTGTGCG 1689

Db 455 GAGGCCAATGCAAGTGGCTGTGCAGAGCGGGCAGAGAGATATCGTGGCATCTGTGCGG 514
Qy 1690 CCGAGGCTGAGAGCTGAGAGCTGTGAGGAGCAAGATGCTGTGCTGCACTGCACTAGCGTGC 1749
Db 515 CCGAGGCTGAGAGCTGAGAGCTGTGAGGAGCAAGATGCTGTGCTGCACTGCACTAGCGTGC 574
Qy 1750 CTGGAAGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 1809
Db 575 CTGGAAGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAG 634
Qy 1810 CGCCCAAGAGCTGTGAG 1869
Db 635 CGCCCAAGAGCTGTGAG 694
Qy 1870 CCGGAG 1929
Db 695 CCGGAG 754
Qy 1930 GACACCCCTGCAAGTGGCCGAG 1989
Db 755 GACACCCCTGCAAGTGGCCGAG 814
Qy 1990 TCGGGGCGCTGCAAG 2049
Db 815 TCGGGGCGCTGCAAG 874
Qy 2050 CCGCAAG 2109
Db 875 CCGCAAG 934
Qy 2110 CCGGAG 2169
Db 935 CCGGAG 994
Qy 2170 GGTGAG 2229
Db 995 GGTGAG 1054
Qy 2230 GGTGAG 2289
Db 1055 GGTGAG 1114
Qy 2290 GGTGAG 2349
Db 1115 GGTGAG 1174
Qy 2350 CCGGAG 2409
Db 1175 CCGGAG 1234
Qy 2410 CCGGAG 2469
Db 1235 CCGGAG 1294
Qy 2470 TTAACCTAAATTTTAAACCAAG 2529
Db 1295 TTAACCTAAATTTTAAACCAAG 1354
Qy 2530 CCGGAG 2589
Db 1355 CCGGAG 1414
Qy 2590 TTAACCTAAATTTTAAACCAAG 2649
Db 1415 TTAACCTAAATTTTAAACCAAG 1474
Qy 2650 TTAACCTAAATTTTAAACCAAG 2709
Db 1475 TTAACCTAAATTTTAAACCAAG 1534
Qy 2710 TTAACCTAAATTTTAAACCAAG 2769

Db 1535 AGGCGAGCCACCTTGGGTTGCTGAGCTCACCAAGCTTTGAGGAGGTGACGGGAAACTG 1594
Qy 2770 TGTATTTTATCTTCATACATGACGGTGGGACAGAGAGCCCTGTCTTAAAGTTTCCATGGA 2829
Db 1595 TGTATTTTATCTTCATACATGACGGTGGGACAGAGAGCCCTGTCTTAAAGTTTCCATGGA 1654
Qy 2830 TGTATTTTATTTAAATCTTAAAGATGAAATACCTTATCAGCGTGTGCTTGAACCTGTGA 2889
Db 1655 TGTATTTTATTTAAATCTTAAAGATGAAATACCTTATCAGCGTGTGCTTGAACCTGTGA 1714
Qy 2890 AAAATGTCATPAACTGGATAGTCTAGCTCTAATGATGAGCTAAGTGGGCTTGGC 2949
Db 1715 AAAATGTCATPAACTGGATAGTCTAGCTCTAATGATGAGCTAAGTGGGCTTGGC 1774
Qy 2950 TTTGAAAACAATGTTTATGCAACAAGAACAAATGTGACGACCAAGCTTTGGGGGCGT 3009
Db 1775 TTTGAAAACAATGTTTATGCAACAAGAACAAATGTGACGACCAAGCTTTGGGGGCGT 1834
Qy 3010 ATGTGTGCGCAGCTCTTAACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 3069
Db 1835 ATGTGTGCGCAGCTCTTAACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 1894
Qy 3070 ACACACAGTGGCCACATGCTCTAGCTGCGTGGCTTCTGCTGGCTTAAAGATGTTTG 3129
Db 1895 ACACACAGTGGCCACATGCTCTAGCTGCGTGGCTTCTGCTGGCTTAAAGATGTTTG 1954
Qy 3130 GCAACTTACAGCCACAGGCTTACAGCTTAAAGATGTTTCTCCCTTGTAACTTCACTTCA 3189
Db 1955 GCAACTTACAGCCACAGGCTTACAGCTTAAAGATGTTTCTCCCTTGTAACTTCACTTCA 2014
Qy 3190 CTGGGAGCTGAGCGACGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 3249
Db 2015 CTGGGAGCTGAGCGACGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2074
Qy 3250 CAGGAGAGCTGTTTATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 3309
Db 2075 CAGGAGAGCTGTTTATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2134
Qy 3310 CCTAGACATGACAGATTAACCTAGTACATGCTCACTTCACTTCACTTCACTTCACTTCA 3369
Db 2135 CCTAGACATGACAGATTAACCTAGTACATGCTCACTTCACTTCACTTCACTTCACTTCA 2194
Qy 3370 TCAATTTTGTAGTATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTG 3429
Db 2195 TCAATTTTGTAGTATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTGGGATTTG 2254
Qy 3430 TGAACCTGCTTACAGCGTGGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 3489
Db 2255 TGAACCTGCTTACAGCGTGGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2314
Qy 3490 TTTCTGATGATTAAGATGCTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 3549
Db 2315 TTTCTGATGATTAAGATGCTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2374
Qy 3550 TAGGGTCTTCTGAACTCTGTTATTAAGTAATTTGTTGCAAGACCTGCTGCTG 3609
Db 2375 TAGGGTCTTCTGAACTCTGTTATTAAGTAATTTGTTGCAAGACCTGCTGCTGCTG 2434
Qy 3610 CAAACATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3669
Db 2435 CAAACATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2494
Qy 3670 ATGTGAATCTGAGGAGATCTTTTCACTGACAGAAATATCCAAAGCTTGTGAACCTG 3729
Db 2495 ATGTGAATCTGAGGAGATCTTTTCACTGACAGAAATATCCAAAGCTTGTGAACCTG 2554
Qy 3730 GCTATGTTTAAATATGCTCATTTGCTTAACTGTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 3789
Db 2555 GCTATGTTTAAATATGCTCATTTGCTTAACTGTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2614
Qy 3790 AAGTTCATTTGATGCTCAATTAAGCAAGTACTGCTACTTTTGAANTGAAATAA 3849
Db 2615 AAGTTCATTTGATGCTCAATTAAGCAAGTACTGCTACTTTTGAANTGAAATAA 2674

Qy 3850 AAAAAAAAA 3858
Db 2675 AAAAAAAAA 2683

RESULT 9
US-10-342-887-324
; Sequence 324, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 324
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-324

Query Match 67.5%; Score 2606.4; DB 18; Length 2691;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2635; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

Qy 1211 GATCTGGGTACCAACAAGCTTCCAGAAAGAAAGCTTGTGATGCTATGCTGCTC-GGGA 1269
Db 36 GATCTGGGTACCAACAAGCTTCCAGAAAGAAAGCTTGTGATGCTATGCTGCTC-GGGA 94
Qy 1270 CACCAAGCAATGATGAAGATCTTGCACGCGCCAGAGACCTGGAACCTGGACCTGGACAGGCG 1329
Db 95 CACCAAGCAATGATGAAGATCTTGCACGCGCCAGAGACCTGGAACCTGGACCTGGACAGGCG 154
Qy 1330 TGGCAGCTGCTGCAACCTGGGAGTGGAGGCGGGCAAGAGAGTGGCCAAAGTGGCTCT 1389
Db 155 TGGCAGCTGCTGCAACCTGGGAGTGGAGGCGGGCAAGAGAGTGGCCAAAGTGGCTCT 214
Qy 1390 GCTCAACATGCAACCCCAACCTGAGCAACCTGAGGGCTTCAACCCCTGTTGCACTGGC 1449
Db 215 GCTCAACATGCAACCCCAACCTGAGCAACCTGAGGGCTTCAACCCCTGTTGCACTGGC 274
Qy 1450 CGTGAGAGAGAGGGTGGGGGTGCTGAGAGCTCTGCTGCGCAAGAGATCAAGTGTAA 1509
Db 275 CGTGAGAGAGAGGGTGGGGGTGCTGAGAGCTCTGCTGCGCAAGAGATCAAGTGTAA 334
Qy 1510 CGCCAAAGATGAGGACAGTGGACAGCCCTCACTTTCAGGCCAGAACGGGGATGATGC 1569
Db 335 CGCCAAAGATGAGGACAGTGGACAGCCCTCACTTTCAGGCCAGAACGGGGATGATGC 394
Qy 1570 TAGCACAAGGCTGCTGTTGAGAGAAAGCCTTGGTCAACGAGGTGAATTGAGAGGCGG 1629
Db 395 TAGCACAAGGCTGCTGTTGAGAGAAAGCCTTGGTCAACGAGGTGAATTGAGAGGCGG 454
Qy 1630 GAGCGCCATGCACTGGCTTGCACAGAGGGCAGAGAAATATCCGAGCCATCTGCTGG 1689
Db 455 GAGCGCCATGCACTGGCTTGCACAGAGGGCAGAGAAATATCCGAGCCATCTGCTGG 514
Qy 1690 CCGAGGCGTGGACGTGAGCTTGCAGGGAGAGATGCTGAGCTGCACTGACCTAGCTGC 1749

Db 515 CCGAGCGCTGACGCTGAGCGCTGACAGGAGATGCTGCTGCCACTGCACTACGCTGC 574
Qy 1750 CTGGCAGGCGCCACTCTGCCATCTGTCAGCTGTGGCCACAGACCGCGGGGTGAGTGAA 1809
Db 575 CTGGCAGGCGCCACTCTGCCATCTGTCAGCTGTGGCCACAGACCGCGGGGTGAGTGAA 634
Qy 1810 CGCCACGACGCTGAGTGGGAGGAGCGCCATGTCACCTGGCCGCAACAGCGCGGGCACTACG 1869
Db 635 CGCCACGACGCTGAGTGGGAGGAGCGCCATGTCACCTGGCCGCAACAGCGCGGGCACTACG 694
Qy 1870 CGTGGCCGCGCATCTCTCATCGACTGTGCTCCGACGTCAACGTCTGCAAGCTGCTGGACA 1929
Db 695 CGTGGCCGCGCATCTCTCATCGACTGTGCTCCGACGTCAACGTCTGCAAGCTGCTGGACA 754
Qy 1930 GACACCCCTGCACTGTGCGCGGAGACGCGGCAACGAGCACTGCAAGCTGCTGCA 1989
Db 755 GACACCCCTGCACTGTGCGCGGAGACGCGGCAACGAGCACTGCAAGCTGCTGCA 814
Qy 1990 TCGGGGCGCTGGCAAGAGGCGCTGACCTTCAGACGGCTTACACCGCTTGCACCTGGCTGC 2049
Db 815 TCGGGGCGCTGGCAAGAGGCGCTGACCTTCAGACGGCTTACACCGCTTGCACCTGGCTGC 874
Qy 2050 CGCACAACGACACTGTGCGCACTGTCAAGCTGCTTGTGAGAGAGAGCGCGATGTGCTGC 2109
Db 875 CGCACAACGACACTGTGCGCACTGTCAAGCTGCTTGTGAGAGAGAGCGCGATGTGCTGC 934
Qy 2110 CGGGGAGCCCTTGAACAGACGCGCGCTGCACTGTGCTGCGCCACGCGCACTCGAGAGT 2169
Db 935 CGGGGAGCCCTTGAACAGACGCGCGCTGCACTGTGCTGCGCCACGCGCACTCGAGAGT 994
Qy 2170 GGTGAGAGAGTTGTGCAAGCGCGAGATGTCATTGACCTGTTCAGACGAGCGGCTCAGGCG 2229
Db 995 GGTGAGAGAGTTGTGCAAGCGCGAGATGTCATTGACCTGTTCAGACGAGCGGCTCAGGCG 1054
Qy 2230 GCTGCACTGTGCGCGCCAGGCGCGCACGACAGCGGTGAGAGCTTGTCTCAGGCACTG 2289
Db 1055 GCTGCACTGTGCGCGCCAGGCGCGCACGACAGCGGTGAGAGCTTGTCTCAGGCACTG 1114
Qy 2290 GGGCCACATCAACTGTGCAAGAGCTCAAGTTCCAGGGCGCGCACTGCGCCGCACT 2349
Db 1115 GGGCCACATCAACTGTGCAAGAGCTCAAGTTCCAGGGCGCGCACTGCGCCGCACT 1174
Qy 2350 CCGGAGGAGAGACACTGACTGCTGCGCGGAGACGCGGGGTTCACGTGGGGCTC 2409
Db 1175 CCGGAGGAGAGACACTGACTGCTGCGCGGAGACGCGGGGTTCACGTGGGGCTC 1234
Qy 2410 TTGTCTGTCTGTGTTCTCTGTGGAGATGAAACGATCTGTGAGGGGCCGTGTGAGC 2469
Db 1235 TTGTCTGTCTGTGTTCTCTGTGGAGATGAAACGATCTGTGAGGGGCCGTGTGAGC 1294
Qy 2470 TTACTTAAATGTTAAACAAAGCAGAGGTGACATGTGTCCATCAGAGGCGGCTGCTGCA 2529
Db 1295 TTACTTAAATGTTAAACAAAGCAGAGGTGACATGTGTCCATCAGAGGCGGCTGCTGCA 1354
Qy 2530 CCGAGGTGCGCTCAGGTGAGAGCTGAGTCAAGTGCACATGCGCGCTCATCATCATC 2589
Db 1355 CCGAGGTGCGCTCAGGTGAGAGCTGAGTCAAGTGCACATGCGCGCTCATCATCATC 1414
Qy 2590 TAGGCACTGTCTGTCTGAAGGAGACGCTGAGTCAATCTTCTGTGTCTCTAATGGG 2649
Db 1415 TAGGCACTGTCTGTCTGAAGGAGACGCTGAGTCAATCTTCTGTGTCTCTAATGGG 1474
Qy 2650 TCGCTGAGGCTGTCTCTGATGATGAGAGCCCAAGCGTGAAGATTCACCTCTCTCG 2709
Db 1475 TCGCTGAGGCTGTCTCTGATGATGAGAGCCCAAGCGTGAAGATTCACCTCTCTCG 1534
Qy 2710 AGGCGAGCCACTGTGGGTGCTGAGCTCAACAGTCTTGAAGGAGGTGAGGGGAAACTG 2769
Db 1535 AGGCGAGCCACTGTGGGTGCTGAGCTCAACAGTCTTGAAGGAGGTGAGGGGAAACTG 1594
Qy 2770 TGTCTTTTATCTTCAATACATGACGCTGAGAGGCGCTGTCTTAAAGTTTCAATGAA 2829

Db 1595 TGTCTTTTATCTTCAATACATGACGCTGAGAGGCGCTGTCTTAAAGTTTCCATGAA 1654
Qy 2830 TGTCTTTTATTTAAATATCTTGAAGATGAATACCTTATCAGCTGTGCTTGAACCTGTTA 2889
Db 1655 TGTCTTTTATTTAAATATCTTGAAGATGAATACCTTATCAGCTGTGCTTGAACCTGTTA 1714
Qy 2890 AAAATGTTCAATTAATTGATGATCTAGTCTTAAATGATGAGTGAAGTGGGTTGGC 2949
Db 1715 AAAATGTTCAATTAATTGATGATCTAGTCTTAAATGATGAGTGAAGTGGGTTGGC 1774
Qy 2950 TTTGAACAAATGTTTATTCACACAGAAACGATGATGACGACCTTTGCGGGCGT 3009
Db 1775 TTTGAACAAATGTTTATTCACACAGAAACGATGATGACGACCTTTGCGGGCGT 1834
Qy 3010 ATGTGTGCGCAGCTTAAACATTCAGTCTAATTAATCTTGGGTGAGTCTTGTGGACAAC 3069
Db 1835 ATGTGTGCGCAGCTTAAACATTCAGTCTAATTAATCTTGGGTGAGTCTTGTGGACAAC 1884
Qy 3070 ACACACAGTGCACACATGATCTAGCTGCGGTTGTTTCTGTTGCTTAAGATGTTTG 3129
Db 1895 ACACACAGTGCACACATGATCTAGCTGCGGTTGTTTCTGTTGCTTAAGATGTTTG 1954
Qy 3130 GCAACTCTGAGCCACAGGCTTAAGATCAATTAACAAATTCCTCTTGTGACCTCAGTG 3189
Db 1955 GCAACTCTGAGCCACAGGCTTAAGATCAATTAACAAATTCCTCTTGTGACCTCAGTG 2014
Qy 3190 CTGGGAGCTAGAGGAGACCCCTCAGGTCGTGAGAGCAACGCTTGGGGAAGAGGTG 3249
Db 2015 CTGGGAGCTAGAGGAGACCCCTCAGGTCGTGAGAGCAACGCTTGGGGAAGAGGTG 2074
Qy 3250 CAGGAGAGCTGTGTTTATCTCAACAGCAGATGAAATTAATTAATATGATTA 3309
Db 2075 CAGGAGAGCTGTGTTTATCTCAACAGCAGATGAAATTAATTAATATGATTA 2134
Qy 3310 CTTTGAATTAACAGATTAATCTTATGATGACCTGCTACCTGCACTCTTCCACTC 3369
Db 2135 CTTTGAATTAACAGATTAATCTTATGATGACCTGCTACCTGCACTCTTCCACTC 2194
Qy 3370 TCAATTTTGTAGGTGATTTGGATGAGATAGTGTGTTGGGATGAGGGGAGTGTTC 3429
Db 2195 TCAATTTTGTAGGTGATTTGGATGAGATAGTGTGTTGGGATGAGGGGAGTGTTC 2254
Qy 3430 TGAAGCTGTTGACAGAGTGCCTCGACCTTCAGCAAGTTTGGGGTGTGCCCCAGGCGG 3489
Db 2255 TGAAGCTGTTGACAGAGTGCCTCGACCTTCAGCAAGTTTGGGGTGTGCCCCAGGCGG 2314
Qy 3490 TTTCTTGAATGTAAGATGTGGCATCTAGCTCTGTAACTTCACTGTGCTCCA 3549
Db 2315 TTTCTTGAATGTAAGATGTGGCATCTAGCTCTGTAACTTCACTGTGCTCCA 2374
Qy 3550 TAGGTCCTTCTGATTAAGTATGATTAATTAAGTTTGTGAGAACTGACCTGCGTG 3609
Db 2375 TAGGTCCTTCTGATTAAGTATGATTAATTAAGTTTGTGAGAACTGACCTGCGTG 2454
Qy 3610 CAACATGATACCTGTGCGCTGTATATGATGATGATTAATTAATGATGATTA 3669
Db 2435 CAACATGATACCTGTGCGCTGTATATGATGATGATTAATTAATGATGATTA 2494
Qy 3670 ATGTGAATCTGTGGCAGATTAATTTTCATGAGAGAAATATCAAGCTGTGAACTG 3729
Db 2495 ATGTGAATCTGTGGCAGATTAATTTTCATGAGAGAAATATCAAGCTGTGTAACTG 2554
Qy 3730 GCTATGTTTAAATATGCTCATTTGCTTACTGTTGTGAGCTGCTGAGAGGAGCAAG 3789
Db 2555 GCTATGTTTAAATATGCTCATTTGCTTACTGTTGTGAGCTGCTGAGAGGAGCAAG 2614
Qy 3790 AAGTTCAATTTGATGTCAATTAACAAAGTACTTGCTTCTTTTGAANTGAAGAAA 3849
Db 2615 AAGTTCAATTTGATGTCAATTAACAAAGTACTTGCTTCTTTTGAANTGAAGAAA 2674
Qy 3850 AAAAAAAAA 3858
Db 2675 AAAAAAAAA 2683

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RESULT 10
US-10-658-904-3
; Sequence 3, Application US/10658904
; Publication No. US20040048305A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 14171 Protein Kinase, A No. US20040048305A1 Human
FILE REFERENCE: MP100-0101RCP1M
CURRENT APPLICATION NUMBER: US/10/658,904
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 09/781,882
PRIOR FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/182,096
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-658-904-3

Query Match      61.0%; Score 2355; DB 18; Length 2355;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ATGAGAGGCGACCGGCGGACCCCATAGGCGCTGCGCGTCATGCGACCTTTCAGCCGCGGC 76
DB 1 ATGAGAGGCGACCGGCGGACCCCATAGGCGCTGCGCGTCATGCGACCTTTCAGCCGCGGC 60
QY 77 GAGTTACGCGGCTGCGGAGAGAGTGGGCTGCGGCGGCTTGGGCGAGGTGTATCAAGTGGCC 136
DB 61 GAGTTACGCGGCTGCGGAGAGAGTGGGCTGCGGCGGCTTGGGCGAGGTGTATCAAGTGGCC 120
QY 137 CATGTCACCTGAGAGACCTGCGCTGACCATCAAGTGTCTGCGCCAGCTTGCATCGACGAC 196
DB 121 CATGTCACCTGAGAGACCTGCGCTGACCATCAAGTGTCTGCGCCAGCTTGCATCGACGAC 180
QY 197 AGGAGCGCATGAGAGCTTTTGGAGAGAGCCAGAGATGAGATGAGATGAGATGAGATGAG 256
DB 181 AGGAGCGCATGAGAGCTTTTGGAGAGAGCCAGAGATGAGATGAGATGAGATGAGATGAG 240
QY 257 ATCTGCTGTGTATGAGCATCTGCGCGGAACTGTGCGGCTGTGTCATGAGATGAGATGAG 316
DB 241 ATCTGCTGTGTATGAGCATCTGCGCGGAACTGTGCGGCTGTGTCATGAGATGAGATGAG 300
QY 317 ACGGGCTCCCTGAGAAAGCTGCTGAGGCAATGCGATGAGATCTCCGGTTCGGA 376
DB 301 ACGGGCTCCCTGAGAAAGCTGCTGAGGCAATGCGATGAGATCTCCGGTTCGGA 360
QY 377 ATATATCAAGAGCGCGGTGGGCAATGATCTTCTGCACTGATGAGCGCCGCACTTCG 436
DB 361 ATATATCAAGAGCGCGGTGGGCAATGATCTTCTGCACTGATGAGCGCCGCACTTCG 420
QY 437 CACTGGAACCTCAAGCCCGGAAATCTGCTGATGAGCCCACTACACGTCAGATTTCT 496
DB 421 CACTGGAACCTCAAGCCCGGAAATCTGCTGATGAGCCCACTACACGTCAGATTTCT 480
QY 497 GATTTGTGTGCGCAAGTGCACCGGCTGTCCACTCGCATGACCTCAGCATGATGAG 556
DB 481 GATTTGTGTGCGCAAGTGCACCGGCTGTCCACTCGCATGACCTCAGCATGATGAG 540
QY 557 CTGTGTGGCAATTCGCTTCTCTCCGAGAGCGATCAAGGAGAGAGCGCGCTTC 616
DB 541 CTGTGTGGCAATTCGCTTCTCTCCGAGAGCGATCAAGGAGAGAGCGCGCTTC 600
QY 617 GACACCAAGCAGATGATACAGCTTTCGATGATGATGATGATGATGATGATGATGATGAT 676
DB 601 GACACCAAGCAGATGATACAGCTTTCGATGATGATGATGATGATGATGATGATGATGAT 660
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QY 677 AAGCGTTTGCAGATGAGAGAAATCATCTGTCATCATGATGAGATGATGAGATGAGATGAG 736
DB 661 AAGCGTTTGCAGATGAGAGAAATCATCTGTCATCATGATGAGATGATGAGATGAGATGAG 720
QY 737 CGCCCGGAGCTGCGCGCGTGTGAGAGCCCGGCGCGCTGCGAGCACTGATATGCG 796
DB 721 CGCCCGGAGCTGCGCGCGTGTGAGAGCCCGGCGCGCTGCGAGCACTGATATGCG 780
QY 797 CTCATGCAAGCGGTGTGCGAGAGGGGATTCGGAAGTTAGGCCCACTTCCAGAAATTA 856
DB 781 CTCATGCAAGCGGTGTGCGAGAGGGGATTCGGAAGTTAGGCCCACTTCCAGAAATTA 840
QY 857 TCTGAAACCGAGAGACTGTGTGAAAGAGCTGATGACGAAGTGAAGAAATGCTCATGAT 916
DB 841 TCTGAAACCGAGAGACTGTGTGAAAGAGCTGATGACGAAGTGAAGAAATGCTCATGAT 900
QY 917 CTGAGCTGAAAGAGCCCGGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 976
DB 901 CTGAGCTGAAAGAGCCCGGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
QY 977 GCCTTGTGCCCCGACTTGTGATTAAGATCAAGCCCTTCCGAGCTTCTCAAGCTGAG 1036
DB 961 GCCTTGTGCCCCGACTTGTGATTAAGATCAAGCCCTTCCGAGCTTCTCAAGCTGAG 1020
QY 1037 TCTGAGTTTCCAGAGCTGTGAGAGGCCCGAGAGCTCAAGCGGCTCTGATGATC 1096
DB 1021 TCTGAGTTTCCAGAGCTGTGAGAGGCCCGAGAGCTCAAGCGGCTCTGATGATC 1080
QY 1097 AAGCTGCAATGTCGCGAGTGGAGAGAGCTCTCGGGGAGTGTCTGCTGAGATCTCGCC 1156
DB 1081 AAGCTGCAATGTCGCGAGTGGAGAGAGCTCTCGGGGAGTGTCTGCTGAGATCTCGCC 1140
QY 1157 TTCTTTTCAAGAGATCACTGTCTGTCTTTTGAAGCGGAACTTCAACCAAGGATCTG 1216
DB 1141 TTCTTTTCAAGAGATCACTGTCTGTCTTTTGAAGCGGAACTTCAACCAAGGATCTG 1200
QY 1217 GGTACCAAGAGCTGCGAGAGAGAGAGCTGTGATGATGATGATGATGATGATGATGATG 1276
DB 1201 GGTACCAAGAGCTGCGAGAGAGAGAGCTGTGATGATGATGATGATGATGATGATGATG 1260
QY 1277 AAATGATGAGATCTCTGAGCGCGAGAGAGCTGAGCACTGAGCACTGAGCACTGAG 1336
DB 1261 AAATGATGAGATCTCTGAGCGCGAGAGAGCTGAGCACTGAGCACTGAGCACTGAG 1320
QY 1337 CTGCTGCACTGCGCGTGGAGGCGGCAAGAGATGCGCAATGCTGCTGCTCAAC 1396
DB 1321 CTGCTGCACTGCGCGTGGAGGCGGCAAGAGATGCGCAATGCTGCTGCTCAAC 1380
QY 1397 AATGCAACCCCAACCTGAGCAACCTGAGGGGCTCAACCCGTTGCAATGAGCGTGGAG 1456
DB 1381 AATGCAACCCCAACCTGAGCAACCTGAGGGGCTCAACCCGTTGCAATGAGCGTGGAG 1440
QY 1457 AGGAGGAGCGGAGTGTGTGAGAGCTCTGCTGAGCAAGAGATGATGATGATGATGATG 1516
DB 1441 AGGAGGAGCGGAGTGTGTGAGAGCTCTGCTGAGCAAGAGATGATGATGATGATGATG 1500
QY 1517 GATGAGAGCAAGTGCACAGCTTCCATTTTGAAGCCGAGAAAGGAGATGATGATGATG 1576
DB 1501 GATGAGAGCAAGTGCACAGCTTCCATTTTGAAGCCGAGAAAGGAGATGATGATGATG 1560
QY 1577 CGGCTGCTGTTGAGAGAGAGAGCTCTGCTGAGCAAGAGTGGATCTTGAAGGAGCGAG 1636
DB 1561 CGGCTGCTGTTGAGAGAGAGAGCTCTGCTGAGCAAGAGTGGATCTTGAAGGAGCGAG 1620
QY 1637 ATGCAAGTGGCTGTCAGAGCAAGGAGAGATATCTGTGCGATCTCTGCGCGAGAG 1696
DB 1621 ATGCAAGTGGCTGTCAGAGCAAGGAGAGATATCTGTGCGATCTCTGCGCGAGAG 1680
QY 1697 GTGAGCTGAGCTGTCAGAGGCAAGATGCTGTGCTGCACTGCACTGATGATGATGATG 1756
DB 1681 GTGAGCTGAGCTGTCAGAGGCAAGATGCTGTGCTGCACTGCACTGATGATGATGATG 1740
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QY 1757 GGCACCTGCCCCATGCTCAAGCTGTGGCCAAAGACGGCGGGGTGATGTAACGCCCCAG 1816
DB 1741 GGCACCTGCCCCATGCTCAAGCTGTGGCCAAAGACGGCGGGGTGATGTAACGCCCCAG 1800
QY 1817 AGCGTGAATGGAGAGACGCATTGTGACCTGGCCGACAGCCGCGGACCTAACCGCGTGGCC 1876
DB 1801 AGCGTGAATGGAGAGACGCATTGTGACCTGGCCGACAGCCGCGGACCTAACCGCGTGGCC 1860
QY 1877 GCGATCTCTATCTGACCTGTGTCTCCGACGTCACGTTCTGCAAGCTGTGGCACAGACACC 1936
DB 1861 GCGATCTCTATCTGACCTGTGTCTCCGACGTCACGTTCTGCAAGCTGTGGCACAGACACC 1920
QY 1997 CTGCACTGTGGCCGCGGAGACGGGGGACACAGACATGCAAGCTGTGGCACAGACACC 1996
DB 1921 CTGCACTGTGGCCGCGGAGACGGGGGACACAGACATGCAAGCTGTGGCACAGACACC 1980
QY 1997 GCTGGCAAGAGAGCCGCTGACCTCAGACGAGCTTACACCGCTGTGACCTGTGGCACAGACACC 2056
DB 1981 GCTGGCAAGAGAGCCGCTGACCTCAGACGAGCTTACACCGCTGTGACCTGTGGCACAGACACC 2040
QY 2057 GAGACCTGTGGCCGCTGTCAAGCTGTGTCTGAGAGAGAGCCGATGTGCTGGCCCGGAG 2116
DB 2041 GAGACCTGTGGCCGCTGTCAAGCTGTGTCTGAGAGAGAGCCGATGTGCTGGCCCGGAG 2100
QY 2117 CCCCAGAACAGAGCCGCTGTGACCTGTGTCTGAGAGAGAGCCGATGTGCTGGCCCGGAG 2176
DB 2101 CCCCAGAACAGAGCCGCTGTGACCTGTGTCTGAGAGAGAGCCGATGTGCTGGCCCGGAG 2160
QY 2177 GAGTTGATCAGCGCCGATGTCAATTGACCTGTGTGACAGAGAGAGCTGACGCGCTGAC 2236
DB 2161 GAGTTGATCAGCGCCGATGTCAATTGACCTGTGTGACAGAGAGAGCTGACGCGCTGAC 2220
QY 2237 CTGGCCGCGCCAGAGCCGCGGACGACAGAGAGCTGTGACCTGTGTGAGAGAGAGCCG 2296
DB 2221 CTGGCCGCGCCAGAGCCGCGGACGACAGAGAGCTGTGACCTGTGTGAGAGAGAGCCG 2280
QY 2297 ATCAACTGTGACAGCTCAAGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2356
DB 2281 ATCAACTGTGACAGCTCAAGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
QY 2357 CGAAGCAAGACCTAG 2371
DB 2341 CGAAGCAAGACCTAG 2355

RESULT 11
US-10-128-174-15
; Sequence 15, Application US/10128174
; Publication No. US2003019462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-174-15

Query Match 60.3%; Score 2327.2; DB 16; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 17 AAGAGAGGCGAGAGCGGAGACCCCATGAGCCCTGTGGCGCTGTGCGACCTTTCAGCGCGGC 76
DB 1 AAGAGAGGCGAGAGCGGAGACCCCATGAGCGCCCTGTGGCGCTGTGCGACCTTTCAGCGCGGC 60
QY 77 GAGTTCAAGGCGGTGGAGAAAGGTGGCTGTGGGCGGCTTGTGGGAGAGTGTAAAGGTGCGC 136

DB 61 GAGTTCAAGGCGGTGGAGAAAGGTGGCTGTGGGCGGCTTGTGGGAGAGTGTAAAGGTGCGC 120
QY 137 CATGTCACTGGAAGACCTGAGCTGTGGCATTAAGTGTCTGCGCCAGCTGTGACGTAAGAC 136
DB 121 CATGTCACTGGAAGACCTGAGCTGTGGCATTAAGTGTCTGCGCCAGCTGTGACGTAAGAC 180
QY 197 AAGAGAGGCGAGAGGCTTTTGAAGAGCAAGAGATGAGATGGCAAGTTTGGTAC 256
DB 181 AAGAGAGGCGATGAGGCTTTTGAAGAGCAAGAGATGAGATGGCAAGTTTGGTAC 240
QY 257 ATCTGCTGTGTATGTGACATCTGCGCGAAGCTGTGCGCTGTGTATGAGATCATGAGAG 316
DB 241 ATCTGCTGTGTATGTGACATCTGCGCGAAGCTGTGCGCTGTGTATGAGATCATGAGAG 300
QY 317 ACGGCTCTCCGGAAGAGCTGTGGCTTGGAGGCAATTTGCAATGGATCTCCGGTTCCGA 376
DB 301 ACGGCTCTCCGGAAGAGCTGTGGCTTGGAGGCAATTTGCAATGGATCTCCGGTTCCGA 360
QY 377 ATCATCAAGAGACGGGAGTGGGATGAATTCCTGTGACATGAGCCCGCACTCTG 436
DB 361 ATCATCAAGAGACGGGAGTGGGATGAATTCCTGTGACATGAGCCCGCACTCTG 420
QY 437 CACCTGACCTCAAGCCCGGAAATCTGTGTGATGACCACTTACACAGCTCAAGATTTCT 496
DB 421 CACCTGACCTCAAGCCCGGAAATCTGTGTGATGACCACTTACACAGCTCAAGATTTCT 480
QY 497 GATTTTGTGTGCGCAAGTGCACAGGAGCTGTCCCATCTGCAATGACCTCAAGATGAGC 556
DB 481 GATTTTGTGTGCGCAAGTGCACAGGAGCTGTCCCATCTGCAATGACCTCAAGATGAGC 540
QY 557 CTGTTTGGCAATATGCTTACCTCCCTCAAGAGGCAATCAAGGAGAGAGAGAGAGAGAGAG 616
DB 541 CTGTTTGGCAATATGCTTACCTCCCTCAAGAGGCAATCAAGGAGAGAGAGAGAGAGAGAG 600
QY 617 GACACCAAGACAGATGATACAGCTTTGCAATCTGATCTGATGAGAGAGAGAGAGAGAGAG 676
DB 601 GACACCAAGACAGATGATACAGCTTTGCAATCTGATCTGATGAGAGAGAGAGAGAGAGAG 660
QY 677 AAGCCGTTTGCAGATGAGAGAAATCTCTGACATCATGTGTGAAGGTGTGAAGAGGAC 736
DB 661 AAGCCGTTTGCAGATGAGAGAAATCTCTGACATCATGTGTGAAGGTGTGAAGAGGAC 720
QY 737 GCGCCGAGAGCGCGCCGCTGTGAGAGAGCCGCGCGCGCTGTGACAGCTGTGATAGC 796
DB 721 GCGCCGAGAGCGCGCCGCTGTGAGAGAGCCGCGCGCGCTGTGACAGCTGTGATAGC 780
QY 797 CTATGCAAGCGGTCTGAG 856
DB 781 CTATGCAAGCGGTCTGAG 840
QY 857 TCTGAACCGAGAGACCTGTGTGAAGAAAGCTGTGATGACAGAGAGAGAGAGAGAGAGAG 916
DB 841 TCTGAACCGAGAGACCTGTGTGAAGAAAGCTGTGATGACAGAGAGAGAGAGAGAGAGAG 900
QY 917 CTGAGCGTGAAGAAAGCCCGCGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 976
DB 901 CTGAGCGTGAAGAAAGCCCGCGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 977 GCTCTGCGCCACCTTGTGATTAAGATTAAGCTTCTGAGCTTCTGTCAAGCTGAGAC 1036
DB 961 GCTCTGCGCCACCTTGTGATTAAGATTAAGCTTCTGAGCTTCTGTCAAGCTGAGAC 1020
QY 1037 TCTGAAGTTTCCAGAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1096
DB 1021 TCTGAAGTTTCCAGAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1097 AAGCGGCAATGTGCGAG 1156
DB 1081 AAGCGGCAATGTGCGAG 1140
QY 1157 TTCTCTTCAAGAGATCAATGTGCTGTCTTTGAGCGGAGAGCTTCAACAGAGATCTG 1216

Db	1141	TTCTCTTCCAGAGGATCACTGTCCGTCTCTTTGAGGGGAACTTTGAACAGAGATCTG	1200
Qy	1217	GGTACCAACAAACGTCCAGAGAAAGACTTGTGAATGCCATCGTGTCC-GGACACACAG	1275
Db	1201	GGACACAC-AGACGTCCAGAGAGAAAGCTTGTGAATGCCATCGTGTCCGGGGACACAG	1259
Qy	1276	CAAACTGATGAAAGATCTTCAGACCCGACAGACGTGTGAACCTGGACACTGGAACAGCCGTGCAG	1335
Db	1260	CAAACTGATGAAAGATCTTCAGACCCGACAGAGGTGTGAACCTGGACACTGGAACAGCCGTGCAG	1319
Qy	1336	CCGTGTGACCCGTGGCGGTGAGAGGCGCGGGCAAGAGAGATGCGCCAAATGGGTCTGTCAA	1395
Db	1320	CCGTGTGACCCGTGGCGGTGAGAGGCGCGGGCAAGAGAGATGCGCCAAATGGGTCTGTCAA	1379
Qy	1396	CAATGCCAAACCCCAACTGAGCAACCTGAGGGGCTCAACCCCTGTGCAATGACCTGTGA	1455
Db	1380	CAATGCCAAACCCCAACTGAGCAACCTGAGGGGCTCAACCCCTGTGCAATGAGCCGTGGA	1439
Qy	1456	GAGAGGGGTGGGGGTGTCTGTGAGACTCTCTCTGTGGCACAGAAAGATCAATGTCAACGGCAA	1515
Db	1440	GAGAGGGGTGGGGGTGTCTGTGAGACTCTCTCTGTGGCACAGAAAGATCAATGTCAACGGCAA	1499
Qy	1516	GGAATAGGAAACAAGTGTGAACAGCCCTTCACTTTGCAAGCCCAAGAACGGGAGTGAAGTCAACAC	1575
Db	1500	GGATAGGAAACAAGTGTGAACAGCCCTTCACTTTGCAAGCCCAAGAACGGGAGTGAAGTCAACAC	1559
Qy	1576	ACGGCTGTCTGTGAGAGAGAAAGCCCTCGGTCAACAGAGTGAACCTTGAAGGGCCGGAAGCC	1635
Db	1560	ACGGCTGTCTGTGAGAGAGAAAGCCCTCGGTCAACAGAGTGAACCTTGAAGGGCCGGAAGCC	1619
Qy	1636	CATGCACTGTGAGCTTGCACACACGGGCAAGAGATATCTGTGTCATCTGTCTGTCCGACAGG	1695
Db	1620	CATGCACTGTGAGCTTGCACACACGGGCAAGAGATATCTGTGTCATCTGTCTGTCCGACAGG	1679
Qy	1696	CGTGAACGTGAGCCCTGCAAGGGCAAGAGATGCGCTGCTGCACATGACATACGCTGCTGAGCA	1755
Db	1680	CGTGAACGTGAGCCCTGCAAGGGCAAGAGATGCGCTGCTGCACATGACATACGCTGCTGAGCA	1739
Qy	1756	GGGCAACCTGAGCCCATCTGTCAAGCTTCTGTGACCAAGAGCCGGGGGTGAATGTGAACGCCCA	1815
Db	1740	GGGCAACCTGAGCCCATCTGTCAAGCTTCTGTGACCAAGAGCCGGGGGTGAATGTGAACGCCCA	1799
Qy	1816	GAAGCTGATGAGAGAGAGGCCATTGCACTGTGCGCACAGAGCCGGGGCTTACCCGCTGTGC	1875
Db	1800	GAAGCTGATGAGAGAGAGGCCATTGCACTGTGCGCACAGAGCCGGGGCTTACCCGCTGTGC	1859
Qy	1876	CGGCAATCCCAATGACCTGTGCTCGAGAGGTCAACGTCTGCAAGCCGTCAGGCAACAGACACC	1935
Db	1860	CGGCAATCCCAATGACCTGTGCTCGAGAGGTCAACGTCTGCAAGCCGTCAGGCAACAGACACC	1919
Qy	1936	CTTGAACGTGAGCCGCGAGAGACGGGGCAACAGAGCACTGCGACAGCTTGTCTTGAATCGGGG	1995
Db	1920	CTTGAACGTGAGCCGCGAGAGACGGGGCAACAGAGCACTGCGACAGCTTGTCTTGAATCGGGG	1979
Qy	1996	CGCTGGCAAGAGAGCCGTGACCTCAAGACGGCTTACACCGCTGTGCACTTGTGCTGCCCGCAA	2055
Db	1980	CGCTGGCAAGAGAGCCGTGACCTCAAGACGGCTTACACCGCTGTGCACTTGTGCTGCCCGCAA	2039
Qy	2056	CGGACACTGTGGCCACTGTCAAGCTGCTTGTGAGAGAGAAAGCCGATGTGGCTGTGGCCCGGG	2115
Db	2040	CGGACACTGTGGCCACTGTCAAGCTGCTTGTGAGAGAGAAAGCCGATGTGTGTGGCCCGGG	2099
Qy	2116	ACCCCTGAACACAGACGGGCGCTGACCTGTGCTGCGCCACAGGGCACTCGAGAGTGTGTGA	2175
Db	2100	ACCCCTGAACACAGACGGGCGCTGACCTGTGCTGCGCCACAGGGCACTCGAGAGTGTGTGA	2159
Qy	2176	GGAGTTGTCAAGCGCCGATGTCAATTGAACCTGTTCCACAGACAGGGGCTCAAGCGGCTGCA	2235
Db	2160	GGAGTTGTCAAGCGCCGATGTCAATTGAACCTGTTCCACAGACAGGGGCTCAAGCGGCTGCA	2219
Qy	2236	CTGTGGCGCCCAAGGGCGGGCAACAGACAGAGGTGTGAAGCTGTGCTCAAGCAATGGGGCCA	2295
Db	2220	CTGTGGCGCCCAAGGGCGGGCAACAGACAGAGGTGTGAAGCTGTGCTCAAGCAATGGGGCCA	2279

QY	2236	CATCAACCTGCAGAGCTCTCAAGTTCCAGGCGGCGCATGAGCCCGCGCCACACTCTCGTG	2355
DB	2280	CATCAACCTGCAGAGCTCTCAAGTTCCAGGCGGCGCATGAGCCCGCGCCACACTCTCGTG	2339
QY	2356	GGGAGCAAGACCTGAG 2371	
DB	2340	GGGAGCAAGACCTGAG 2355	
RESULT 12			
US-10-128-174-16			
; Sequence 16, Application US/10128174			
; Publication No. US2003019462A1			
GENERAL INFORMATION:			
APPLICANT: Nunez, Gabriel			
APPLICANT: Inohara, Naohiro			
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling			
FILE REFERENCE: UM-06967			
CURRENT APPLICATION NUMBER: US/10/128.174			
CURRENT FILING DATE: 2002-04-23			
NUMBER OF SEQ ID NOS: 44			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 16			
LENGTH: 2355			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-10-128-174-16			
Query Match			
Best Local Similarity 99.8%; Score 2327.2; DB 16; Length 2355;			
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;			
QY	17	ATGAGAGGCGAGCGGCGGAGCCCATAGGCGCCCTGCGGCTGCGGCACTTCAGACGCGGCG	76
DB	1	ATGAGAGGCGAGCGGCGGAGCCCATAGGCGCCCTGCGGCTGCGGCACTTCAGACGCGGCG	60
QY	77	GAGTTCAACGGGCTGGGAGAGGTGGCTCGGCGGCTTCGGGCGAGGTGTACAAAGTTCGCG	136
DB	61	GAGTTCAACGGGCTGGGAGAGGTGGCTCGGCGGCTTCGGGCGAGGTGTACAAAGTTCGCG	120
QY	137	CATGTCACATGGAAGACCTGGCTGGCTCATGAGTCTCGCCAGCCTGCACGTTGACAGAC	196
DB	121	CATGTCACATGGAAGACCTGGCTGGCTCATGAGTCTCGCCAGCCTGCACGTTGACAGAC	180
QY	197	AGGAGCGCATGAGCTTTTGGAGAAAGCCAAAGAAATGAGAGTGGCAAGTTTCGTAC	256
DB	181	AGGAGCGCATGAGCTTTTGGAGAAAGCCAAAGAAATGAGAGTGGCAAGTTTCGTAC	240
QY	257	ATCCTGCGCTGTGATGTGACATGCGCGGACCTGTGGGCTGTGATGAGTACATGAG	316
DB	241	ATCCTGCGCTGTGATGTGACATGCGCGGACCTGTGGGCTGTGATGAGTACATGAG	300
QY	317	ACGGGCTCCCTGGAAGAGCTGGCTTGGAGCCATTGCAATGGAGATCTCCGGTTCCGA	376
DB	301	ACGGGCTCCCTGGAAGAGCTGGCTTGGAGCCATTGCAATGGAGATCTCCGGTTCCGA	360
QY	377	ATCATCACAGAGCGGCGGTGGGCAATGTTCTCTGCACTGCAATGCGCCCGCACTCTG	436
DB	361	ATCATCACAGAGCGGCGGTGGGCAATGTTCTCTGCACTGCAATGCGCCCGCACTCTG	420
QY	437	CACCTGGAACCTCAAGCCCGCGAATCTGCTGCTGAGAGCCCATACACGTCMAAGATTCT	496
DB	421	CACCTGGAACCTCAAGCCCGCGAATCTGCTGCTGAGAGCCCATACACGTCMAAGATTCT	480
QY	497	GATTTTGTCTGGCCAAAGTCAACGGGCTGTCCCATCTGCAATGACCTCAGCATGATGAGC	556
DB	481	GATTTTGTCTGGCCAAAGTCAACGGGCTGTCCCATCTGCAATGACCTCAGCATGATGAGC	540
QY	557	CTGTTTGGCAATATGCGCTACTCTCTCTCCAGAGCGCATCAGGAGAAAGACCGGCTTTC	616
DB	541	CTGTTTGGCAATATGCGCTACTCTCTCTCCAGAGCGCATCAGGAGAAAGACCGGCTTTC	600

QY 617 GACACAAAGCAAGATATACAGCTTTGCGATCGTATCTGGGGGCTGCAACAGAG 676
 DB 601 GACACAAAGCAAGATATACAGCTTTGCGATCGTATCTGGGGGCTGCAACAGAG 660
 QY 677 AAGCGTTTGCAGATGAGAAAGACATCTGCAATCATATGTGAAAGTGTGAAGGCGAC 736
 DB 661 AAGCGTTTGCAGATGAGAAAGACATCTGCAATCATATGTGAAAGTGTGAAGGCGAC 720
 QY 737 CGCGCCGAGCTGCG 796
 DB 721 CGCGCCGAGCTGCG 780
 QY 797 CTGACGAGCGGCTGCGAGGCGGAGATCGGAGTTAGGCGCCACTTCAGAAATTAAT 856
 DB 781 CTGACGAGCGGCTGCGAGGCGGAGATCGGAGTTAGGCGCCACTTCAGAAATTAAT 840
 QY 857 TCTGAACCGAGAGCACTGTGTGAAAAAGCTGATGACGAATGTAAGAAATCTGCTAT 916
 DB 841 TCTGAACCGAGAGCACTGTGTGAAAAAGCTGATGACGAATGTAAGAAATCTGCTAT 900
 QY 917 CTGACGTAAGAAAGCCCGCGAGCCCGAGAGCGAGTGTGTCTGCGAGGCTCAAGCGG 976
 DB 901 CTGACGTAAGAAAGCCCGCGAGCCCGAGAGCGAGTGTGTCTGCGAGGCTCAAGCGG 960
 QY 977 GCTCTGCGCCCGACCTTGATTAACGACTACAGCTCTGCGAGCTTCTCAAGCTGAGC 1036
 DB 961 GCTCTGCGCCCGACCTTGATTAACGACTACAGCTCTGCGAGCTTCTCAAGCTGAGC 1020
 QY 1037 TCTGAGTTTCCAGAGCTGTGAGGAGCCCGAGAGCTTCAAGCGAGCTCTCTGAGTCC 1096
 DB 1021 TCTGAGTTTCCAGAGCTGTGAGGAGCCCGAGAGCTTCAAGCGAGCTCTCTGAGTCC 1080
 QY 1097 AAGCTGCGCATCTGCGGCGAGTGAAGAGCTCTGCGGCGTCTCTGCGTGAATCCGCG 1156
 DB 1081 AAGCTGCGCATCTGCGGCGAGTGAAGAGCTCTGCGGCGTCTCTGCGTGAATCCGCG 1140
 QY 1157 TCTCTCTGAGAGATCACTGTGCTGTCTCTTGAAGCGGAACTTCAACAGCATCTG 1216
 DB 1141 TCTCTCTGAGAGATCACTGTGCTGTCTCTTGAAGCGGAACTTCAACAGCATCTG 1200
 QY 1217 GGTACCAAGAGCTTCAGAGAGAGAGAGCTTGTGATGCTGATCTGTCTC-GGAGACAG 1275
 DB 1201 GGTACCAAGAGCTTCAGAGAGAGAGAGCTTGTGATGCTGATCTGTCTC-GGAGACAG 1259
 QY 1276 CAATGATGATGATCTCTGCAAGCGCGAGAGCTGGAATCTGGAATCTGGAATCTG 1335
 DB 1260 CAATGATGATGATCTCTGCAAGCGCGAGAGCTGGAATCTGGAATCTGGAATCTG 1319
 QY 1336 CCGTCTGACCTGCGGCTGAGAGGCGGCGAGAGAGTCTGCGCAAGTGTCTCTCA 1395
 DB 1320 CCGTCTGACCTGCGGCTGAGAGGCGGCGAGAGAGTGTCTCTCTCA 1379
 QY 1396 CAATGCAACCCCAACTGAGCAACCTGAGGAGCTTCAACCCCGTTGACATGCGGTGA 1455
 DB 1380 CAATGCAACCCCAACTGAGCAACCTGAGGAGCTTCAACCCCGTTGACATGCGGTGA 1439
 QY 1456 GAGGAGGAGGCGGCGGCTGAGAGCTCTGCGAGAGAGTCAAGTGAAGAGCGCA 1515
 DB 1440 GAGGAGGAGGCGGCGGCTGAGAGCTCTGCGAGAGAGTCAAGTGAAGAGCGCA 1499
 QY 1516 GATGAGAGCAAGTGAAGAGCTTCACTTTCAGCGCAAGAGCGGAGTGAATGATGAGC 1575
 DB 1500 GATGAGAGCAAGTGAAGAGCTTCACTTTCAGCGCAAGAGCGGAGTGAATGATGAGC 1559
 QY 1576 ACGGCTGCTGTGTGAGAGAGAGCTCTGCTCAACGAGGTTGAATTTGAGGCGCGAC 1635
 DB 1560 ACGGCTGCTGTGTGAGAGAGAGCTCTGCTCAACGAGGTTGAATTTGAGGCGCGAC 1619
 QY 1636 CATGCAAGTGTGCTGCAAGCGGAGAGAGATTAAGTGTGATCTGCTGCGCGAGG 1695
 DB 1620 CATGCAAGTGTGCTGCAAGCGGAGAGAGATTAAGTGTGATCTGCTGCGCGAGG 1679
 QY 1696 CGTGACGTGAGCTGCAAGGAGCGGAGATCTGCTGCACTGACATGCTGCTGCA 1755

DB 1680 GGTGAGGTGAGCGCTGCAAGGCGCAAGAGATGCTGCGCTGCACTGCACTGCTGCGCA 1739
 QY 1756 GGGCCACTTGTCCCATCTCTCAAGCTGTCTGCGCAAGAGCGGCGGTGATGAAACGCCCA 1815
 DB 1740 GGGCCACTTGTCCCATCTCTCAAGCTGTCTGCGCAAGAGCGGCGGTGATGAAACGCCCA 1799
 QY 1816 GAGCGTGAATGAGAGAGAGCGCATTTGACCTGCGCGCAAGCGGCGGCACTAACCGGTGGC 1875
 DB 1800 GAGCGTGAATGAGAGAGAGCGCATTTGACCTGCGCGCAAGCGGCGGCACTAACCGGTGGC 1859
 QY 1876 CCGCATCTCATGACCTGTGTCTTCCAGCTCAACGTTCTGAGCTGTGCGACAGACACC 1935
 DB 1860 CCGCATCTCATGACCTGTGTCTTCCAGCTCAACGTTCTGAGCTGTGCGACAGACACC 1919
 QY 1936 CTGCAAGTGTGCGCGGAGAGCGGCGCAAGAGCATGCGCAAGGCTGCTCTGCAATCGGGG 1995
 DB 1920 CTGCAAGTGTGCGCGGAGAGCGGCGCAAGAGCATGCGCAAGGCTGCTCTGCAATCGGGG 1979
 QY 1996 CGCTGCGAAGAGCGGCTGACCTGACAGGCTACACCGCTCTGCACTGCGCTGCGCGCA 2055
 DB 1980 CGCTGCGAAGAGCGGCTGACCTGACAGGCTACACCGCTCTGCACTGCGCTGCGCGCA 2039
 QY 2056 CGGACACTGCGCACTGTCAAGCTGTCTGAGAGAGAGCGGATGTGCTGCGCGG 2115
 DB 2040 CGGACACTGCGCACTGTCAAGCTGTCTGAGAGAGAGCGGATGTGCTGCGCGG 2099
 QY 2116 ACCCTGAACTGAGCGGCGCTGACCTGTGCTGCGCGCGCCAGCGGCACTCGAGGTGTGA 2175
 DB 2100 ACCCTGAACTGAGCGGCGCTGACCTGTGCTGCGCGCGCCAGCGGCACTCGAGGTGTGA 2159
 QY 2176 GAGTGTGTGAGCGGCGGATGATTTGACCTGTTGAGAGAGAGAGGCTCAGCGGCTGCA 2235
 DB 2160 GAGTGTGTGAGCGGCGGATGATTTGACCTGTTGAGAGAGAGAGGCTCAGCGGCTGCA 2219
 QY 2236 CTTGCGCGCCAGCGGCGGCGCAAGAGAGAGCTGCTGAGAGATGAGGCGCCCA 2295
 DB 2220 CTTGCGCGCCAGCGGCGGCGCAAGAGAGAGCTGCTGAGAGATGAGGCGCCCA 2279
 QY 2296 CATCAACTGAGAGCTTCAAGGTTTCCAGGCGGCGCAAGGCGCGCACTGCGG 2355
 DB 2280 CATCAACTGAGAGCTTCAAGGTTTCCAGGCGGCGCAAGGCGCGCACTGCGG 2339
 QY 2356 GCGAAGCAAGCATG 2371
 DB 2340 GCGAAGCAAGCATG 2355

RESULT 13
 US-10-128-174-18
 ; Sequence 18, Application US/10128174
 ; Publication NO. US20030199462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nunez, Gabriel
 ; APPLICANT: Inohara, Naohiro
 ; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
 ; FILE REFERENCE: UM-06967
 ; CURRENT APPLICATION NUMBER: US/10/128,174
 ; CURRENT FILING DATE: 2002-04-23
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 2355
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-128-174-18

Query Match 60.3%; Score 2327.2; DB 16; Length 2355;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
 QY 17 ATGAGGGCGAGCGGCGGAGCCCATGAGGCGCTGCGCTGCTGCGCATCTTGAACGCGGCG 76

Db 1 ATGAGGGGAGACGGGGGAGCCCATGGGCGCTGGCGACTGGACACTTTCGAGCGGGG 60
Qy 77 GAGTTCA CGGGCTGGAGAGAGGTGGGCTTGCGGGGCTTCGGGCAAGTGTACAAAGTGGC 136
Db 61 GAGTTCA CGGGCTGGAGAGAGGTGGGCTTGCGGGGCTTCGGGCAAGTGTACAAAGTGGC 120
Qy 137 CATGTCACATGGAAGACTGGCTGGCTCATCAAGTGTCTGGCCGACGTGACGTGACGAC 196
Db 121 CATGTCACATGGAAGACTGGCTGGCTCATCAAGTGTCTGGCCGACGTGACGACGAC 180
Qy 197 AGGAGCGCATGAGAGCTTTTGGAGAGAGCCAGAGAGATGAGATGGCCAGTTTGGCTAC 256
Db 181 AGGAGCGCATGAGAGCTTTTGGAGAGAGCCAGAGAGATGAGATGGCCAGTTTGGCTAC 240
Qy 257 ATCTGGCTGTGTATGAGCATCTGCGCGAACCCTGTGGGCTGTGTATGAGATCATGAG 316
Db 241 ATCTGGCTGTGTATGAGCATCTGCGCGAACCCTGTGGGCTGTGTATGAGATCATGAG 300
Qy 317 AGGGGCTCCCTGGAGAGAGCTGTGGCTTTGGAGGCCATTGGCCATGGGATTCCTGGTTCCGA 376
Db 301 AGGGGCTCCCTGGAGAGAGCTGTGGCTTTGGAGGCCATTGGCCATGGGATTCCTGGTTCCGA 360
Qy 377 ATCATTCACAGAGCGGGGATGGGCAATTCCTGCACTGCACTGCACTGCACTGCACTGCACTG 436
Db 361 ATCATTCACAGAGCGGGGATGGGCAATTCCTGCACTGCACTGCACTGCACTGCACTGCACTG 420
Qy 437 CACTGGAACCTCAAGCCCGGACATCTGCTGATGACCACCTACCAAGTCAAGATTCT 496
Db 421 CACTGGAACCTCAAGCCCGGACATCTGCTGATGACCACCTACCAAGTCAAGATTCT 480
Qy 497 GATTTTGTGTGGCCAAAGTGCACAGGGCTGTCCCACTGCGCATGACCTTCAGCATGATGAGC 556
Db 481 GATTTTGTGTGGCCAAAGTGCACAGGGCTGTCCCACTGCGCATGACCTTCAGCATGATGAGC 540
Qy 557 CTGTTTGGGCAATGGCTCAACCTCCGAGAGCGCATGAGGAGAGAGCGGCTCTTC 616
Db 541 CTGTTTGGGCAATGGCTCAACCTCCGAGAGCGCATGAGGAGAGAGCGGCTCTTC 600
Qy 617 GACACCAAGCAGATGTATACAGCTTTGGATGTGATCTGGGGCGTGTCAACAGAG 676
Db 601 GACACCAAGCAGATGTATACAGCTTTGGATGTGATCTGGGGCGTGTCAACAGAG 660
Qy 677 AAGCCGTTTGCAGATGAGAGAACATCTGCAATCATGTGTGAGGTGTGAGGGCCAGC 736
Db 661 AAGCCGTTTGCAGATGAGAGAACATCTGCAATCATGTGTGAGGTGTGAGGGCCAGC 720
Qy 737 CGCCCGAGCTGCGGCCGCTGTCAGAGCCCGGCGCGGCGCTGACGCCACCTGATACCG 796
Db 721 CGCCCGAGCTGCGGCCGCTGTCAGAGCCCGGCGCGGCGCTGACGCCACCTGATACCG 780
Qy 797 CTGATGCAAGCTGTCGAGGAGGATCCGAGATTAGGCCCACTTTCAGAGAAATTACT 856
Db 781 CTGATGCAAGCTGTCGAGGAGGATCCGAGATTAGGCCCACTTTCAGAGAAATTACT 840
Qy 857 TCTGAACCGAGGACCTGTGTGAAAAGCTGTATGACGAAAGTGAAGAAATCTGCTATGAT 916
Db 841 TCTGAACCGAGGACCTGTGTGAAAAGCTGTATGACGAAAGTGAAGAAATCTGCTATGAT 900
Qy 917 CTGGAAGTGAAGAGCCCGGAGGCCAGGAGGAGGTGTGCTGAGAGCTCAAGCGG 976
Db 901 CTGGAAGTGAAGAGCCCGGAGGCCAGGAGGAGGTGTGCTGAGAGCTCAAGCGG 960
Qy 977 GCCTGCGCCCACTTTCAGTAACGATACAGCCTCTCCGAGCTTCTTCAACAGCTGAC 1036
Db 961 GCCTGCGCCCACTTTCAGTAACGATACAGCCTCTCCGAGCTTCTTCAACAGCTGAC 1020
Qy 1037 TCTGAGTTTCCAGAGCTGTGAGAGGCCCGGAGAGAGTCAAGCCGACGCTCTTGAGTCC 1096
Db 1021 TCTGAGTTTCCAGAGCTGTGAGAGGCCCGGAGAGAGTCAAGCCGACGCTCTTGAGTCC 1080
Qy 1097 AAGCTGCATGTGTCGGCAGTGGAGAGAGGCTCTCGGGGGGTGTCTCGGTGACCTCGCC 1156
Db 1081 AAGCTGCATGTGTCGGCAGTGGAGAGAGGCTCTCGGGGGGTGTCTCGGTGACCTCGCC 1140

Qy 1157 TTCTCTTCAGAGGATCATGTGCTGTCTCTTTGAGCGGGAACCTTCAACGAGCATCTG 1216
Db 1141 TTCTCTTCAGAGGATCATGTGCTGTCTCTTTGAGCGGGAACCTTCAACGAGCATCTG 1200
Qy 1217 GGTACCAAGACGCTCCAGAGAGAGAGAGCTTGTGATGCCATGCTGTCC -GGAGACAG 1275
Db 1201 GGTACCAAGACGCTCCAGAGAGAGAGAGCTTGTGATGCCATGCTGTCCCGGGGACACAG 1259
Qy 1276 CAATGTGATGAAGTCTGTGAGCCGCGAGAGAGTGTGACCTGGCACTGGAACAAGGCGCAG 1335
Db 1260 CAATGTGATGAAGTCTGTGAGCCGCGAGAGAGTGTGACCTGGCACTGGAACAAGGCGCAG 1319
Qy 1336 CCGTGTGACCTGGCGGTGGAGGCGGGCAAGAGAGTGTGAGCCCAAGTGGCTGTGCA 1395
Db 1320 CCGTGTGACCTGGCGGTGGAGGCGGGCAAGAGAGTGTGAGCCCAAGTGGCTGTGCA 1379
Qy 1396 CAATGCCAACCCCAACCTGACCAACCGTAGGGGCTCCACCCGTTGCAATGAGCGTGA 1455
Db 1380 CAATGCCAACCCCAACCTGACCAACCGTAGGGGCTCCACCCGTTGCAATGAGCGTGA 1439
Qy 1456 GAGAGGGTGGGGGTGTGTGAGACTCTGTGCAAGAGATCACTGTCAACGCCAA 1515
Db 1440 GAGAGGGTGGGGGTGTGTGAGACTCTGTGCAAGAGATCACTGTCAACGCCAA 1499
Qy 1516 GAGATGAGACAGATGAGACAGCCCTCCACTTTGCAAGCCAGAACGGGAGATGATAGAC 1575
Db 1500 GAGATGAGACAGATGAGACAGCCCTCCACTTTGCAAGCCAGAACGGGAGATGATAGAC 1559
Qy 1576 ACGCTGTGTGTGAGAGAGAGCCTCGGTCAACGAGGTGACCTTTGAGGGCGGAGCGC 1635
Db 1560 ACGCTGTGTGTGTGAGAGAGAGCCTCGGTCAACGAGGTGACCTTTGAGGGCGGAGCGC 1619
Qy 1636 CATGCACTGTGCTGTCCAGCACGGGCAAGAAATTCGTGGCATCTGTGTGCGGAGG 1695
Db 1620 CATGCACTGTGCTGTCCAGCACGGGCAAGAAATTCGTGGCATCTGTGTGCGGAGG 1679
Qy 1656 CGTGACGTGAGCCCTGACGGGCAAGAGATGCGGTGCGCATGCACTACGCTGCTGCA 1755
Db 1640 CGTGACGTGAGCCCTGACGGGCAAGAGATGCGGTGCGCATGCACTACGCTGCTGCA 1739
Qy 1756 GGGCCACCTGCGCATCTGTCAAGCTGCTGCGCAAGAGCCGGGGGTGAGTGTGAACGCCA 1815
Db 1740 GGGCCACCTGCGCATCTGTGTCAAGCTGCTGCGCAAGAGCCGGGGGTGAGTGTGAACGCCA 1799
Qy 1816 GACGCTGATGAGAGAGCGCAATTGCACTGAGCGGCAAGGGCGGCACTACCGGCTGGC 1875
Db 1800 GACGCTGATGAGAGAGCGCAATTGCACTGAGCGGCAAGGGCGGCACTACCGGCTGGC 1859
Qy 1876 CCGCATCTGTCAATGACCTGTGTCTCCAGATGTCAACGTGTGCAAGCCGTGGGCAAGACCC 1935
Db 1860 CCGCATCTGTCAATGACCTGTGTCTCCAGATGTCAACGTGTGCAAGCCGTGGGCAAGACCC 1919
Qy 1936 CCGTGAAGTGGCGGCGAGAGACGGGCAACAGGACTGTCCAGGCTGTCTGTGATCGGG 1995
Db 1920 CCGTGAAGTGGCGGCGAGAGACGGGCAACAGGACTGTGTGAGGAGAGAGCTGTGATCGGG 1979
Qy 1996 CGCTGGCAAGAGAGCGTGTACCTGACAGCGCTACACCGCTGTGCACTGTGCTGCCAA 2055
Db 1980 CGCTGGCAAGAGAGCGTGTACCTGACAGCGCTACACCGCTGTGCACTGTGCTGCCAA 2039
Qy 2056 CGGACACCTGGGCACTGTCAAGCTGTTGTGAGAGAGAGCGCGATGTGCTGGCCGGGG 2115
Db 2040 CGGACACCTGGGCACTGTCAAGCTGTTGTGAGAGAGAGCGCGATGTGCTGGCCGGGG 2099
Qy 2116 ACCCTGAAACAGACGGGCTGTGCACTGAGCTGCCGCCACAGGCACTGGAGGTGTGA 2175
Db 2100 ACCCTGAAACAGACGGGCTGTGCACTGAGCTGCCGCCACAGGCACTGGAGGTGTGA 2159
Qy 2176 GGAATTTGTCAAGCGCGATGTCAATTGACCTGTTTCAACAGACGGGGCTCAAGCGCTGCA 2235
Db 2160 GGAATTTGTCAAGCGCGATGTCAATTGACCTGTTTCAACAGACGGGGCTCAAGCGCTGCA 2219

2236 CCTGGCCGCGCAGGCGCGGACGACAGACGGGTGGAGACTGCTCAGGCAATGGGGCCCA 2295
|||||
2220 CTTGGCCGCGCGGCGGACGACAGACGGGTGGAGACTGCTCAGGCAATGGGGCCCA 2279
|||||
2236 CATCAACCTGCAAGACCTCAAGTTCCAGGCGCGCCATGGCCCGCGGCAACTCTCTCG 2355
2280 CATCAACCTGCAAGACCTCAAGTTCCAGGCGCGCCATGGCCCGCGGCAACTCTCTCG 2339
2356 GCGAAGCAAGACTG 2371
2340 GCGAAGCAAGACTG 2355

RESULT 14
US-10-128-174-19
; Sequence 19, Application US/10128174
; Publication No. US2003019462A1
; GENERAL INFORMATION:
; APPLICANT: Inohara, Gabriel
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-174-19

Query Match 60.3%; Score 2327.2; DB 16; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

17 ATGAGAGGCGACGGGCGGACCCCATGGGCTTGCGGCTGCGACCTTCGACCGGGGC 76
1 ATGAGAGGCGACGGGCGGACCCCATGGGCTTGCGGCTGCGACCTTCGACCGGGGC 60
77 GAGTTCACGGGCTGAGAGAGGTGGGCTTCGGGCGGCTTCGGGCAAGGTGCGC 136
61 GAGTTCACGGGCTGAGAGAGGTGGGCTTCGGGCGGCTTCGGGCAAGGTGCGC 120
137 CATGTCACATGGAAGACCTGCGGCTGCGACATGAGTCTGCGGCAAGGTGCGC 196
121 CATGTCACATGGAAGACCTGCGGCTGCGACATGAGTCTGCGGCAAGGTGCGC 180
197 AGGAGAGCGCATGGAGCTTTTGGAGAAGCCAGAAGATGAGATGGAGCTTTCGCTAC 256
181 AGGAGAGCGCATGGAGCTTTTGGAGAAGCCAGAAGATGAGATGGAGCTTTCGCTAC 240
257 ATTCGCGCTGTATGACATCTGCGGCGAACCTGTGCGGCTGTGATGAGATGAGAG 316
241 ATTCGCGCTGTATGACATCTGCGGCGAACCTGTGCGGCTGTGATGAGATGAGAG 300
317 AGGAGCTCCCTGGAGAAAGCTGCTGCTTCGAGGCAATGGGCAATGGGCAATGGG 376
301 AGGAGCTCCCTGGAGAAAGCTGCTGCTTCGAGGCAATGGGCAATGGGCAATGGG 360
377 ATTCATCCAGAGAGCGGCGGTGGGCAATGAACTTCGACATGAGAGCGGCGCACTCTG 436
361 ATTCATCCAGAGAGCGGCGGTGGGCAATGAACTTCGACATGAGAGCGGCGCACTCTG 420
437 CATCTGACCTCAAGAGCGGCGGCAATCTGCTGATGAGAGCGGCGCACTCAAGATTCT 496
421 CATCTGACCTCAAGAGCGGCGGCAATCTGCTGATGAGAGCGGCGCACTCAAGATTCT 480
497 GATTTTGGCTGCGGCAAGTGAACGGGCTGTCTCCCACTGCAATGAGCTCAAGTGAATGC 556
481 GATTTTGGCTGCGGCAAGTGAACGGGCTGTCTCCCACTGCAATGAGCTCAAGTGAATGC 540
557 CTGTTTGGCAATGCGCTTACCTCCCTCAGAGCGGCAATGAGGAGAGAGCGGCTTTC 616

541 CTGTTTGGCAATGCGCTTACCTCCCTCAGAGCGGCAATGAGGAGAGAGCGGCTTTC 600
617 GACACCAAGACGATGTATACAGCTTTTGCATGTCTCTGCGGCGGCTTCACAGAG 676
601 GACACCAAGACGATGTATACAGCTTTTGCATGTCTCTGCGGCGGCTTCACAGAG 660
677 AAGCGTTTGCATGAGTGAAGAACATCTGCAATCATGAGTGAAGTGAAGGAGGAC 736
661 AAGCGTTTGCATGAGTGAAGAACATCTGCAATCATGAGTGAAGTGAAGGAGGAC 720
737 GCGCCGAGCTGCGGCGGCTGTCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 796
721 GCGCCGAGCTGCGGCGGCGGCTGTCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
797 CTCAATGCAAGGCTGTCGAGAGGAGATCCGCGAGTTAGGCGGCGGCGGCGGCGGCGG 856
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841 TCTGAACCGAGGACCTGTGTGAAGAACCTGATGAGAGTGAAGAACCTGTGTATGAT 900
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901 CTGACCTGTAAGAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
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961 GCGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
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1097 AAGCTGCGATGTCGCGGCAAGTGGAGAGGCTCTGCGGAGTGTCTGCTGAGACTCGGC 1156
1081 AAGCTGCGATGTCGCGGCAAGTGGAGAGGCTCTGCGGAGTGTCTGCTGAGACTCGGC 1140
1157 TTTCTCTTCCAGAGATCATCTGTCTCTTGAAGCGGAGAACCTTGAACAGAGGACTG 1216
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1217 GGTACCAAGACCTTCCAGAGAGAGAGAGTGTGATGCCATCTGTCC-GGGACACAG 1275
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1500 GAGATGAGAGCCAGTGAAGACGCGCTTCACTTTGAGAGCCGAGAGAGAGTGAAGTGAACAC 1559
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1560 AAGCGTGTGTTTGAAGAGAGAGCGCTGCGTCAAGAGTGAAGTGAAGGAGCGGAGCGG 1619
1636 CATGCAAGTGGCTGTCAGAGCGGCGGAGAGAGATATGCTGTGCAATCTGCTGCGCGAGG 1695

Db	1620	CATGCACGTGGCCCTGGCCAGCAGCAGGCGAGAGAAATATCGTGGCAATCTGTCTGGCCGAGG	1679
Qy	1696	CGTGGACGTGAGCCCTTGCAGGGCGAAGATGCTGTGGCTGCACCTGACCTACGCTGCTTGGCA	1755
Db	1680	COTGGACGTGAGCCCTTGCAGGGCGAAGATGCTGTGGCTGCACCTGACCTACGCTGCTTGGCA	1739
Qy	1756	GGGCGCACCTTGGCCCATTCGTCAAGCTGTGTGGCCCAAGAGCGCGGGGGTGAATGGAACGCCCA	1815
Db	1740	GGGCGCACCTTGGCCCATTCGTCAAGCTGTGTGGCCCAAGAGCGCGGGGGTGAATGGAACGCCCA	1799
Qy	1816	GACGCTGATGGAGAGAGCGCCATTGCACTTGGCCCGCAGACGCGGGGCACTACCGGTGGC	1875
Db	1800	GACGCTGATGGAGAGAGCGCCATTGCACTTGGCCCGCAGACGCGGGGCACTACCGGTGGC	1859
Qy	1876	CCGACATCTTCATCGACTCTGTGCTCCGAGCTCAAGCTCTGACGCTGTGGCAACAACACC	1935
Db	1860	CCGACATCTTCATCGACTCTGTGCTCCGAGCTCAAGCTCTGACGCTGTGGCAACAACACC	1919
Qy	1936	CCTGACGTTGGCGCGGAGACGGGGGCAACAGAGCATGCGACGGCTGTCTCTGACTGCGGG	1995
Db	1920	CCTGACGTTGGCGCGGAGACGGGGGCAACAGAGCATGCGACGGCTGTCTCTGACTGCGGG	1979
Qy	1996	CGCTGGCAAGAGAGCGCTGACCTCAGACGGCTACACCGCTCTGCACTTGGCTGCGCCAA	2055
Db	1980	CGCTGGCAAGAGAGCGCTGACCTCAGACGGCTACACCGCTCTGCACTTGGCTGCGCCAA	2039
Qy	2056	CGGACATCTTGGGCACTGTCAAGCTGTGTCCAGAGAGAAAGCGCGATGTGGCCCGGGG	2115
Db	2040	CGGACATCTTGGGCACTGTCAAGCTGTGTCCAGAGAGAAAGCGCGATGTGGCCCGGGG	2099
Qy	2116	ACCCCTGAACAGAGCGGCGCTGCACCTTGGCTGCGCCACGCGGCACTCGAGGTGGTGA	2175
Db	2100	ACCCCTGAACAGAGCGGCGCTGCACCTTGGCTGCGCCACGCGGCACTCGAGGTGGTGA	2159
Qy	2176	GGAGTTGGTCAAGCGCCGATGTCAATTGACCTGTTCCAGAGCAGGGGCTCAGCGCGCTGCA	2235
Db	2160	GGAGTTGGTCAAGCGCCGATGTCAATTGACCTGTTCCAGAGCAGGGGCTCAGCGCGCTGCA	2219
Qy	2236	CCTGGCCCGCCGAGGGCGGGGCGGCAAGCAGACGAGGGTGGAGCTGTCTCAGGCAATGGGGCCA	2295
Db	2220	CCTGGCCCGCCGAGGGCGGGGCGGCAAGCAGACGAGGGTGGAGCTGTCTCAGGCAATGGGGCCA	2279
Qy	2296	CATCAACTTGCAGAGGCTTCAAGTTCAGGGGCGGCAATGGCCCGCGCCACACTCTCTGG	2355
Db	2280	CATCAACTTGCAGAGGCTTCAAGTTCAGGGGCGGCAATGGCCCGCGCCACACTCTCTGG	2339
Qy	2356	GCGAAGCAAGACCTAG 2371	
Db	2340	GCGAAGCAAGACCTAG 2355	

RESULT 15

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/ Sequence 1, Application US/10128174

/ Publication No. US20030199462A1

/ GENERAL INFORMATION:

/ APPLICANT: Nunez, Gabriel

/ APPLICANT: Inohara, Naohiko

/ TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

/ FILE REFERENCES: UM-06967

/ CURRENT APPLICATION NUMBER: US/10/128,174

/ CURRENT FILING DATE: 2002-04-23

/ NUMBER OF SEQ ID NOS: 44

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 1

/ LENGTH: 2355

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-128-174-1

Query Match	60.2%	Score 2325.6;	DB 16;	Length 2355;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 2350; Conservative	0;	Mismatches 4;	Indels 2;	Gaps 2;

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Db	1	ATGGAAGGGGCGA	CGGGCGGGGACCCCATGGAGCCCTGAGCTGTGCGGACCTTCAACGCGGGC	60
OY	77	GAGTTCA	CGGGCTGGGAGAAAGTGAGGCTCGGGCGGCTTCTGGGCGAGGTGACAAAGTGTCGC	136
Db	61	GAGTTCA	CGGGCTGGGAGAAAGTGAGGCTCGGGCGGCTTCTGGGCGAGGTGACAAAGTGTCGC	120
OY	137	CATGTCCA	CTGGAAGAACCTTGCTGGCCATCTAAATGTCTGGCCGACCGCTGCACCGTCAAGAC	196
Db	121	CATGTCCA	CTGGAAGAACCTTGCTGGCCATCTAAATGTCTGGCCGACCGCTGCACCGTCAAGAC	180
OY	197	AGGAGAGCGCAT	GTGAGCTTTTGGAAAGACCAAGACAAAGATGAGATGGCCAAAGTTTCGTAC	256
Db	181	AGGAGAGCGCAT	GTGAGCTTTTGGAAAGACCAAGACAAAGATGAGATGGCCAAAGTTTCGTAC	240
OY	257	ATCTGCTCTGTGTAT	TGGCATCTCTGCGCGAACCTGTGTGGCCCTGGTGCATGAGTTCATGGAG	316
Db	241	ATCTGCTCTGTGTAT	TGGCATCTCTGCGCGAACCTGTGTGGCCCTGGTGCATGAGTTCATGGAG	300
OY	317	ACGGGCTCCCTG	GAAGAAAGCTGTGGGCTTCCGAGCCATTTGCATGGAGATCTCCGGTTCCGA	376
Db	301	ACGGGCTCCCTG	GAAGAAAGCTGTGGGCTTCCGAGCCATTTGCATGGAGATCTCCGGTTCCGA	360
OY	377	ATCATCCACG	AGACGGGCGGTGGGCGATGAACTTCTCTGCATGTAGCGCCCGCCACCTCTCG	436
Db	361	ATCATCCACG	AGACGGGCGGTGGGCGATGAACTTCTCTGCATGTAGCGCCCGCCACCTCTCG	420
OY	437	CACCTGGA	ACCTCAAGCCCGCGAACATCTCTCTGTGATGGCCCACTAACACGTCAGAATTTCT	496
Db	421	CACCTGGA	ACCTCAAGCCCGCGAACATCTCTCTGTGATGGCCCACTAACACGTCAGAATTTCT	480
OY	497	GATTTGGTCTG	GCAGATGCACGGGCTGTCCCACTCGCATGAACCTCAGCATGATGATGC	556
Db	481	GATTTGGTCTG	GCAGATGCACGGGCTGTCCCACTCGCATGAACCTCAGCATGATGATGATGC	540
OY	557	CTGTTTGGCA	CAATGCGCTTACCTTCCCTTCAGAGCGCATCAGGAGAAAGACCCGGCTTTTC	616
Db	541	CTGTTTGGCA	CAATGCGCTTACCTTCCCTTCAGAGCGCATCAGGAGAAAGACCCGGCTTTTC	600
OY	617	GACACCAAGCA	CGATGTATACAGCTTTGGCATGCTCATCTGGGGCGTGTCAACACAGAG	676
Db	601	GACACCAAGCA	CGATGTATACAGCTTTGGCATGCTCATCTGGGGCGTGTCAACACAGAG	660
OY	677	AAGCGCTTTG	CAGATGAGAAAGATCTCTGCACATCATCTGTAAGGTGTGAAGGGCCAC	736
Db	661	AAGCGCTTTG	CAGATGAGAAAGATCTCTGCACATCATCTGTAAGGTGTGAAGGGCCAC	720
OY	737	CGCCCGGAC	CTGCGCCGTGTGCAGAGCCCGCGCGCGCCCTGGCAACCACTGATACGC	796
Db	721	CGCCCGGAC	CTGCGCCGTGTGCAGAGCCCGCGCGCGCCCTGGCAACCACTGATACGC	780
OY	797	CTCATGTAC	GGCGGTGTGAGAGGATCCCGGATTTAGGCCACCTTCCAAAGAAATTACT	856
Db	781	CTCATGTAC	GGCGGTGTGAGAGGATCCCGGATTTAGGCCACCTTCCAAAGAAATTACT	840
OY	857	TCGTGAAC	CCGAGACCTGTGTGAAGAGCTGTATGACGAATGTAAGAAAGAACTGCTCATGAT	916
Db	841	TCGTGAAC	CCGAGACCTGTGTGAAGAGCTGTATGACGAATGTAAGAAAGAACTGCTCATGAT	900
OY	917	CTGGAACGT	GAAGAAAGCCCCCGGAGCCCAAGAGCGAGGAGGTGTCTGCGAGGCTCAAGCGG	976
Db	901	CTGGAACGT	GAAGAAAGCCCCCGGAGCCCAAGAGCGAGGAGGTGTCTGCGAGGCTCAAGCGG	960
OY	977	GCCTCTG	CCCCACCTTGTGATTAACGATACAGCTTCTCGAGCTTCTCTCAACAGCTGAC	1036
Db	961	GCCTCTG	CCCCACCTTGTGATTAACGATTAACGATTAACGATTAACGATTAACGATTAAC	1020
OY	1037	TCGTGAAGTTT	CCCAAGGCTGTGTGAAGAGGCCCGAGAGAGCTCAAGCCGCACTCTCTGAATTC	1096
Db	1021	TCGTGAAGTTT	CCCAAGGCTGTGTGAAGAGGCCCGAGAGAGCTCAAGCCGCACTCTCTGAATTC	1080

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Db 1091 AAGGCGCATCGTCCGGGAGTGGGAGAGGCTCTCGGGGGTGTCTCGGTGGACCTCCGCC 1140
QY 1157 TTCTCTTCCAGAGATCACTGTGCTGTCTTGTGAGCGGGAACTTCAACGAGCATGTG 1216
Db 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTGTGAGCGGGAACTTCAACGAGCATGTG 1200
QY 1217 GGTACCAAGAAGCTTCCAGAGAGAAGCTTGTGATGCTGTGTCC-GGAGACAG 1275
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Db 1260 CAATCTGATGAGATCTGCAAGCCGACGAGAGCTGTGACCTGGACCTGGAACAGCGGTGCCAG 1319
QY 1336 CTTGTGCACTGTGCGGTGAGAGCGGGCAAGAGAGTGCAGCAAGTGTGCTGTCA 1395
Db 1320 CTTGTGCACTGTGCGGTGAGAGCGGGCAAGAGAGTGCAGCAAGTGTGCTGTCA 1379
QY 1396 CAATGCCAACCCCAACTGAGCAACCTGAGGGGCTTCAACCCGTTGCAATGGCCGTGA 1455
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Db 1560 ACGGCTGCTGTTGGAGAGAAAGCTTGGTCAACGAGGTGACTTTGAGGGCCGACGCC 1619
QY 1636 CATGCAAGTGGCTGCGCAAGCAAGGGGAGAGATATCGTGCATCTGCTGCGCGAGAG 1695
Db 1620 CATGCAAGTGGCTGCGCAAGCAAGGGGAGAGATATCGTGCATCTGCTGCGCGAGAG 1679
QY 1696 CTTGGAAGTGAAGCTTGCAGAGGGCAAGATGCTGTGCTGCCACTGACCTAGCTTGGCA 1755
Db 1680 CTTGGAAGTGAAGCTTGCAGAGGGCAAGATGCTGTGCTGCCACTGACCTAGCTTGGCA 1739
QY 1756 GGGCCCACTGCTCCATCTGTCAAGCTGTGCTGCAAGCGAGGGGTGAGTGTAAAGCCCA 1815
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QY 1816 GACGCTGAGTGGGAGGAGCGCAATTGCACTTGGCCGCAAGCGCGGGCACTAACGGGTGGC 1875
Db 1800 GACGCTGAGTGGGAGGAGCGCAATTGCACTTGGCCGCAAGCGCGGGCACTAACGGGTGGC 1859
QY 1876 CCGCATCTCATGACCTGTGTCTCGACGTCAACGTCTTGCAGCTGTGGCAAGACACC 1935
Db 1860 CCGCATCTCATGACCTGTGTCTCGACGTCAACGTCTTGCAGCTGTGGCAAGACACC 1919
QY 1936 CTTGCAAGTGGCGCGGAGAGACGGGGCAACAGACACTGCAAGCTGTCTTGCATTGGGG 1995
Db 1920 CTTGCAAGTGGCGCGGAGAGACGGGGCAACAGACACTGCAAGCTGTCTTGCATTGGGG 1979
QY 1996 CGCTGGCAAGAGAGCGGTGACCTCAGACGGCTTACACCGCTTGCACCTTGGCTGGCCGCA 2055
Db 1980 CGCTGGCAAGAGAGCGGTGACCTCAGACGGCTTACACCGCTTGCACCTTGGCTGGCCGCA 2039
QY 2056 CGGACACTGTGCACTGTCAAGCTGTGTGAGAGAGAGCGCATGTGCTGTGCGCGGG 2115
Db 2040 CGGACACTGTGCACTGTCAAGCTGTGTGAGAGAGAGCGCATGTGCTGTGCGCGGG 2099
QY 2116 ACCCTTGAACAGACGGCGCTGCACTGTGCTGCGCGCACTGGAAGTGTGTGA 2175
Db 2100 ACCCTTGAACAGACGGCGCTGCACTGTGCTGCGCGCACTGGAAGTGTGTGA 2159
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QY 2296 CATCACTGTGAGAGCTTCAAGGTTCAGAGGCGGCAATGGGCGCGCCCAACTTGTGGC 2355
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Search completed: September 17, 2005, 02:18:44
Job time : 8808.61 secs

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Dh 61 GAGTTCAACGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAGTGGCC 120
Qy 121 CATGTCCACTGGAAGACCTGGCTGGGCAATCAAGTGTCTGGCCAGCTTCACGTCGACGAC 180
Dh 121 CATGTCCACTGGAAGACCTGGCTGGGCAATCAAGTGTCTGGCCAGCTTCACGTCGACGAC 180
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Qy 361 ATCAATCCAGAGACGGCGGTGGGCAATGAATCTTCGCACTGCAATGAGCCCGCACTCCG 420
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Qy 901 CTGGAACGTAAGAGCCCGCGAGGCCAGAGACGAGTGTGCTTCGAGGCTCAAGCGG 960
Dh 901 CTGGAACGTAAGAGCCCGCGAGGCCAGAGACGAGTGTGCTTCGAGGCTCAAGCGG 960
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Qy 1081 AAGCTGCATGTCGGAGTGGAGAGAGCTTCGAGGAGTGTCTCTCGTGGATCTCCGCC 1140
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Qy 1141 TTCTTTCCAGAGATCACTGTGCTGTCTTGTGAGCGGGAACCTTCAACAGCGATCTG 1200
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Dh 1321 CTGCTGACCTGGCGGTGAGAGCGCGGCAAGAGAGTGCSCCAAGTGTGCTGTCAAC 1380
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Qy 1441 AGAGGCTGCGGAGTGTCTGTGAGCTTCGTGTGACGAGAAATCAATGTCAACGCCAG 1500
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Dh 1741 GGCACCTGCGCCATCTGTCAAGCTGTGCGCAAGCGCGGAGTGAATGGAACGCCAG 1800
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Dh 1801 ACGTGTGATGAGAGAGCGCATTTGCACTTGGCCGCAAGCGCGGCGCATACCGCTGGCC 1860
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Dh 1861 CGCATCTCATGACCTGTGCTCGAGCTGCAACGTCGTGACGCTGTGGCAAGACACC 1920
Qy 1921 CTGCACTGTGCGCGGAGACGAGGCAACGAGCATTCGACAGCTGTCTCATGTCGGAGC 1980
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Qy 1981 GCTGGCAAGAGAGCGCTGACCTGACAGCGCTTACACGCTTGTGACCTGTGCGCCGAC 2040
Dh 1981 GCTGGCAAGAGAGCGCTGACCTGACAGCGCTTACACGCTTGTGACCTGTGCGCCGAC 2040
Qy 2041 GGAACCTGAGCACTGTCAAGCTGTGTGAGAGAGAGCGATGTGCTGAGCCGGGGA 2100
Dh 2041 GGAACCTGAGCACTGTGTCAAGCTGTGTGAGAGAGAGCGATGTGCTGAGCCGGGGA 2100
Qy 2101 CCCCTGAACCAAGACGAGCTGTGACCTTGTGACCGGCCACGAGCATTCGAGAGTGTGAG 2160
Dh 2101 CCCCTGAACCAAGACGAGCTGTGACCTTGTGACCGGCCACGAGCATTCGAGAGTGTGAG 2160
Qy 2161 GAGTTGTGACGCGCGATGTATTAAGCTTGTGAGAGAGAGGAGCTCAAGCGGCTGAC 2220
Dh 2161 GAGTTGTGACGCGCGATGTATTAAGCTTGTGAGAGAGAGGAGCTCAAGCGGCTGAC 2220

Accession	Gene	Strain	Position (nt)	Sequence	Position (nt)	Sequence
QY	CTGGCCGCCAGGCGCGGACGCA	CGA	CGGTGGAGACTCTGCTC	TAGGCAATGGGGCCAC	2280	
Db	CTGGCCGCCAGGCGCGGACGCA	CAG	CGGTGGAGACTCTGCTC	TAGGCAATGGGGCCAC	2280	
QY	ATCAACTGCGAGAGCTCAAGTT	CGA	GGGGCGGCTATGGCCCCGCGCA	CACTCTGTCGG	2340	
Db	ATCAACTGCGAGAGCTCAAGTT	CGA	GGGGCGGCTATGGCCCCGCGCA	CACTCTGTCGG	2340	
QY	CGAAGCAAGACTTAG	2355				
Db	CGAAGCAAGACTTAG	2355				

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RESULT 2
US-10-658-904-1
; Sequence 1, Application US/10658904
; Publication No. US20040048305A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OR INVENTION: 14171 Protein Kinase, A No. US20040048305A1el Human
; TITLE OR INVENTION: Protein Kinase and Uses Thereof
; FILE REFERENCE: MPI00-010PISCPLM
; CURRENT APPLICATION NUMBER: US/10/658,904
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 09/781,882
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/182,096
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)..(2371)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3860)
; OTHER INFORMATION: n = A,T,C or G
US-10-658-904-1

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Query March	100.0%;	Score 2355;	DB 18;	Length 3860;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2355; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

OY	1	ATGAGAGGGGAGACGGGCGGGACCCCATATGGGGCCCTGGGGCTGCTGCGACCTTTCGACGCGGGG	60
Db	17	ATGAGAGGGGAGCGGCGGGACCCCATATGGGGCCCTGGGGCTGCTGCGACCTTTCGACGCGGGG	76
OY	61	GAGTTTCACGGGCTGGAGAGAGTGGGCTCGGGCGGGCTTTCGGGCAAGGTGTACAAGGTGGCG	120
Db	77	GAGTTTCACGGGCTGGAGAGAGTGGGCTCGGGCGGGCTTTCGGGCAAGGTGTACAAGGTGGCGC	136
OY	121	CATGTCCATATGGAAAGACCTGGGCTGGCATCAAGTGTGGCCGACGCTGCACGCTGCAGC	180
Db	137	CATGTCCATATGGAAAGACCTGGGCTGGCATCAAGTGTGGCCGACGCTGCACGCTGCAGC	196
OY	181	AGGGAGCGCATGGAGCTTTTGGAAAGAGCCAAAGAAAGTGAAGTGGCCAAAGTTTGGCTAC	240
Db	197	AGGGAGCGCATGGAGCTTTTGGAAAGAGCCAAAGAAAGTGAAGTGGCCAAAGTTTGGCTAC	256
OY	241	ATTCCTGCGCTGTATATGGCATCTGGCGGAAACCTGTGGGCTGGTCAATGGAGTACATGAG	300
Db	257	ATTCCTGCGCTGTATATGGCATCTGGCGGAAACCTGTGGGCTGGTCAATGGAGTACATGAG	316
OY	301	ACGGGCTCTCCCTGGAAAGCTGCTGGCTTTCGGAGCCATTGCATATGGGATCTCCGGTTCCGA	360
Db	317	ACGGGCTCTCCCTGGAAAGCTGCTGGCTTTCGGAGCCATTGCATATGGGATCTCCGGTTCCGA	376

QY	361	ATCATCCACGAGACGCGCGGTGGGATGAACCTTCTGTGACATGAGTGGCCCCGCCACTCTCTG	420
Db	377	ATCATCCACGAGACGCGCGGTGGGATGAACCTTCTGTGACATGAGTGGCCCCGCCACTCTCTG	436
QY	421	CACCTGGAACCTCAAGCCCCGGGAAACATCTCTGTGGATGCCCCACTACAGCTCAAGATTCTT	480
Db	437	CACCTGGAACCTCAAGCCCCGGGAAACATCTCTGTGGATGCCCCACTACAGCTCAAGATTCTT	496
QY	481	GATTTTGGTCTGGCCCAAGTCAACGAGCTGTCCCACTCGATGACCTCAAGATGATGGC	540
Db	497	GATTTTGGTCTGGCCCAAGTCAACGAGCTGTCCCACTCGATGACCTCAAGATGATGGC	556
QY	541	CTGTTTGGCACAATGCGCTTACTCTCTTCAGAGCGCATCAGGAGAAAGAGCGGCTCTTC	600
Db	557	CTGTTTGGCACAATGCGCTTACTCTCTTCAGAGCGCATCAGGAGAAAGAGCGGCTCTTC	616
QY	601	GACATCCAAAGCAAGATGATATACAGTTTGCAATGCTCATCTGGGGCGGTCTCAACAGAA	660
Db	617	GACATCCAAAGCAAGATGATATACAGTTTGCAATGCTCATCTGGGGCGGTCTCAACAGAA	676
QY	661	AAGCGTTTGCAGATGAGAGAAACATCTCGACATCATGCTGTAAGTGTGTAAGAGGCGAC	720
Db	677	AAGCGTTTGCAGATGAGAGAAACATCTCGACATCATGCTGTAAGTGTGTAAGAGGCGAC	736
QY	721	CGCCCCGAGCTGCCGCCCTGTGTGAGAGACCCGCGCGCTGTGACGCACTGTATAGC	780
Db	737	CGCCCCGAGCTGCCGCCCTGTGTGAGAGACCCGCGCGCTGTGACGCACTGTATAGC	796
QY	781	CTCATGCAAGCGGTCTGTGGCAGGGGGATCCGGAATTTAGGGCCACCTTCCAAAGAAATTCT	840
Db	797	CTCATGCAAGCGGTCTGTGGCAGGGGGATCCGGAATTTAGGGCCACCTTCCAAAGAAATTCT	856
QY	841	TCTGAAACCGAGAGACCTGTGTGAAAAGCCTGTATGACGAAGTGAAGAAACTGTCTATGAT	900
Db	857	TCTGAAACCGAGAGACCTGTGTGAAAAGCCTGTATGACGAAGTGAAGAAACTGTCTATGAT	916
QY	901	CTGGAACGTGAAGAACCCGCCGAGCCCAAGAGCGAGAGTGTTGCTGTGAGGCTCAAGCGG	960
Db	917	CTGGAACGTGAAGAACCCGCCGAGCCCAAGAGCGAGAGTGTTGCTGTGAGGCTCAAGCGG	976
QY	961	GCGTCTGCCCCCACTTTTGATTAAGACATACAGCTCTCCGAGCTTCTCTCAAGCTGGAC	1020
Db	977	GCGTCTGCCCCCACTTTTGATTAAGACATACAGCTCTCCGAGCTTCTCTCAAGCTGGAC	1036
QY	1021	TCTGAGATTTTCCAGAGCTGTGAGGGGCCCCGAGAGAGCTCAACCGCAGCTCTCTGAGTCC	1080
Db	1037	TCTGAGATTTTCCAGAGCTGTGAGGGGCCCCGAGAGAGCTCAACCGCAGCTCTCTGAGTCC	1096
QY	1081	AAGCTGCCATCGTCCGGGAGTGGGAGAGGCTCTCGGGGGTGTCTCTCGTGGATCTCCGCC	1144
Db	1097	AAGCTGCCATCGTCCGGGAGTGGGAGAGGCTCTCGGGGGTGTCTCTCGTGGATCTCCGCC	1160
QY	1141	TTCTCTTTCAGAGATCATCTGTCCGTGTCTTTTACGGGGAAACCTTCAACAGAGATCTG	1200
Db	1157	TTCTCTTTCAGAGATCATCTGTCCGTGTCTTTTACGGGGAAACCTTCAACAGAGATCTG	1216
QY	1201	GGTACCAACAAGACGTCGAGAGAAAGAACTTGTGGATCCCAATCGTGTCCGAGAACACAGC	1260
Db	1217	GGTACCAACAAGACGTCGAGAGAAAGAACTTGTGGATCCCAATCGTGTCCGAGAACACAGC	1276
QY	1261	AAACTGATGAAGATCTTGCAGCCGCGAGGACGTGGAACCTTGGACCTGGACAGCGGTCCAGC	1320
Db	1277	AAACTGATGAAGATCTTGCAGCCGCGAGGACGTGGAACCTTGGACCTGGACAGCGGTCCAGC	1336
QY	1321	CTGCTGCAACCTGGCGGTGGAAGGCCCGGGGAAAGAGAGTGGCGCAATGGCTGTCTCAAC	1380
Db	1337	CTGCTGCAACCTGGCGGTGGAAGGCCCGGGGAAAGAGAGTGGCGCAATGGCTGTCTCAAC	1396
QY	1381	AATGCAACCCCAACCTGAGCAACCGTATGGGGTCTCAACCCCGTTTGCAATAGCCGCTGGAG	1440
Db	1397	AATGCAACCCCAACCTGAGCAACCGTATGGGGTCTCAACCCCGTTTGCAATAGCCGCTGGAG	1456
QY	1441	AGAGAGGTGCGGGGTGTGTGTGAGCTCTCTGTGCAACGAAAGATGTCTAAGCCCAAG	1500

Db 1457 AGAGAGGCGGCGGCTGTGTGAGACTCTGCTGGACGGAAGATCAAGTCAACGCCAAG 1516
Qy 1501 GATGAGACCACTGAGACACCTCTTCACTTTGCAAGCCCAAGACGAGATGAGTCTTACACA 1560
Db 1517 GATGAGACCACTGAGACACCTCTTCACTTTGCAAGCCCAAGACGAGATGAGTCTTACACA 1576
Qy 1561 CGGCTGCTGTGAG 1620
Db 1577 CGGCTGCTGTGAG 1636
Qy 1621 ATGCACTGCTGCTGCAAG 1680
Db 1637 ATGCACTGCTGCTGCAAG 1696
Qy 1681 GTGCACTGCTGCTGCAAG 1740
Db 1697 GTGCACTGCTGCTGCAAG 1756
Qy 1741 GGGCACTGCTGCTGCTGCAAG 1800
Db 1757 GGGCACTGCTGCTGCTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1816
Qy 1801 AGCTGATGAG 1860
Db 1817 AGCTGATGAG 1876
Qy 1861 CGCATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Db 1877 CGCATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1936
Qy 1921 CTGACAGTGGCGCGGAG 1980
Db 1937 CTGACAGTGGCGCGGAG 1996
Qy 1981 GCTGGCAAG 2040
Db 1997 GCTGGCAAG 2056
Qy 2041 GGAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Db 2057 GGAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2116
Qy 2101 CCCCTGAACAAG 2160
Db 2117 CCCCTGAACAAG 2176
Qy 2161 GAGTTGCTCAGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2220
Db 2177 GAGTTGCTCAGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2236
Qy 2221 CTGGCGCGCGCAAG 2280
Db 2237 CTGGCGCGCGCAAG 2296
Qy 2281 ATCAACTGCTGAGAGCTCAAGTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Db 2297 ATCAACTGCTGAGAGCTCAAGTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2356
Qy 2341 CGAAGCAAG 2355
Db 2357 CGAAGCAAG 2371

RESULT 3
US-10-354-358-37

; Sequence 37, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying

APPLICANT: Lesoon, Andrea
APPLICANT: Lightcap, Eric S.
APPLICANT: Williamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5691, 6428,
TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 3703, 14111, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
FILE REFERENCE: MP102-020P1RNOXIM
CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/364,517
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/382,995
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/388,853
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 3860
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (17)...(2371)
US-10-354-358-37

Query Match 99.9%; Score 2332; DB 16; Length 3860;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2354; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 ATGAGAGGCGACCGCGGAGACCCCATGAGCGCTGCTGCGACCTTCAGCGCGGC 60
Db 17 ATGAGAGGCGACCGCGGAGACCCCATGAGCGCTGCTGCGACCTTCAGCGCGGC 76
Qy 61 GAGTTCAAGGCTGAG 120
Db 77 GAGTTCAAGGCTGAG 136
Qy 121 CATGTCACTGAG 180
Db 137 CATGTCACTGAG 196
Qy 181 AGGAGGCGATGAG 240
Db 197 AGGAGGCGATGAG 256
Qy 241 ATCTGCTGCTGATGAG 300
Db 257 ATCTGCTGCTGATGAG 316
Qy 301 ACGGCTCCTGAGAAAG 360

Db 317 ACGGGCTCCCTGGAAAAGCTGCTTGCGAGGCCATTGGCAATGGAATCTCCGGTTCCGA 376
 Qy 361 ATCATCCACGAGACGGCGGTGGGCAATGAATTTCTTGCACTGCAATGCGCCGCACTCTCG 420
 Db 377 ATCATCCACGAGACGGCGGTGGGCAATGAATTTCTTGCACTGCAATGCGCCGCACTCTCG 436
 Qy 421 CACCTGGACCTCAAGCCCGGAGAACATCTGCTGGATGCGCACTGCAATGCAATGATTTCT 480
 Db 437 CACCTGGACCTCAAGCCCGGAGAACATCTGCTGGATGCGCACTGCAATGCAATGATTTCT 496
 Qy 481 GATTTGGTCTGGCCAAATGCAACGGCTGTCCCACTGCAATGAATGATGATGCG 540
 Db 497 GATTTGGTCTGGCCAAATGCAACGGCTGTCTCCCACTGCAATGAATGATGATGCG 556
 Qy 541 CTGTTTGGCACAATGCTTACTCTCTCAGAGCGCATCAGGAGAGAGCGCGCTCTTC 600
 Db 557 CTGTTTGGCACAATGCTTACTCTCTCAGAGCGCATCAGGAGAGAGCGCGCTCTTC 616
 Qy 601 GACACCAAGCAGATGATTAACGCTTTGGATGCTGATCTGCGGCGTGTGCAACAGAG 660
 Db 617 GACACCAAGCAGATGATTAACGCTTTGGATGCTGATCTGCGGCGTGTGCAACAGAG 676
 Qy 661 AAGCGTTTGGAGATGAGAAAGAACATCTTGCAATCATGATGATGATGATGATGCG 720
 Db 677 AAGCGTTTGGAGATGAGAAAGAACATCTTGCAATCATGATGATGATGATGATGCG 736
 Qy 721 CGCCCGAGCTGCGCGCGGTGTGCAAGACCGCGCGCGCGCTGAGCCACCTGATACGC 780
 Db 737 CGCCCGAGCTGCGCGCGGTGTGCAAGACCGCGCGCGCGCTGAGCCACCTGATACGC 796
 Qy 781 CTGATGACGGGTGTGCGAGAGGGGATTCGCGAGATTAAGCCCACTTTCAAGAAATTAAT 840
 Db 797 CTGATGACGGGTGTGCGAGAGGGGATTCGCGAGATTAAGCCCACTTTCAAGAAATTAAT 856
 Qy 841 TCTGAACCGAGAGACCTGTGTGAAAAGCTGATGACGAGTGAAGAAAGAAATGCTCATGAT 900
 Db 857 TCTGAACCGAGAGACCTGTGTGAAAAGCTGATGACGAGTGAAGAAAGAAATGCTCATGAT 916
 Qy 901 CTGAGCGTGAAGAACCCCGGAGGCCAGAGACGAGGTGTGTCTGCGAGGCTCAAGCGG 960
 Db 917 CTGAGCGTGAAGAACCCCGGAGGCCAGAGACGAGGTGTGTCTGCGAGGCTCAAGCGG 976
 Qy 961 GCTCTGCCCCCACTTTGATTAACGATCAAGCTCTTCAAGCTTCTCTCAAGCTGAGAC 1020
 Db 977 GCTCTGCCCCCACTTTGATTAACGATCAAGCTCTTCAAGCTTCTCTCAAGCTGAGAC 1036
 Qy 1021 TCTGAGTTTCCAGAGCTGTGAGAGGCCCCGAGAGAGCTCAGCGCGAGCTCTTGAATCC 1080
 Db 1037 TCTGAGTTTCCAGAGCTGTGAGAGGCCCCGAGAGAGCTCAGCGCGAGCTCTTGAATCC 1096
 Qy 1081 AAGCTGCATGCTCCGAGAGTGGGAAAGAGCTCTCGGGGGTGTCTCGGTGAGCTCCGCC 1140
 Db 1097 AAGCTGCATGCTCCGAGAGTGGGAAAGAGCTCTCGGGGGTGTCTCGGTGAGCTCCGCC 1156
 Qy 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAAACTTTCAACAGAGATATG 1200
 Db 1157 TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAAACTTTCAACAGAGATATG 1216
 Qy 1201 GGTACCAAGAGCTCAGAGAGAGAGCTTTGAGATGCAATGATGTC-GGGACACAG 1259
 Db 1217 GGTACCAAGAGCTCAGAGAGAGAGAGCTTTGAGATGCAATGATGTC-GGGACACAG 1275
 Qy 1260 CAAATGATGAAGATCTGCAACCGCAGAGAGCTGAGACCTGAGCACTGAGACGCGATGCCAG 1319
 Db 1276 CAAATGATGAAGATCTGCAACCGCAGAGAGAGCTGAGACCTGAGCACTGAGACGCGATGCCAG 1335
 Qy 1320 CCTGCTGCACTGCGGTGAGAGCGGGGCAAGAGAGTGGCGCAATGCTGCTCTCA 1379
 Db 1336 CCTGCTGCACTGCGGTGAGAGCGGGGCAAGAGAGTGGCGCAATGCTGCTCTCA 1395
 Qy 1380 CAATGCAACCCCAACTGAGCAACGATGAGGGCTCAACCCGTTGCAATGCGCGTGA 1439
 Db 1396 CAATGCAACCCCAACTGAGCAACGATGAGGGCTCAACCCGTTGCAATGCGCGTGA 1455

Qy 1440 GAGAGGGTGGCGGGGTGTGCTGAGAGCTCTGCTGAGACGGAAGATCATGTCAACGCCAA 1499
 Db 1456 GAGAGGGTGGCGGGGTGTGCTGAGAGCTCTGCTGAGACGGAAGATCATGTCAACGCCAA 1515
 Qy 1500 GATGAGGACCAATGAGCAAGCCCTTCCACTTTGAGCGCCAGAGCGGGATGATGTAGAC 1559
 Db 1516 GATGAGGACCAATGAGCAAGCCCTTCCACTTTGAGCGCCAGAGCGGGATGATGTAGAC 1575
 Qy 1560 ACGGCTGCTGTGAGAAAGAACCTCTGCTGCAAGAGTGAATTTGAGGGCGGAGAGCC 1619
 Db 1576 ACGGCTGCTGTGAGAAAGAACCTCTGCTGCAAGAGTGAATTTGAGGGCGGAGAGCC 1635
 Qy 1620 CATGCACTGCGCGGAGAGACGAGGAGAGAAATATGTCGCAATCTGCTGCGCGAGG 1679
 Db 1636 CATGCACTGCGCGGAGAGACGAGGAGAGAAATATGTCGCAATCTGCTGCGCGAGG 1695
 Qy 1680 CTGGAAGTGAAGCTGAGAGGCAAGATGCTGAGCTGCACTGCACTAGCTGCTGCGCA 1739
 Db 1696 CTGGAAGTGAAGCTGAGAGGCAAGATGCTGAGCTGCACTGCACTAGCTGCTGCGCA 1755
 Qy 1740 GGGCCACTGCGCATGCTGCAAGCTGTGCGCAAGACCGGGGTGAATGAAAGGCCA 1799
 Db 1756 GGGCCACTGCGCATGCTGCAAGCTGTGCGCAAGACCGGGGTGAATGAAAGGCCA 1815
 Qy 1800 GACGCTGATGAGAGAGAGAGCATTTGCACTGAGCGGCAACAGCGGGCACTAACGCTGAGC 1859
 Db 1816 GACGCTGATGAGAGAGAGAGCATTTGCACTGAGCGGCAACAGCGGGCACTAACGCTGAGC 1875
 Qy 1860 CCGCATCTCATGCACTGTGTCTCCAGCTTCAACGCTTGAAGCTGTGCGCAACAGACC 1919
 Db 1876 CCGCATCTCATGCACTGTGTCTCCAGCTTCAACGCTTGAAGCTGTGCGCAACAGACC 1935
 Qy 1920 CTGCACTGCGCGGAGAGAGGGGCAACAGAGCACTGCGAGCTGTCTCTGCACTCGGGG 1979
 Db 1936 CTGCACTGCGCGGAGAGAGGGGCAACAGAGCACTGCGAGCTGTCTCTGCACTCGGGG 1995
 Qy 1980 CGCTGGGAAGAGAGCGGTGACCTGACAGGCTTCAACGCTCTGCACTGAGCTGCGCCAA 2039
 Db 1996 CGCTGGGAAGAGAGCGGTGACCTGACAGGCTTCAACGCTCTGCACTGAGCTGCGCCAA 2055
 Qy 2040 CGGACACTGCGCACTGTCAAGCTGTCTTGAAGAGAGAGCCGATGTCTGCGCGGG 2099
 Db 2056 CGGACACTGCGCACTGTCAAGCTGTCTTGAAGAGAGAGCCGATGTGTGCGCGGG 2115
 Qy 2100 ACCCTGAACCAAGCGCGCTGCACTGCGCTGCGGCCAGGGCACTTGGAGGTGTGGA 2159
 Db 2116 ACCCTGAACCAAGCGCGCTGCACTGCGCTGCGGCCAGGGCACTTGGAGGTGTGGA 2175
 Qy 2160 GGAATTTGTGAGCGCGGATGCAATTTGACTGTTGAGAGAGAGGGGCTCAGCGGCTGCA 2219
 Db 2176 GGAATTTGTGAGCGCGGATGCAATTTGACTGTTGAGAGAGAGGGGCTCAGCGGCTGCA 2235
 Qy 2220 CCTGCGCGCCAGAGGCGGCGCAAGAGAGAGAGCTTGTCTGAGCAATGAGGCGCA 2279
 Db 2236 CCTGCGCGCCAGAGGCGGCGCAAGAGAGAGAGAGCTTGTCTGAGCAATGAGGCGCA 2295
 Qy 2280 CATCAACTGAGAGCTTCAAGTTTCAAGGGGCGCATGAGCCCGCGCATCTCTGCG 2339
 Db 2296 CATCAACTGAGAGCTTCAAGTTTCAAGGGGCGCATGAGCCCGCGCATCTCTGCG 2355
 Qy 2340 GCGAAGCAAGACTGAG 2355
 Db 2356 GCGAAGCAAGACTGAG 2371

RESULT 4
 US-10-172-118-1840
 ; Sequence 1840, Application US/10172118
 ; Publication No. US20030224374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong

APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIORITY FILING DATE: 2002-05-14
PRIORITY FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1840
LENGTH: 3879
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_020639
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1840

Query Match 99.0%; Score 2330.4; DB 17; Length 3879;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2353; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

1 ATGAGAGGCGACGGCGGAGCCCAATGGCCCTGTGGCGCTGCGCACCCTTGAGCGGGC 60
49 ATGAGAGGCGACGGCGGAGCCCAATGGCCCTGTGGCGCTGCGCACCCTTGAGCGGGC 108
61 GAGTTACGCGGCTGCGGAGAGGTGGCTCGGGCGGCTTCGGGCAAGTATCAAGGTGGC 120
109 GAGTTACGCGGCTGCGGAGAGGTGGCTCGGGCGGCTTCGGGCAAGTATCAAGGTGGC 168
121 CATGTCACTGGAAGACTGGCTGGCCATCAAGTGTCTGCCCAAGCTTGACGTGAGAC 180
169 CATGTCCACTGGAAGACTGGCTGGCCATCAAGTGTCTGCCCAAGCTTGACGTGAGAC 228
181 AGGAGGCGCATGAGCTTTTGAAGAAGCCAAAGATGAGATGGCCCAATTCGGCTAC 240
229 AGGAGGCGCATGAGCTTTTGAAGAAGCCAAAGATGAGATGGCCCAATTCGGCTAC 288
241 ATCTGCTGTGTATGTGATCTGCGCGCAACCTGTGCGCTGTGTATGAGATGATGAG 300
289 ATCTGCTGTGTATGTGATCTGCGCGCAACCTGTGCGCTGTGTATGAGATGATGAG 348
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349 ACGGAGCTCTGGAAGACTGTGGCTTGGAGCCATTGGCATGGAGATCTCGGTTCCGA 408
361 ATCATCCAGAGCGGCGGTGGGATGAACTTCTGCACTGCAATGAGCCCGGCACTCCG 420
409 ATCATCCAGAGCGGCGGTGGGATGAACTTCTGCACTGCAATGAGCCCGGCACTCCG 468
421 CACCTGGACTCAAGCCCGGCAACATCTGTGTGATGCCCACTACAGTCAAGATTCT 480
469 CACCTGGACTCAAGCCCGGCAACATCTGTGTGATGCCCACTACAGTCAAGATTCT 528
481 GATTTGTGTGCGCAAGTGAAGCGGCTGTCCCACTGCAATGACCTCAAGATGATGGC 540
529 GATTTGTGTGCGCAAGTGAAGCGGCTGTCCCACTGCAATGACCTCAAGATGATGGC 588
541 CTGTTTGGCAATGCGCTACCTCCCTCAAGGCGCATCAAGGAGAAAGCGCGCTCTTC 600
589 CTGTTTGGCAATGCGCTACCTCCCTCAAGGCGCATCAAGGAGAAAGCGCGCTCTTC 648
601 GACACCAAGCAAGATGTATACAGCTTTGCAATGCTGATCTGGGCGTGTCAACAAG 660
649 GACACCAAGCAAGATGTATACAGCTTTGCAATGCTGATCTGGGCGTGTCAACAAG 708
661 AAGCGTTTGCAGATGAGAAAGCAATCTGCAATCATGATGATGAGGTGTGAAGGCGCAC 720
709 AAGCGTTTGCAGATGAGAAAGCAATCTGCAATCATGATGATGAGGTGTGAAGGCGCAC 768

Qy 721 CGCCCCAGCTGCGCCCGGTGTGACAGCCCGGCGGCTGTGAGCCACTGATACGC 780
Db 769 CGCCCCAGCTGCGCCCGGTGTGACAGCCCGGCGGCTGTGAGCCACTGATACGC 828
Qy 781 CTATGCAAGCGGTGTGCGAGGGGATTCGCGGATTTAGGCCACTTCCAGAAATTACT 840
Db 829 CTATGCAAGCGGTGTGCGAGGGGATTCGCGGATTTAGGCCACTTCCAGAAATTACT 888
Qy 841 TCTGAACCGAGAGCCTGTGTGAAGCCGTGATGAAGTGAAGTGAAGTGAAGTGAAGT 900
Db 889 TCTGAACCGAGAGCCTGTGTGAAGCCGTGATGAAGTGAAGTGAAGTGAAGTGAAGT 948
Qy 901 CTGAGCTGGAAGAGCCCGGCGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCG 960
Db 949 CTGAGCTGGAAGAGCCCGGCGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCG 1008
Qy 961 GCCTGTGCCCCCACTTTCATTAACGATCAAGCTTCTCGAGCTTCTCAAGCTGAGC 1020
Db 1009 GCCTGTGCCCCCACTTTCATTAACGATCAAGCTTCTCGAGCTTCTCAAGCTGAGC 1068
Qy 1021 TCTGAGTTTCCAGAGCTGTGTGAGGGCCCGAGAGGTGACGCGGCTCTGAGTCC 1080
Db 1069 TCTGAGTTTCCAGAGCTGTGTGAGGGCCCGAGAGGTGACGCGGCTCTGAGTCC 1128
Qy 1081 AAGCTGCAATGCTTCGGCAGTGGGAAGAGCTCTCGGGGCTGTCTCGATGAGCTCGGC 1140
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Qy 1141 TTCTCTTCAGAGATATCATGTGTCTGTCTTTGAGGCGGACCTTCAACAGCATCTG 1200
Db 1189 TTCTCTTCAGAGATATCATGTGTCTGTCTTTGAGGCGGACCTTCAACAGCATCTG 1248
Qy 1201 GGTATCCAGAGAGTCCAGAGAAAGCTTGTGGAATGCCATGATGCC-GGAGAACAG 1259
Db 1249 GGTATCCAGAGAGTCCAGAGAAAGCTTGTGGAATGCCATGATGCCAGAACAG 1307
Qy 1260 CAATGATGATGATCTGTGAGCGCGAGAGCTGTGACCTGTGACCTGAGACCGGATG 1319
Db 1308 CAATGATGATGATCTGTGAGCGCGAGAGCTGTGACCTGTGACCTGAGACCGGATG 1367
Qy 1320 CTGTGCTGACCTGTGAGGAGGCGCGGCAAGAGAGTGGCCCAAGTGTGCTCTCAA 1379
Db 1368 CTGTGCTGACCTGTGAGGAGGCGCGGCAAGAGAGTGGCCCAAGTGTGCTCTCAA 1427
Qy 1380 CAATGCCAACCCCACTGTAGCAACGCTAGGGGCTCCACCCGTTGACATGCGCGTGA 1439
Db 1428 CAATGCCAACCCCACTGTAGCAACGCTAGGGGCTCCACCCGTTGACATGCGCGTGA 1487
Qy 1440 GAGGAGGCTCGGGGTGTCTGTGAGCTCTGTGAGCAAGAGATCATGTCTCAAGCCCAA 1499
Db 1488 GAGGAGGCTCGGGGTGTCTGTGAGCTCTGTGAGCAAGAGATCATGTCTCAAGCCCAA 1547
Qy 1500 GATGAGAGCAAGTGAAGAGCCCTTCCACTTTGACGCCAGAACGGGATGATGTAGCAC 1559
Db 1548 GATGAGAGCAAGTGAAGAGCCCTTCCACTTTGACGCCAGAACGGGATGATGTAGCAC 1607
Qy 1560 ACGGCTGCTGTGGAAGAAAGCGCTGTGCAACGAGTGTGAAGGAGGCGGAGCGC 1619
Db 1608 ACGGCTGCTGTGGAAGAAAGCGCTGTGCAACGAGTGTGAAGGAGGCGGAGCGC 1667
Qy 1620 CATGCAAGTGGCTGCGACAGCGGCGAGAAATATGTGCGATCTGTGCGCGCAGG 1679
Db 1668 CATGCAAGTGGCTGCGACAGCGGCGAGAAATATGTGCGATCTGTGCGCGCAGG 1727
Qy 1680 CGTGAAGTGAAGCTGTGAGGCGCAAGATGCTGTGCTGCACTGCACTAGCTGTGCA 1739
Db 1728 CGTGAAGTGAAGCTGTGAGGCGCAAGATGCTGTGCTGCACTGCACTAGCTGTGCA 1787
Qy 1740 GGGGCACTTCCCATCTCTCAAGCTGTGTGAGCAAGCGGCGGAGTGAAGCGGCGCA 1799
Db 1788 GGGGCACTTCCCATCTCTCAAGCTGTGTGAGCAAGCGGCGGAGTGAAGCGGCGCA 1847

QY 1800 GACCTGATGGAGAGACCCATTGCACTTGGCCGACACAGCGCGGCACTACCCGCTGGC 1859
 DB 1848 GACCCTGATGGAGAGACCCATTGCACTTGGCCGACACAGCGCGGCACTACCCGCTGGC 1907
 QY 1860 CGGATCCTCATTCAGACCTGTGTCTCCAGAGTGAAGTCTGAGACCTGCTGAGACAGACACC 1919
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 DB 1968 CCTGCACTGTGCGCGGAGAGACGAGGCAACAGACACTGCGAGGCTGCTCTGCAATCGGGG 2027
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 QY 2160 GAGATTGCTCAGCGCGCATGTTCATTGACCTGTTGCAAGAGAGAGGCTCAAGCGCTGCA 2219
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 DB 2328 CATCAACCTGACAGACCTCAAGTTCAGAGGCGGCAATGAGGCGCGCGCACTCTGCG 2387
 QY 2340 GCGAAGCAAGACTAG 2355
 DB 2388 GCGAAGCAAGACTAG 2403

RESULT 5
 US-10-342-887-1840
 ; Sequence 1840, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yundong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernard, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 1840
 ; LENGTH: 3879
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-342-887-1840

Query Match 99.0%; Score 2330.4; DB 18; Length 3879;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 2353; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
 QY 1 ATGAGAGGCGACCGCGGAGACCCCATGAGCCCTGCGCTGTGTGCACTTCAGACGCGGGC 60
 DB 49 ATGAGAGGCGACCGCGGAGACCCCATGAGCCCTGCGCTGTGTGCACTTCAGACGCGGGC 108
 QY 61 GAGTTCAAGGAGGAGAGAGTGTGAGGCTGAGGCGGCTTCCGAGAGGTGTACAAAGTTCGC 120
 DB 109 GAGTTCAAGGAGGAGAGAGTGTGAGGCTGAGGCGGCTTCCGAGAGGTGTACAAAGTTCGC 168
 QY 121 CATGTCACTGGAAGACCTGCTGAGCATCAAGTGTCTGCTGAGCTGCACTGTGAGAC 180
 DB 169 CATGTCACTGGAAGACCTGCTGAGCATCAAGTGTCTGCTGAGCTGCACTGTGAGAC 228
 QY 181 AGGAGGCGCATGAGACTTTTGGAGAGAGCCAGAGATGAGATGAGCAAGTTTGGCTAC 240
 DB 229 AGGAGGCGCATGAGACTTTTGGAGAGAGCCAGAGATGAGATGAGCAAGTTTGGCTAC 288
 QY 241 ATCTGCTGTGTATGAGCATCTGCGCGGACCTGTGCGGCTGTGATGAGATACATGAG 300
 DB 289 ATCTGCTGTGTATGAGCATCTGCGCGGACCTGTGCGGCTGTGATGAGATACATGAG 348
 QY 301 ACGGCTCTCCGTGAAAAGCTGTGAGCTTGTGAGACCATTTGCAATGAGATCTTCGATCGA 360
 DB 349 ACGGCTCTCCGTGAAAAGCTGTGAGCTTGTGAGACCATTTGCAATGAGATCTTCGATCGA 408
 QY 361 ATCATTCACAGAGAGGCGGTGTGAGTAACTTCTGTGACAGTGAAGGCGCGGCACTCTG 420
 DB 409 ATCATTCACAGAGAGGCGGTGTGAGTAACTTCTGTGACAGTGAAGGCGCGGCACTCTG 468
 QY 421 CACCTGAGCTCAAGCCCGGAGACATCTGTGATGAGCCCATCAAGTCAAGATTTCT 480
 DB 469 CACCTGAGCTCAAGCCCGGAGACATCTGTGATGAGCCCATCAAGTCAAGATTTCT 528
 QY 481 GATTGTGTGTGAGCAAGTGTGCAAGGCTGTCCCATCTGCAATGACCTCAAGTGTGTG 540
 DB 529 GATTGTGTGTGAGCAAGTGTGCAAGGCTGTCCCATCTGCAATGACCTCAAGTGTGTG 588
 QY 541 CTGTTTGGCACATGCGCTTACCTCCCTCAGAGGCGATCAAGGAGAGAGCGGCTCTTC 600
 DB 589 CTGTTTGGCACATGCGCTTACCTCCCTCAGAGGCGATCAAGGAGAGAGCGGCTCTTC 648
 QY 601 GACACCAAGGACAGATGATACAGCTTGTGAGTGTGATCTGAGGCGGTGCTACACAGAG 660
 DB 649 GACACCAAGGACAGATGATGATACAGCTTGTGAGTGTGATCTGAGGCGGTGCTACACAGAG 708
 QY 709 AAGCGTTTGCAGATGAGAGAACATCTGTGACATCATGTGTGAGAGTGTGAGAGGCGCAC 768
 DB 721 CGCCCGAGCTGCGCGCGGTGTGCAAGGCTCGCGCGCGGTGTGCAAGGCGCACATGATGCG 780
 QY 769 CGCCCGAGCTGCGCGCGGTGTGCAAGGCTCGCGCGCGGTGTGCAAGGCGCACATGATGCG 828
 QY 781 CTCAATGAGCGGTGTGCAAGGAGATCTGCGGAGTGTGAGGCGCACCTTCCAGAAATTA 840
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 QY 841 TCTGAAACCGAGACCTGTGTGAAAAGCTGTATGACGAAGTGAAGAAATGCTCATAT 900
 DB 889 TCTGAAACCGAGACCTGTGTGAAAAGCTGTATGACGAAGTGAAGAAATGCTCATAT 948
 QY 901 CTGAGCTGAAAAGCCCCCGAGAGCCGAGAGGAGGTGTGCTGCAAGGCTCAAGGCG 960
 DB 949 CTGAGCTGAAAAGCCCCCGAGAGCCGAGAGGAGGTGTGCTGCAAGGCTCAAGGCG 1008
 QY 961 GCTCTGCGCCCACTTGTATTAAGATCAAGCTCTCCAGCTTCTCTCAAGCTGAGC 1020
 DB 1009 GCTCTGCGCCCACTTGTATTAAGATCAAGCTCTCCAGCTTCTCTCAAGCTGAGC 1068
 QY 1021 TCTGAGATTTCAGAGCTGTGAGAGGCGCGAGAGACTCAAGCGGAGCTCTCTGATGCC 1080
 DB 1069 TCTGAGATTTCAGAGCTGTGAGAGGCGCGAGAGACTCAAGCGGAGCTCTCTGATGCC 1128

[illegible][illegible]

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Db 529 GATTTTGTCTGGCCCAAGTGCACACGGGCTGTTCCTCCATCTGCATGACCTTCAGATGATGGC 588
Qy 541 CTGTTTGGCAACATGGCTTACTCTCTCTCCAGAGCCGATCAGAGAGAAAGCCGCTCTTC 600
Db 589 CTGTTTGGCAACATGGCTTACTCTCTCCAGAGCCGATCAGAGAGAAAGCCGCTCTTC 648
Qy 601 GACACCAAGCAAGATGATATACAGCTTTGGATGATCTGATCTGGGGGCTCTCAACAGAG 660
Db 649 GACACCAAGCAAGATGATATACAGCTTTGGATGATCTGATCTGGGGGCTCTCAACAGAG 708
Qy 661 AAGCGTTTGGCAAGTGAAGAAACATCTGCAATCATGATGATGAGGTGTGAGAGGCCAC 720
Db 709 AAGCGTTTGGCAAGTGAAGAAACATCTGCAATCATGATGATGAGGTGTGAGAGGCCAC 768
Qy 721 GCGCCCGAGCTGCGCCGCTGTGCAAGAGCCCGCGCGCTGTGAGCCACTGTATAGC 780
Db 769 GCGCCCGAGCTGCGCCGCTGTGCAAGAGCCCGCGCGCTGTGAGCCACTGTATAGC 828
Qy 781 CTGATGACAGCGGTGCTGAGAGGGGATCCGAGATTAGGCCCACTTCCAGAAATTAAT 840
Db 829 CTGATGACAGCGGTGCTGAGAGGGGATCCGAGATTAGGCCCACTTCCAGAAATTAAT 888
Qy 841 TCTGAAACCGAGAGACCTGTGTGAAAAAGCTGTATGACGAAGTGAAGAAATGCTCATGAT 900
Db 889 TCTGAAACCGAGAGACCTGTGTGAAAAAGCTGTATGACGAAGTGAAGAAATGCTCATGAT 948
Qy 901 CTGAGACGTGAAGAAAGCCCCCGAGAGCCAGAGAGCGAGGTGTGCTGCGAGGCTCAAGGG 960
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Qy 961 GCGTGTGCGCCGACCTTGTGATTAACGACTCTCTCCAGCTTCTCTCAAGCTGAGC 1020
Db 1009 GCGTGTGCGCCGACCTTGTGATTAACGACTCTCTCCAGCTTCTCTCAAGCTGAGC 1068
Qy 1021 TCTGAGATTTCACAGCTGTGACAGGAGCCCGAGAGCTCAGCGCAGCTCTCTGATGTC 1080
Db 1069 TCTGAGATTTCACAGCTGTGACAGGAGCCCGAGAGCTCAGCGCAGCTCTCTGATGTC 1128
Qy 1081 AAGCTGCACTGCTCGGCGAGTGGAGAGAGGCTCTCGGGGTGTCTCTGCTGAGCTCCGCG 1140
Db 1129 AAGCTGCACTGCTCGGCGAGTGGAGAGAGGCTCTCGGGGTGTCTCTGCTGAGCTCCGCG 1188
Qy 1141 TCTCTTCCAGAGGATCACTGTGTGCTGTGAGCGGGAACCTTCAACAGAGATCTG 1200
Db 1189 TCTCTTCCAGAGGATCACTGTGTGCTGTGAGCGGGAACCTTCAACAGAGATCTG 1248
Qy 1201 GGTACCAACAGAGCTTCCAGAGAGAGAGCTTGTGATGCTCATGCTGTGTC-GGGAACAG 1259
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Qy 1440 GAGGAGGGGTGCGGGGTGTGTGTGAGCTCTCTGCTGGAAGAGATAGTGTCAAGCCCA 1499
Db 1488 GAGGAGGGGTGCGGGGTGTGTGTGAGCTCTCTGCTGGAAGAGATAGTGTCAAGCCCA 1547
Qy 1500 GAGTGAAGACAGTGAAGAGCCCTTCCATTTGCAAGCCAGAAACGGGGATGAGTCTGAGAC 1559
Db 1548 GAGTGAAGACAGTGAAGAGCCCTTCCATTTGCAAGCCAGAAACGGGGATGAGTCTGAGAC 1607

Qy 1560 ACCGCTGCTGTGGAGAGAGACGCTGCTCAACGAGGTGGAATTGTGAGGGCCGAGCGCC 1619
Db 1608 ACCGCTGCTGTGGAGAGAGACGCTGCTCAACGAGGTGGAATTGTGAGGGCCGAGCGCC 1667
Qy 1620 CATGCAAGTGGCTGTGCAAGAGAGCGGCGAGAGAAATATGTGTCGATCTCTGCTGCGCGAGG 1679
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Qy 1680 CTGGAAGTGAAGCTGTGCAAGAGAGTGTGCTGTGCTGCACTGACCTTACCTGTGCGCA 1739
Db 1728 CTGGAAGTGAAGCTGTGCAAGAGAGTGTGCTGTGCTGCACTGACCTTACCTGTGCGCA 1787
Qy 1740 GGGCCACTGCGCATGTGCAAGCTGTGCAAGAGCAAGCAAGCGAGGAGTGTGAAAGCCCA 1799
Db 1788 GGGCCACTGCGCATGTGCAAGCTGTGCAAGAGCAAGCAAGCGAGGAGTGTGAAAGCCCA 1847
Qy 1800 GACGCTGATGAGAGAGAGCGCATTTGCACTGTGCGCAAGCGCGGCACTTACCGCTGTGCGC 1859
Db 1848 GACGCTGATGAGAGAGAGCGCATTTGCACTGTGCGCAAGCGCGGCACTTACCGCTGTGCGC 1907
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Db 1968 CCGTCAAGTGGCCGCGAGAGAGCGGCGCAAGAGCACTGCGAGGCTGTGCTGTGCACTGCGAGG 2027
Qy 1980 CGCTGGAAGAGAGCGCTGTGACCTTCAAGAGGCTTCAACCGCTTGTGCAAGCTTGTGCGCA 2039
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Qy 2040 CGGACACTGCGCACTGTCAAGCTGTGTGTGAGAGAGAGCGGCTGATGTGCTGCGCGG 2099
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Qy 2100 ACCCTGAAACAGAGAGCGGCGCTGCACTGTGCGCGCCAGCGGCACTCGAGGTGTGGA 2159
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Qy 2160 GAGATTGTGACGCGCGGATGTCAATTGAACCTGTGGAAGAGAGGGCTCAAGCGCTGCA 2219
Db 2208 GAGATTGTGACGCGCGGATGTCAATTGAACCTGTGGAAGAGAGGGCTCAAGCGCTGCA 2267
Qy 2220 CCGGCGCGCCAGCGGCGCGCAAGAGAGAGCTTGTGAGAGAGCTTGTGAGAGATGGGGCCCA 2279
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Qy 2280 CATCAACCTGAGAGAGCTTCAAGTTCAGAGGCGGCGCATGAGCCGCGCAACTCTGCG 2339
Db 2328 CATCAACCTGAGAGAGCTTCAAGTTCAGAGGCGGCGCATGAGCCGCGCAACTCTGCG 2387
Qy 2340 GCGAAGCAAGACTAG 2355
Db 2388 GCGAAGCAAGACTAG 2403

RESULT 7
US-10-128-174-15
; Sequence 15, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: US-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 2355

TYPE: DNA
ORGANISM: Homo sapiens
US-10-128-174-15
Query Match 98.8%; Score 2327.2; DB 16; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY 1 ATGAGGCGCAGCGCGGAGCCCATGGGCTCGCGCTGCTGCCCATCTTGAGCGCGGC 60
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DB 61 GAGTTCAAGGCTGGGAGAGAGTGGGCTCGGCGGCTTCGGGAGTGAAGAAGTGGCGC 120
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DB 121 CATGTCCACTGGAAGACTGGCTGGCCATCAAGTCTCGCCAGCTTGCAAGTGCAGC 180
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DB 181 AGGAGCGCATAGAGCTTTTGAAGAGCCAAAGAGATGAGATGGCCAAATTTCGCTAC 240
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DB 241 ATCCGCTGTGTATGGCATCTGCGCGAACCTGTGGCTGTGTATGAGATGATGAGAG 300
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DB 301 ACGGCTCTCTGAAAGCTGTGCTTCGAGCCATTGCGATGGGATCTCCGGTTCGA 360
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DB 901 CTGGAACGTAAGAGCGCGCGAGCCAGAGCGAGCGGTGCTGCGAGGCTCAAGGCG 960
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DB 1021 TCTGAAGTTTCCAGAGCTGTGAGAGGCGCCGAGAGCTCAGCGGAGCTCTTGAGTCC 1080
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DB 1081 AAGCTGCATATGTCGCGAGTGGAGAGAGCTTCGCGGAGTGTCTCGGTGAGCTCGGC 1140
QY 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAACCTTCACAGCATCTG 1200
DB 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAACCTTCACAGCATCTG 1200
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DB 1201 GGTATCCAAAGAGCTCCAGAAAGAAAGCTTTGTGATGCTCATGTGTCC -GGACACAG 1259
QY 1260 CAAATGATGAAGATCTTGACGCGAGCGAGAGTGGCCAAAGTGTGCTGTCAA 1319
DB 1260 CAAATGATGAAGATCTTGACGCGAGCGAGAGTGGCCAAAGTGTGCTGTCAA 1319
QY 1320 CTGTGTCACCTGAGCGGTGAGGCGCGGCAAGAGATGCGCAAGTGTGCTGTCAA 1379
DB 1320 CTGTGTCACCTGAGCGGTGAGGCGCGGCAAGAGATGCGCAAGTGTGCTGTCAA 1379
QY 1380 CAATGCCAACCCCAACCTTGAGCAACGTTAGGGCTCAACCCGTTGCACTTGCCTGGA 1439
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DB 1440 GAGGAGGATGCGGGGTGTGTGTGAGCTCTGTGTCAGAGAAATCAGTGTGTCAACGCAA 1499
QY 1500 GATGAGAGCAAGTGAACAGCCCTTCACTTTGCAAGCCAGAAAGGAGTGAAGTCTAGAC 1559
DB 1500 GATGAGAGCAAGTGAACAGCCCTTCACTTTGCAAGCCAGAAAGGAGTGAAGTCTAGAC 1559
QY 1560 ACGGCTCTGTGTGAGAAAGAACGCTGTGTCACAGAGTGAAGCTTTGAGGCGCGAGGCC 1619
DB 1560 ACGGCTCTGTGTGAGAAAGAACGCTGTGTCACAGAGTGAAGCTTTGAGGCGCGAGGCC 1619
QY 1620 CATGCAAGTGAAGCTGCAAGCGGCAAGGAGATATGTGTGCACTGTGCTGCGCGAGG 1679
DB 1620 CATGCAAGTGAAGCTGCAAGCGGCAAGGAGATATGTGTGCACTGTGCTGCGCGAGG 1679
QY 1680 CGTGAAGTGAAGCTGCAAGGCAAGAGATGCTGTGTCACATGCACTGCTGCTGCGCA 1739
DB 1680 CGTGAAGTGAAGCTGCAAGGCAAGAGATGCTGTGTCACATGCACTGCTGCTGCGCA 1739
QY 1740 GGGCAACCTGCTCAATGCTCAAGCTGTGTCACAGCGCGGAGTGTGAAGCGCCA 1799
DB 1740 GGGCAACCTGCTCAATGCTCAAGCTGTGTCACAGCGCGGAGTGTGAAGCGCCA 1799
QY 1800 GAGCGTGAATGGAAGAGCGCAATGCACTGCGCGCAACGCGGGGCACTACCGCGTGGC 1859
DB 1800 GAGCGTGAATGGAAGAGCGCAATGCACTGCGCGCAACGCGGGGCACTACCGCGTGGC 1859
QY 1860 CCGGATCTCATGCACTGTGTCTTCCAGGTGAAGTGTGCAAGCTGTGCGCAACAC 1919
DB 1860 CCGGATCTCATGCACTGTGTCTTCCAGGTGAAGTGTGCAAGCTGTGCGCAACAC 1919
QY 1920 CTGTCAGTGTGCGCGGAGAGCGGGGCAAGAGCACTGCAAGGCTGTCTGCAATCGGGG 1979
DB 1920 CTGTCAGTGTGCGCGGAGAGCGGGGCAAGAGCACTGCAAGGCTGTCTGCAATCGGGG 1979
QY 1980 CGCTGCAAGAGAGCGCTGACCTTCAAGCGGCTACACGCTTCAAGCTTGCCTGCGCAA 2039
DB 1980 CGCTGCAAGAGAGCGCTTGAACCTTCAAGCGGCTACACGCTTCAAGCTTGCCTGCGCAA 2039
QY 2040 CGGCAACTGAGCACTGTCAAGCTGTGTGAGAGAGAGCGGATGTGTGCTGCGCGGG 2099

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RESULT 8
US-10-128-174-16
; Sequence 16, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohito
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-174-16

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Query Match	98.8%	Score 2337.2	DB 16	Length 2355
Best Local Similarity	99.8%	Pred. No. 0		
Matches 2351	Conservative 0	Mismatches 3	Indels 2	Gaps 2
Qy	1	ATGAGAGCGGAGCGGCGGAGCCCATATGGCCCTGGCGCTGCTCGGCACTTTGACGCGGCG	60	
Db	1	ATGAGAGGCGGAGCGGCGGAGCCCATATGGCCCTGGCGCTGCTCGGCACTTTGACGCGGCG	60	
Qy	61	GAGTTCACGGCGCTGGGAGAAAGTGGGCTTGGGCGGCTTTGGGCAAGTGTCAAAAGTGGCG	120	
Db	61	GAGTTCACGGCGCTGGGAGAAAGTGGGCTTGGGCGGCTTTGGGCAAGTGTCAAAAGTGGCG	120	
Qy	121	CATGTCCACTGGAGAACTGTGCTGGCCATCAATGTCTGCCAGCCTGCACGTCGACGAC	180	
Db	121	CATGTCCACTGGAGAACTGTGCTGGCCATCAATGTCTGCCAGCCTGCACGTCGACGAC	180	
Qy	181	AGGGAGCGCATGAGCTTTTGGAGAGAGCCAAAGAGATGAGATGGCCAAAGTTTGGCTAC	240	
Db	181	AGGGAGCGCATGAGCTTTTGGAGAGAGCCAAAGAGATGAGATGGCCAAAGTTTGGCTAC	240	
Qy	241	ATCTGCGCTGTGATATGGCATCTGCCGCGAAACCGTGGCGCTGTCATGTGAGATCAATGAG	300	
Db	241	ATCTGCGCTGTGATATGGCATCTGCCGCGAAACCGTGGCGCTGTCATGTGAGATCAATGAG	300	
Qy	301	ACGGGCTCCCTGGAAAGCTGTGGCTTGGAGCCATTGCCAATGGGATCTCCGGTTCCGA	360	
Db	301	ACGGGCTCCCTGGAAAGCTGTGGCTTGGAGCCATTGCCAATGGGATCTCCGGTTCCGA	360	
Qy	361	ATCATTCACAGAGACGCGCGTGGGCAATGAACTTCTGCACTGCAATGGCCCCGCGCACTCCG	420	
Db	361	ATCATTCACAGAGACGCGCGTGGGCAATGAACTTCTGCACTGCAATGGCCCCGCGCACTCCG	420	

QY	421	CACCTGGACCTTCAAGACCCGCGCAACATCTCTGTGATGCCCATACACAGTCCAGATTTCT	480
Db	421	CACCTGGACCTTCAAGACCCGCGCAACATCTCTGTGATGCCCATACACAGTCCAGATTTCT	480
QY	481	GATTTGGTCTGCGCCAAAGTCGAAGGGCTGTCCCATCTGCATGACCTTGACATGATAGCC	540
Db	481	GATTTGGTCTGCGCCAAAGTCGAAGGGCTGTCCCATCTGCATGACCTTGACATGATAGCC	540
QY	541	CTGTTTGGCAAAATCGCCTACCTCCCTCAGAGGCGATCAGGGGAGAGAGCCGCGCTCTTC	600
Db	541	CTGTTTGGCAAAATCGCCTACCTCCCTCAGAGGCGATCAGGGGAGAGAGCCGCGCTCTTC	600
QY	601	GACACCAAGCAAGATGTATACAGCTTTTGCATCTGTGAGGCGTGTCTCACACAGAAG	660
Db	601	GACACCAAGCAAGATGTATACAGCTTTTGCATCTGTGAGGCGTGTCTCACACAGAAG	660
QY	661	AAAGCGTTTGCAGATGAGAGAAACAATCTGTCACTCATGTGTGAAGGTGTGAAGGGCCAC	720
Db	661	AAAGCGTTTGCAGATGAGAGAAACAATCTGTCACTCATGTGTGAAGGTGTGAAGGGCCAC	720
QY	721	GCGCCCGAGCTGCGCGCCGCTGTGCGAGAGCCGCGCGCGCGCTGCAGCCACTGATAGCG	780
Db	721	GCGCCCGAGCTGCGCGCCGCTGTGCGAGAGCCGCGCGCGCGCTGCAGCCACTGATAGCG	780
QY	781	CTCATGACGCGTGTGCGCAGGGGAGTCCGCGAGTTAGGCCCACCTTTCAGAGAAATTACT	840
Db	781	CTCATGACGCGTGTGCGCAGGGGAGTCCGCGAGTTAGGCCCACCTTTCAGAGAAATTACT	840
QY	841	TCTGAAACCGAGAGACTTGTGTGAAGAAAGCTGTGATGACAAAGTGAAGAAAGAACTGTAT	900
Db	841	TCTGAAACCGAGAGACTTGTGTGAAGAAAGCTGTGATGACAAAGTGAAGAAAGAACTGTAT	900
QY	901	CTGACAGTGAAGAAAGCCCCCGAGCGCCAGAGCGAGAGGTGTGCTGTGCGAGGCTCAAGCGG	960
Db	901	CTGACAGTGAAGAAAGCCCCCGAGCGCCAGAGCGAGAGGTGTGCTGTGCGAGGCTCAAGCGG	960
QY	961	GCTCTGCCCCCACTTGTGATTAACAATCAAGCTCTTCCAGCTTCTTCAACAAGTGGAC	1020
Db	961	GCTCTGCCCCCACTTGTGATTAACAATCAAGCTCTTCCAGCTTCTTCAACAAGTGGAC	1020
QY	1021	TCTGAGTTTCCAGAGTGTGAGAGGCGCCAGAGAGCTCAAGCCGAGCTCTCTGAGTCC	1080
Db	1021	TCTGAGTTTCCAGAGTGTGAGAGGCGCCAGAGAGCTCAAGCCGAGCTCTCTGAGTCC	1080
QY	1081	AAAGTGCATCTCTCCGCGATGTGAGAGAGGCTCTCGGGGAGTGTCTCGTGTGAATCTCGCGC	1140
Db	1081	AAAGTGCATCTCTCCGCGATGTGAGAGAGGCTCTCGGGGAGTGTCTCGTGTGAATCTCGCGC	1140
QY	1141	TTCTCTTTCAGAGATCACTGTCTGTCTTTTGAAGCGGAACTTTCAACAAGCGATCTG	1200
Db	1141	TTCTCTTTCAGAGATCACTGTCTGTCTTTTGAAGCGGAACTTTCAACAAGCGATCTG	1200
QY	1201	GGTACCAAGAGCTGTGAGAGAAAGAACTTGTGATGTCATCTGTGTCCGAGACAACAG	1260
Db	1201	GGTACCAAGAGCTGTGAGAGAAAGAACTTGTGATGTCATCTGTGTCCGAGACAACAG	1260
QY	1260	CAAACTGATGAAGATCTGTGACCGCGCAAGAGCTGTGACTTGGCACTGCAACGCGTGTG	1320
Db	1260	CAAACTGATGAAGATCTGTGACCGCGCAAGAGCTGTGACTTGGCACTGCAACGCGTGTG	1320
QY	1320	CGTGTGCACTGTGCGGTGTGAGAGCGCGGCAAGAGAGTGTGCGCAAGTGTGTGTCTCA	1380
Db	1320	CGTGTGCACTGTGCGGTGTGAGAGCGCGGCAAGAGAGTGTGCGCAAGTGTGTGTCTCA	1380
QY	1380	CAATGCAACCCCACTGTAGCAACCTGTAGGGGCTCAACCCCGTTTGCATATGGCCGTGGA	1440
Db	1380	CAATGCAACCCCACTGTAGCAACCTGTAGGGGCTCAACCCCGTTTGCATATGGCCGTGGA	1440
QY	1440	GAGAGAGGTGTGTGTGAGACTCTGTGTGCGGAGAAAGATCAAGTGTACAGCCAA	1499
Db	1440	GAGAGAGGTGTGTGTGAGACTCTGTGTGCGGAGAAAGATCAAGTGTACAGCCAA	1499


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QY 1500 GGATGAGGACCAAGTGGAGACGAGCCCTCCACTTTTGACGCCGAGAACGGGGATGAGTCTAGAC 1559
DB 1500 GGATGAGGACCAAGTGGAGACGAGCCCTCCACTTTTGACGCCGAGAACGGGGATGAGTCTAGAC 1559
QY 1560 ACGGCTGCTGTTGGAGAGAAAGCCCTCGGTCAACGAGGTGACCTTTGAGGGCCGAGCGCC 1619
DB 1560 ACGGCTGCTGTTGGAGAGAAAGCCCTCGGTCAACGAGGTGACCTTTGAGGGCCGAGCGCC 1619
QY 1620 CATGCACTGGCTCTGCGCAGCAGCGGCAAGAGAAATCTGTGGCATCTCTGCTGCGCCGAG 1679
DB 1620 CATGCACTGGCTCTGCGCAGCAGCGGCAAGAGAAATCTGTGGCATCTCTGCTGCGCCGAG 1679
QY 1680 CGTGAACGTGAGCCCTGACGAGGCAAGATGCTGTGCTGCACTGCACTAGCTGCTGAGCA 1739
DB 1680 CGTGAACGTGAGCCCTGACGAGGCAAGATGCTGTGCTGCACTGCACTAGCTGCTGAGCA 1739
QY 1740 GGGGCACTGCGCCATCTGCAAGCTGCTGCGCAAGCAAGCCGGGGGTGAGTGTGAACGCCCA 1799
DB 1740 GGGGCACTGCGCCATCTGCAAGCTGCTGCGCAAGCAAGCCGGGGGTGAGTGTGAACGCCCA 1799
QY 1800 GACGCTGATGAGAGAGAGCCCATTTGCACTGCGCGCAAGCGCGGCACTACCGCGTGGC 1859
DB 1800 GACGCTGATGAGAGAGAGCCCATTTGCACTGCGCGCAAGCGCGGCACTACCGCGTGGC 1859
QY 1860 CGGATCTCTCATGACCTGTGCTCGACGTCACGTCGACGCTGCTGCGCAGACAGACC 1919
DB 1860 CGGATCTCTCATGACCTGTGCTCGACGTCACGTCGACGCTGCTGCGCAGACAGACC 1919
QY 1920 CCTGCACTGCGCGCGGAGACGGGGCACAAGCACTGCGCAGCTGCTCTGCAATCGGGG 1979
DB 1920 CCTGCACTGCGCGCGGAGACGGGGCACAAGCACTGCGCAGCTGCTCTGCAATCGGGG 1979
QY 1980 CGCTGAGCAAGAGAGCGGTGACCTGACAGCGCTACACGCGCTGCACTGCGTGGCCCGCA 2039
DB 1980 CGCTGAGCAAGAGAGCGGTGACCTGACAGCGCTACACGCGCTGCACTGCGTGGCCCGCA 2039
QY 2040 CGGACACCTGCGCACTGCTCAAGCTGCTTGTGAGGAGAGAGCGCATGTGCTGCGCGGG 2099
DB 2040 CGGACACCTGCGCACTGCTCAAGCTGCTTGTGAGGAGAGAGCGCATGTGCTGCGCGGG 2099
QY 2100 ACCCTGAAACGAGCGGCGCTGACCTGCGCTGCGCCCAAGGCACTGAGAGTGTGA 2159
DB 2100 ACCCTGAAACGAGCGGCGCTGACCTGCGCTGCGCCCAAGGCACTGAGAGTGTGA 2159
QY 2160 GGAATTGCTCAAGCGCGCATGTCATTTGACTGTGTCAGAGAGGGGCTCAAGCGCTGCA 2219
DB 2160 GGAATTGCTCAAGCGCGCATGTCATTTGACTGTGTCAGAGAGGGGCTCAAGCGCTGCA 2219
QY 2220 CCTGCGCGCCGAGGCGCGGCAAGCAGACGCTGAGACTCTGCTCAGGCAATGGGCCCA 2279
DB 2220 CCTGCGCGCCGAGGCGCGGCAAGCAGACGCTGAGACTCTGCTCAGGCAATGGGCCCA 2279
QY 2280 CATCAACTGCAAGACCTCAAGTTCCAGGCGGCGCATGGCCCGCGCACAATCTCTCG 2339
DB 2280 CATCAACTGCAAGACCTCAAGTTCCAGGCGGCGCATGGCCCGCGCACAATCTCTCG 2339
QY 2340 GCGAAGCAAGACTTG 2355
DB 2340 GCGAAGCAAGACTTG 2355
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RESULT 9

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US-10-128-174-18
; Sequence 18, Application US/10128174
; Publication No. US2003019462A1
; GENERAL INFORMATION:
; APPLICANT: Inohara, Naohiro
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT FILING DATE: US/10/128,174
; NUMBER OF SEQ ID NOS: 44
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-174-18
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Query Match 98.8%; Score 2327.2; DB 16; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
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QY 1 ATGAGGCGACGCGCGGACCCCATGAGCCCTGCGCTGCTGCGCACTTTGACGCGGC 60
DB 1 ATGAGGCGACGCGCGGACCCCATGAGCCCTGCGCTGCTGCGCACTTTGACGCGGC 60
QY 61 GAGTTCAAGGCTGAGAGAAAGTGGCTCGGGCGGCTTCGGGCAAGGTGACAAAGTGGC 120
DB 61 GAGTTCAAGGCTGAGAGAAAGTGGCTCGGGCGGCTTCGGGCAAGGTGACAAAGTGGC 120
QY 121 CATGTCCACTGGAAGACCTGGCTGGCCATGAGTGTGCTGCGCAGCTGCAAGTGTGAC 180
DB 121 CATGTCCACTGGAAGACCTGGCTGGCCATGAGTGTGCTGCGCAGCTGCAAGTGTGAC 180
QY 181 AGGAGCGCATGAGCTTTTGGAAAGACCAAGAAAGATGAGATGGCAAGTTTCTAC 240
DB 181 AGGAGCGCATGAGCTTTTGGAAAGACCAAGAAAGATGAGATGGCAAGTTTCTAC 240
QY 241 ATCTGCTGTGTATGACATCTGCGCGGAACTGTGCGCTGTGATGAGTACATGAG 300
DB 241 ATCTGCTGTGTATGACATCTGCGCGGAACTGTGCGCTGTGATGAGTACATGAG 300
QY 301 ACGGCGCTCCCTGGAAGAGCTGAGCTTGGAGCATTTGCAATGGATCTCCGGTTCCGA 360
DB 301 ACGGCGCTCCCTGGAAGAGCTGAGCTTGGAGCATTTGCAATGGATCTCCGGTTCCGA 360
QY 361 ATCATCCAGAGACGCGGATGGCATGAACTTCTGTGACATGATGAGCCCGCATCTCTG 420
DB 361 ATCATCCAGAGACGCGGATGGCATGAACTTCTGTGACATGATGAGCCCGCATCTCTG 420
QY 421 CACTGGAACCTCAAGCCCGGAACTATCTGCTGAGATGCCATACCAAGTCAAGATTTCT 480
DB 421 CACTGGAACCTCAAGCCCGGAACTATCTGCTGAGATGCCATACCAAGTCAAGATTTCT 480
QY 481 GATTTGCTGAGCAAGTCAAGGCTGTCCACTCGCATGACCTCAAGATGATGGC 540
DB 481 GATTTGCTGAGCAAGTCAAGGCTGTCCACTCGCATGACCTCAAGATGATGGC 540
QY 541 CTGTTTGGCAAAATCGCTTACCTTCCAGAGCGCATCAGGAGAAAGCCGGCTCTTC 600
DB 541 CTGTTTGGCAAAATCGCTTACCTTCCAGAGCGCATCAGGAGAAAGCCGGCTCTTC 600
QY 601 GACACCAAGACATGATACATTTGACATGTCATCTGGGGCGGTGCTCAACAGAG 660
DB 601 GACACCAAGACATGATACATTTGACATGTCATCTGGGGCGGTGCTCAACAGAG 660
QY 661 AAGCGTTTCAAGATGAGAGAAATCTCTGCAATCATGATGAGTGAAGTGAAGGCGCAC 720
DB 661 AAGCGTTTCAAGATGAGAGAAATCTCTGCAATCATGATGAGTGAAGTGAAGGCGCAC 720
QY 721 CGCCCGAGCTGCGCGCGGTGTGCAAGAGCCGCGCGGTGCTGCAAGCACTGATACGC 780
DB 721 CGCCCGAGCTGCGCGCGGTGTGCAAGAGCCGCGCGGTGCTGCAAGCACTGATACGC 780
QY 781 CTCATGCAAGGCTGTGCGAGGGGAGATCCCGAGTTAGGCGCCACTTCCAAAGAAATTAAT 840
DB 781 CTCATGCAAGGCTGTGCGAGGGGAGATCCCGAGTTAGGCGCCACTTCCAAAGAAATTAAT 840
QY 841 TCTGAACCGAGGACCTGTGTGAAGAACTGATGACGAATGGAAGAACTGCTCATGAT 900
DB 841 TCTGAACCGAGGACCTGTGTGAAGAACTGATGACGAATGGAAGAACTGCTCATGAT 900
QY 901 CTGGAAGTGAAGAGCCCGCGAGAGCCAGAGCGAGGTGTGCTTGTGAGGCTCAAGCGG 960
DB 901 CTGGAAGTGAAGAGCCCGCGAGAGCCAGAGCGAGGTGTGCTTGTGAGGCTCAAGCGG 960
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QY	361	ATCATTCACGAGACGGCGGTGGGCATGAACTTCTCTGCACTGCANTGAGCCCGCACTCTG	420
Db	361	ATCATTCACGAGACGGCGGTGGGCATGAACTTCTCTGCACTGCANTGAGCCCGCACTCTG	420
QY	421	CACCTGGACCTTCAGACCCCGCGCAACATCCGTGCTGATGGCCATCCACATGCAAGATTCT	480
Db	421	CACCTGGACCTTCAGACCCCGCGCAACATCCGTGCTGATGGCCATCCACATGCAAGATTCT	480
QY	481	GATTTTGGTCTGGCAGATGACACGGGCTGTCCCACTGCATGACTTCAGAGATGATGGC	540
Db	481	GATTTTGGTCTGGCAGATGACACGGGCTGTCCCACTGCATGACTTCAGAGATGATGGC	540
QY	541	CTGTTTGGCAACATGCGCTACTCTCCCTCCAGAGCCCATCAGGAGAAAGCGGCTCTTC	600
Db	541	CTGTTTGGCAACATGCGCTACTCTCCCTCCAGAGCCCATCAGGAGAAAGCGGCTCTTC	600
QY	601	GACACCAAGCAGATGATACAGCTTTGCGATCGATCTGGGGGTGTCTCACAGAG	660
Db	601	GACACCAAGCAGATGATACAGCTTTGCGATCGATCTGGGGGTGTCTCACAGAG	660
QY	661	AAGCGTTTGAGATGAGAGAAGACCTCTGCATCATGAGTGAAGTGAAGGGCAC	720
Db	661	AAGCGTTTGAGATGAGAGAAGACCTCTGCATCATGAGTGAAGTGAAGGGCAC	720
QY	721	CGCCCGAGCTCGCCGCGGTGTGCAGAGCCGGCCGGCGGCTCGAGCCACTGTATCGC	780
Db	721	CGCCCGAGCTCGCCGCGGTGTGCAGAGCCGGCCGGCGGCTCGAGCCACTGTATCGC	780
QY	781	CTCATGCAAGCGGTGTGTCGAGGGGGATCCGCGATTAAGGCCACTTCACAGAAATTACT	840
Db	781	CTCATGCAAGCGGTGTGTCGAGGGGGATCCGCGATTAAGGCCACTTCACAGAAATTACT	840
QY	841	TCTGAAACCGAGACCTGTGTGAAGACCTGATGACGAATGAAGAAACTGCTCATGAT	900
Db	841	TCTGAAACCGAGACCTGTGTGAAGACCTGATGACGAATGAAGAAACTGCTCATGAT	900
QY	901	CTGACGCTGAAAAAGCCCCCGAGGCCAGAGACGAGGTGTGCTCGAGGCTCAAGCGG	960
Db	901	CTGACGCTGAAAAAGCCCCCGAGGCCAGAGACGAGGTGTGCTCGAGGCTCAAGCGG	960
QY	961	GCGTCTGCCCCCACTTGATTAACGACTACAGCTCTCCGAGCTTCTCAAGCTGGAC	1020
Db	961	GCGTCTGCCCCCACTTGATTAACGACTACAGCTCTCCGAGCTTCTCAAGCTGGAC	1020
QY	1021	TCTGAGATTTCACAGGCTGTGAGGGGCCCGAGAGACTCAGCGAGCTCTCTGAGTCC	1080
Db	1021	TCTGAGATTTCACAGGCTGTGAGGGGCCCGAGAGACTCAGCGAGCTCTCTGAGTCC	1080
QY	1081	AAGCTGCATCGTCCGGCAGTGGGAAGAGCTCTCGGGGGTGTCTCGGTGACTCCGC	1140
Db	1081	AAGCTGCATCGTCCGGCAGTGGGAAGAGCTCTCGGGGGTGTCTCGGTGACTCCGC	1140
QY	1141	TTCCTCTCCAGAGATCACTGTGCGTGTCTTTGAGCCGGAACTTCAACAGCGATCTG	1200
Db	1141	TTCCTCTCCAGAGATCACTGTGCGTGTCTTTGAGCCGGAACTTCAACAGCGATCTG	1200
QY	1201	GGTACCAACAAGACGTTCAGAAAGAAGAGCTTGTGATGCACTGATGCC-GGACACAG	1258
Db	1201	GGTACCAACAAGACGTTCAGAAAGAAGAGCTTGTGATGCACTGATGCC-GGACACAG	1258
QY	1260	CAAACTGATGAAGATCTTGACCCGAGAGCGTGGACCTGGACCTGACACGCGTGGCAG	1318
Db	1260	CAAACTGATGAAGATCTTGACCCGAGAGCGTGGACCTGGACCTGACACGCGTGGCAG	1318
QY	1320	CCTGCTGCACCTTGGCGGTGGAAGCCGGGGCAAGAAGATGCGCAAGTGTCTCTCA	1378
Db	1320	CCTGCTGCACCTTGGCGGTGGAAGCCGGGGCAAGAAGATGCGCAAGTGTCTCTCA	1378
QY	1380	CAATGCAACCCCAACCTGAGCAACCGTGAAGGGCTCAACCCGTTGCACATGCGCTGGA	1438
Db	1380	CAATGCAACCCCAACCTGAGCAACCGTGAAGGGCTCAACCCGTTGCACATGCGCTGGA	1438
QY	1440	GAGGAGGGTGCGGGGTGTCTGAGAGTCTCTGTCGACGGAAGATCAGTTTCACGCCA	1498

Db	1440	GAGAGGGGTGGGGGTGTCTGTGAAGCTCTGTGGCGGGAGATCAAGTGTCAAGCCCA	1499
QY	1500	GGATGAGGACCAAGTGAAGAGCCCTCCACTTTTGACCCAGAACGGGAGATGATCTAGCAC	1559
Db	1500	GGATGAGGACCAAGTGAAGAGCCCTCCACTTTTGAGCCCAAGAACGGGAGATGATCTAGCAC	1559
QY	1560	ACGGCTGTCTTTGGAGAAAGACGCTTGGGTCAACAGATGTGACTTTGAAGGGCCCGACGCC	1619
Db	1560	ACGGCTGTCTTTGGAGAAAGACGCTTGGGTCAAGAGGTGTGACTTTGAAGGGCCCGAGGCC	1619
QY	1620	CATGCAAGTGGCTGTGCCAGCACGGGACGAGAGAAATATGTTGGCAATCTGTGCGCCAGAG	1679
Db	1620	CATGCAAGTGGCTGTGCCAGCACGGGACGAGAGAAATATGTTGGCAATCTGTGCGCCAGAG	1679
QY	1680	CGTGAACGTGAGCCTGCAGGGGCAAGATGCTGGCTGTGCACGTGACTACGCTGCTTGGCA	1739
Db	1680	CGTGAACGTGAGCCTGCAGGGGCAAGATGCTGGCTGTGCACGTGACTACGCTGCTTGGCA	1739
QY	1740	GGGGCACTTGCCCATCTGTCAACGCTGTGCGCCAAACACACCGGGGGTGTGAACGCCCA	1799
Db	1740	GGGGCACTTGCCCATCTGTCAAGCTGTGGCCAAACACCGGGGGTGTGAACGCCCA	1799
QY	1800	GACGCTGTGATGGAGAGACGCCATTGTGCACCTGTGGCGCACAGCGCGGCACTACCGCGTGGC	1859
Db	1800	GACGCTGTGATGGAGAGACGCCATTGTGCACCTGTGGCGCACAGCGCGGCACTACCGCGTGGC	1859
QY	1860	CCGCATCTCATCGACCTGTGCTCCGACGTCAACGTCTGCAGCCTGCTGTGGCAACGACCC	1919
Db	1860	CCGCATCTCTCATCGACCTGTGCTCCGACGTCAACGTCTGCAGCCTGCTGTGGCAACGACCC	1919
QY	1920	CCTGGAAGTGGCCCGCGAGACGGGGCAACGAGGACTGGCGGTGCTCCGTCAATCGGGG	1979
Db	1920	CCTGGAAGTGGCCCGCGAGACGGGGCAACGAGGACTGGCGGTGCTCCGTCAATCGGGG	1979
QY	1980	CGCTTGGCAAGAGGCGCTGTGACCTGACAGCGGTACACGCTTGTGCACCTGTGCGCCGCA	2039
Db	1980	CGCTTGGCAAGAGGCGCTGTGACCTGACAGCGGTACACGCTTGTGCACCTGTGCGCCGCA	2039
QY	2040	CGAGCACTTGGCCCATGTCAAGCTGTGTTCAGAGAGAAAGCCGATGTGCTTGGCCCGGGG	2099
Db	2040	CGAGCACTTGGCCCATGTCAAGCTGTGTTCAGAGAGAAAGCCGATGTGCTTGGCCCGGGG	2099
QY	2100	AACCCCTGAACAGACGGGCGTGCACCTTGGCTGCCGCCACGAGGCACTCGAGAGTGTGTGA	2159
Db	2100	AACCCCTGAACAGAGGCGCTGCACCTTGGCTGCCGCCACGAGGCACTCGAGAGTGTGTGA	2159
QY	2160	GGAAGTTGTGTCAGCGCCGATGTCAATTGACCTTGTTCGACGAGCAGGAGGAGCTCAGCGCGTCA	2219
Db	2160	GGAAGTTGTGTCAGCGCCGATGTCAATTGACCTTGTTCGACGAGCAGGAGGAGCTCAGCGCGTCA	2219
QY	2220	CTTGGCCGCCCCAGAGGCGCGGCAACGACAGTGTGGAATCTTGTCAAGGCATATGGGGCCCA	2279
Db	2220	CTTGGCCGCCCCAGAGGCGCGGCAACGACAGTGTGGAATCTTGTCAAGGCATATGGGGCCCA	2279
QY	2280	CATCAACCTGTGAGAGCTCAAGATTTCAGAGGGGGCCATATGGCCCGCGCCACACTTCTTGG	2339
Db	2280	CATCAACCTGTGAGAGCTCAAGATTTCAGAGGGGGCCATATGGCCCGCGCCACACTTCTTGG	2339
QY	2340	GCGAAGCAAGACTTAG 2355	
Db	2340	GCGAAGCAAGACTTAG 2355	

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RESULT 11
US-10-128-174-1
; Sequence 1, Application US/10128174
; Publication No. US2003019462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohito
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967

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CURRENT APPLICATION NUMBER: US/10/128,174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2355
TYPE: DNA
ORGANISM: Homo sapiens
US-10-128-174-1

Query Match 98.8%; Score 2325.6; DB 16; Length 2355;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2350; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 ATGAGGCGGACGCGGGGACCCCATGAGGCGCTGAGCTGCGACCTTGACGCGGCG 60
DB 1 ATGAGGCGGACGCGGGGACCCCATGAGGCGCTGAGCTGCGACCTTGACGCGGCG 60
QY 61 GAGTTCAAGGCTGGGAGAGAGTGGGCTGCGGCGGCTTGCGGAGAGTGAAGAGTGGG 120
DB 61 GAGTTCAAGGCTGGGAGAGAGTGGGCTGCGGCGGCTTGCGGAGAGTGAAGAGTGGG 120
QY 121 CATGTCATGGAAGACCTGCTGGCATCAAGTCTGAGCCGCTGCAAGTTCAGAC 180
DB 121 CATGTCATGGAAGACCTGCTGGCATCAAGTCTGAGCCGCTGCAAGTTCAGAC 180
QY 181 AGGAGCGCATGACCTTTTGGAGAGGCAAGAGATGAGATGAGGCAAGTTTGTAC 240
DB 181 AGGAGCGCATGACCTTTTGGAGAGGCAAGAGATGAGATGAGGCAAGTTTGTAC 240
QY 241 ATCTGCTGTGTATGAGCATCTGCGCGGACCTGTGCGCTGTGATGAGAGTGAAG 300
DB 241 ATCTGCTGTGTATGAGCATCTGCGCGGACCTGTGCGCTGTGATGAGAGTGAAG 300
QY 301 AGGAGCTCCCTGGAGAGAGCTGCTGGCTTGAAGCCATGAGATGAGGATTCGAGTTCGA 360
DB 301 AGGAGCTCCCTGGAGAGAGCTGCTGGCTTGAAGCCATGAGATGAGGATTCGAGTTCGA 360
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DB 361 ATCATCGACGAGACGCGGTGGGATGAATTCCTGCACTGCACTGAGGCGCGCATCTCTG 420
QY 421 CACCTGAGACTCAAGCCCGGACATCTCTGATGAGCCACTTACCACTCAAGATTC 480
DB 421 CACCTGAGACTCAAGCCCGGACATCTCTGATGAGCCACTTACCACTCAAGATTC 480
QY 481 GATTTTGTGCTGCAAGTGAAGAGAGGCTGCTGCACTGCACTGCACTGCACTGCACTG 540
DB 481 GATTTTGTGCTGCAAGTGAAGAGAGGCTGCTGCACTGCACTGCACTGCACTGCACTG 540
QY 541 CTGTTTGGACATCGCTTACCTCCCTCGAGAGCGCATGAGGAGAGAGCGGCTTTC 600
DB 541 CTGTTTGGACATCGCTTACCTCCCTCGAGAGCGCATGAGGAGAGAGCGGCTTTC 600
QY 601 GACCAAGACGAGATGATACAGCTTGGATGCTATCTGGGCGCTGCTCAACAGAG 660
DB 601 GACCAAGACGAGATGATACAGCTTGGATGCTATCTGGGCGCTGCTCAACAGAG 660
QY 661 AAGCGCTTGGAGATGAAGAGACATCTGCACTGCACTGCACTGCACTGCACTGCACTG 720
DB 661 AAGCGCTTGGAGATGAAGAGACATCTGCACTGCACTGCACTGCACTGCACTGCACTG 720
QY 721 CCGCCGAGCTGCGCGCTGTGCAAGGCGCGCGCGCGCTGCACTGCACTGCACTGCACTG 780
DB 721 CCGCCGAGCTGCGCGCTGTGCAAGGCGCGCGCGCGCTGCACTGCACTGCACTGCACTG 780
QY 781 CTGATGAGAGGCTGCGAGAGGAGATCCGAGATTAAGCCACTTCAAGAAATTAAT 840
DB 781 CTGATGAGAGGCTGCGAGAGGAGATCCGAGATTAAGCCACTTCAAGAAATTAAT 840
QY 841 TCTGAAGCGAGGACCTGTGTGAAGAGCTGATGAAGAGTGAAGAACTGCTCATGAT 900
DB 841 TCTGAAGCGAGGACCTGTGTGAAGAGCTGATGAAGAGTGAAGAACTGCTCATGAT 900

QY 901 CTGAGAGTGAAGAGCGCGGAGCGGAGAGAGAGTGTGCTGAGAGCTCAAGCGG 960
DB 901 CTGAGAGTGAAGAGCGCGGAGCGGAGAGAGAGTGTGCTGAGAGCTCAAGCGG 960
QY 961 GCTTCTGCGGACCTTGAATTAAGAGTCAAGCTTCTGAGCTTCTCAACAGTGAAC 1020
DB 961 GCTTCTGCGGACCTTGAATTAAGAGTCAAGCTTCTGAGAGCTTCTCAACAGTGAAC 1020
QY 1021 TCTGAGATTTTCCAGAGTGTGAGAGGCGCGGAGAGTCAAGGCTGCTGAGTTC 1080
DB 1021 TCTGAGATTTTCCAGAGTGTGAGAGGCGCGGAGAGTCAAGGCTGCTGAGTTC 1080
QY 1081 AAGCTGCAATGCTCGGAGAGTGAAGAGCTCTCGGAGGCTGCTGCTGAGCTCGGCG 1140
DB 1081 AAGCTGCAATGCTCGGAGAGTGAAGAGCTCTCGGAGGCTGCTGCTGAGCTCGGCG 1140
QY 1141 TTCTCTTCCAGAGATCACTGTGCTGCTTGAAGCGGAACTTCAACAGCGATCTG 1200
DB 1141 TTCTCTTCCAGAGATCACTGTGCTGCTTGAAGCGGAACTTCAACAGCGATCTG 1200
QY 1201 GGTACCAAGAGCTTCAAGAGAGAGCTTGTGATGCTTCTGCTGCTGCTGCTGCTG 1259
DB 1201 GGTACCAAGAGCTTCAAGAGAGAGCTTGTGATGCTTCTGCTGCTGCTGCTGCTG 1259
QY 1260 CAAATGATGAAGATCTGAGAGCGGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1319
DB 1260 CAAATGATGAAGATCTGAGAGCGGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1319
QY 1320 CCTGCTGCACTGCGGCTGAGAGCGGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1379
DB 1320 CCTGCTGCACTGCGGCTGAGAGCGGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1379
QY 1380 CAATGCCAACCTCAACTGAGCAACCTGAGGAGCTTCAACCTGCTGCTGCTGCTGCTG 1439
DB 1380 CAATGCCAACCTCAACTGAGCAACCTGAGGAGCTTCAACCTGCTGCTGCTGCTGCTG 1439
QY 1440 GAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1499
DB 1440 GAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1499
QY 1500 GATGAGAGACAGTGAAGAGCTTCACTTGAAGCGGCAAGAGTGAAGTGAAGTGAAG 1559
DB 1500 GATGAGAGACAGTGAAGAGCTTCACTTGAAGCGGCAAGAGTGAAGTGAAGTGAAG 1559
QY 1560 ACGGCTGTGTTGAAGAGAGAGCTGCTGCTGCAAGAGTGAAGTGAAGTGAAGTGAAG 1619
DB 1560 ACGGCTGTGTTGAAGAGAGAGCTGCTGCTGCAAGAGTGAAGTGAAGTGAAGTGAAG 1619
QY 1620 CATGCAAGTGTGCTGCGGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1679
DB 1620 CATGCAAGTGTGCTGCGGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1679
QY 1680 CBTGACAGTGTGCTGCGGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1739
DB 1680 CBTGACAGTGTGCTGCGGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1739
QY 1740 GGGCCACTGCGCAATCTCAAGCTGTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1799
DB 1740 GGGCCACTGCGCAATCTCAAGCTGTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1799
QY 1800 GACGCTGATGAG 1859
DB 1800 GACGCTGATGAG 1859
QY 1860 CCGCATCTTCAATGAG 1919
DB 1860 CCGCATCTTCAATGAG 1919
QY 1920 CCGCATCTTCAATGAG 1979
DB 1920 CCGCATCTTCAATGAG 1979

Db 1380 CAATGCCAACCCCACTGAGCAACCGTAAAGGGGCTCCACCCCGTTGACATGGCCGTGGA 1439
Qy 1440 GAGAGGGTGGGGGTGTCTGTGAGCTCTCTGCGACAGAAATCACTGTCAACGCCAA 1499
Db 1440 GAGAGGGTGGGGGTGTCTGTGAGCTCTCTGCGCGGGAAGATCACTGTCAACGCCAA 1499
Qy 1500 GAATGAGACCAATGAGACAGCCCTCCACTTTTGACGCCCAAGACGGGATGAGTCTAGAC 1559
Db 1500 GAATGAGACCAATGAGACAGCCCTCCACTTTTGACGCCCAAGACGGGATGAGTCTAGAC 1559
Qy 1560 ACGGCTGTGTGAGAGAAAGCGCTCGGTCAAGAGGTGACTTTGAGGGCCGAGCGCC 1619
Db 1560 ACGGCTGTGTGAGAGAAAGCGCTCGGTCAAGAGGTGACTTTGAGGGCCGAGCGCC 1619
Qy 1620 CATGACCTGGCTCTGCGACAGCGGACAGAAATATCGTGGCACTCTGCGCGAGG 1679
Db 1620 CATGACCTGGCTCTGCGACAGCGGACAGAAATATCGTGGCACTCTGCGCGAGG 1679
Qy 1680 CTGTGACCTGAGCTCTGCGAGGAGAGATCTGCTGCGCACTGACCTACCTGCTGGCA 1739
Db 1680 CTGTGACCTGAGCTCTGCGAGGAGAGATCTGCTGCGCACTGACCTACCTGCTGGCA 1739
Qy 1740 GGGGCACTGCGCCATCGTCAAGCTGCTGGCCAAGACGCGGGGAGTGTGAAGCGCCA 1799
Db 1740 GGGGCACTGCGCCATCGTCAAGCTGCTGGCCAAGACGCGGGGAGTGTGAAGCGCCA 1799
Qy 1800 GACGCTGATGAGAGAGAGCGCCATTGCACTGCGCGCAAGCGCGGCACTACCGGCTGGC 1859
Db 1800 GACGCTGATGAGAGAGAGCGCCATTGCACTGCGCGCAAGCGCGGCACTACCGGCTGGC 1859
Qy 1860 CCGCATCTCATGCACTGTGCTCGGAGCTCAACTCTGCAAGCTCTGCGCGCAAGCAACC 1919
Db 1860 CCGCATCTCATGCACTGTGCTCGGAGCTCAACTCTGCAAGCTCTGCGCGCAAGCAACC 1919
Qy 1920 CTGTGACCTGCGCGGAGAGAGCGGCGCAAGAGCACTGCGAGGCTCTGCGCACTGGAG 1979
Db 1920 CTGTGACCTGCGCGGAGAGAGCGGCGCAAGAGCACTGCGAGGCTCTGCGCACTGGAG 1979
Qy 1980 CGCTGCGAAGAGAGCGGCTGCACTGAGCGCTTACACCGCTCTGCACTGGCTGGCGCA 2039
Db 1980 CGCTGCGAAGAGAGCGGCTGCACTGAGCGCTTACACCGCTCTGCACTGGCTGGCGCA 2039
Qy 2040 CGGACACTGCGCACTGTCAAGCTGTCTGAGGAGAGCGGCACTGTGCTGCGCGGAG 2099
Db 2040 CGGACACTGCGCACTGTCAAGCTGTCTGAGGAGAGCGGCACTGTGCTGCGCGGAG 2099
Qy 2100 ACCCTTGAACCAAGAGCGGCTGCACTGCGCGCGCAAGCGGCACTGCGAGGTGTGA 2159
Db 2100 ACCCTTGAACCAAGAGCGGCTGCACTGCGCGCGCAAGCGGCACTGCGAGGTGTGA 2159
Qy 2160 GAGATTGATCAGCGCGGATGTATGACTGTTCAGAGAGAGGAGCTCAGGCGCTGCA 2219
Db 2160 GAGATTGATCAGCGCGGATGTATGACTGTTCAGAGAGAGGAGCTCAGGCGCTGCA 2219
Qy 2220 CTTGGCCGCGCGGCGCGGCGCAAGAGCGGTGAGACTCTGCTCAGGAGAGGCGCA 2279
Db 2220 CTTGGCCGCGCGGCGCGGCGCAAGAGCGGTGAGACTCTGCTCAGGAGAGGCGCA 2279
Qy 2280 CATCAACCTGAGAGCTTCAAGTTCAGGCGGCGCAAGGCGCGCGCACTCTGCG 2339
Db 2280 CATCAACCTGAGAGAGCTTCAAGTTCAGGCGGCGCAAGGCGCGCGCACTCTGCG 2339
Qy 2340 GCGAAGCAAGACTAG 2355
Db 2340 GCGAAGCAAGACTAG 2355

RESULT 13
US-10-128-174-17
; Sequence 17, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohiro
; TITLE OR INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: US-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-174-17
Query Match 98.7%; Score 2324; DB 16; Length 2355;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2349; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
Qy 1 ATGAGAGGCGACCGCGGAGCCCATGAGGCGCTGCGCTGCGCACTTGCAGCGCGGC 60
Db 1 ATGAGAGGCGACCGCGGAGCCCATGAGGCGCTGCGCTGCGCACTTGCAGCGCGGC 60
Qy 61 GAGTTCAAGGCTGAGAGAGTGGGCTCGGCGGCTTTCGAGAGTGTCAAGGTGCGC 120
Db 61 GAGTTCAAGGCTGAGAGAGTGGGCTCGGCGGCTTTCGAGAGTGTCAAGGTGCGC 120
Qy 121 CATGTCCATGAGAAAGCTTGGCTGCGCATCAAGTCTCGCCAGCCCTGCGCATGAGAGC 180
Db 121 CATGTCCATGAGAAAGCTTGGCTGCGCATCAAGTCTCGCCAGCCCTGCGCATGAGAGC 180
Qy 181 AGGAGGCGCATGAGCTTTTGAAGAGCAAGAGATGAGATGCGCAAGTTTCGCTAC 240
Db 181 AGGAGGCGCATGAGCTTTTGAAGAGCAAGAGATGAGATGCGCAAGTTTCGCTAC 240
Qy 241 ATCTGCTGTGTATGAGCATTCGCGGAACTGTGCGCTGTGTATGAGATCATGAG 300
Db 241 ATCTGCTGTGTATGAGCATTCGCGGAACTGTGCGCTGTGTATGAGATCATGAG 300
Qy 301 ACGGCTCTCTGAGAAAGCTGCTGGAGGCACTTGCATGAGAGATCTCGGTTCCGA 360
Db 301 ACGGCTCTCTGAGAAAGCTGCTGGAGGCACTTGCATGAGAGATCTCGGTTCCGA 360
Qy 361 ATCATCCAGAGAGCGGCGTGGCATGAACTTCTGTGACATGAGGCGCCGCACTCTG 420
Db 361 ATCATCCAGAGAGCGGCGTGGCATGAACTTCTGTGACATGAGGCGCCGCACTCTG 420
Qy 421 CACCTGGAAGCTCAAGCCCGGAAATCTGCTGAGTCCCATACAGTCAAGATTTCT 480
Db 421 CACCTGGAAGCTCAAGCCCGGAAATCTGCTGAGTCCCATACAGTCAAGATTTCT 480
Qy 481 GATTTTGTGTGCGCAAGTGAAGAGAGGCTGTCCCATCTGCACTGAGATGAGTGGC 540
Db 481 GATTTTGTGTGCGCAAGTGAAGAGAGGCTGTCCCATCTGCACTGAGATGAGTGGC 540
Qy 541 CTGTTTGGCAATTCGCTTACCTCTCCAGAGGCGCATCAGGAGAGAGCGGCTCTTC 600
Db 541 CTGTTTGGCAATTCGCTTACCTCTCCAGAGGCGCATCAGGAGAGAGCGGCTCTTC 600
Qy 601 GACACCAAGCAGATGATTAAGCTTTGCAATCTGCACTCATGTGAGAGTGTGAAGGCGAC 720
Db 601 GACACCAAGCAGATGATTAAGCTTTGCAATCTGCACTCATGTGAGAGTGTGAAGGCGAC 720
Qy 661 AAGCGTTTGAAGATGAGAGAAATCATCTGCACTCATGTGAGAGTGTGAAGGCGAC 780
Db 661 AAGCGTTTGAAGATGAGAGAAATCATCTGCACTCATGTGAGAGTGTGAAGGCGAC 780
Qy 721 GCGCCGAGCTGCGCGCGTGTGAGAGCGCGCGCGGCTGCGCACTGATAGC 780
Db 721 GCGCCGAGCTGCGCGCGTGTGAGAGCGCGCGCGGCTGCGCACTGATAGC 780
Qy 781 CTGATGAGCGGTCTGCGAGAGGAGATCCGAGTGTAGGCCCATCTTCAAGAAATTA 840
Db 781 CTGATGAGCGGTCTGCGAGAGGAGATCCGAGTGTAGGCCCATCTTCAAGAAATTA 840

QY	841	1CTGAAACCGAGAGACTGTGTGAAAAAGCTTGATGACGAATGAAAAAATCTGTCTAT	900
Db	841	1CTGAAACCGAGAGACTGTGTGAAAAAGCTTGATGACGAATGAAAAAATCTGTCTAT	900
QY	901	CTGGACGTGAAAAAGCCCCCGAGAGCCGAGAGCGAGGTGTGTCCGACAGGCTCAAGCGG	960
Db	901	CTGGACGTGAAAAAGCCCCCGAGAGCCGAGAGCGAGGTGTGTCCGACAGGCTCAAGCGG	960
QY	961	GCCCTTCGCCCCCACTTTGATTAACAAGCTTCCGAGCTTCTCAACAGCTGGAC	1020
Db	961	GCCCTTCGCCCCCACTTTGATTAACAAGCTTCCGAGCTTCTCAACAGCTGGAC	1020
QY	1021	1CTGGAAGTTTCCCAAGGCTGTGAGGGCCCCGAGAGCTCAGCCGAGCTCCTTGAATCC	1080
Db	1021	1CTGGAAGTTTCCCAAGGCTGTGAGGGCCCCGAGAGCTCAGCCGAGCTCCTTGAATCC	1080
QY	1081	1AAGCTGCCATCGTCCGGGACGTGGAGAGAGGCTCTGGGGGGTGTCTCGGTGGAATCCGCG	1140
Db	1081	1AAGCTGCCATCGTCCGGGACGTGGAGAGAGGCTCTGGGGGGTGTCTCGGTGGAATCCGCG	1140
QY	1141	1TTCTCTTCCAGAGATCACTGTGCTGTCTTTGACCGGAAACCTTCAACAGCGATCTG	1200
Db	1141	1TTCTCTTCCAGAGATCACTGTGCTGTCTTTGACCGGAAACCTTCAACAGCGATCTG	1200
QY	1201	1GGTACCAACAAGCTCTCGAAGAGAGACTTGTGATGCACTCGTGTCC-GGACACAG	1255
Db	1201	1GGACACAC-AGA-CGTCCAGAAAGAAACCTTGTGATGCACTCGTGTCCGGGGACACAG	1255
QY	1260	1CAAATGATGAAGATCTTGAGCCGACAGAGCGTGGACCTGGACACTGGACACCGGTGCAG	1315
Db	1260	1CAAATGATGAAGATCTTGAGCCGACAGAGCGTGGACCTGGACACTGGACACGGGTGCAG	1315
QY	1320	1CTGTCTGACCTGGCGGTGTGAGAGCCGGGCAAGAGAGTGCACAAGTGGCTGTCAA	1375
Db	1320	1CTGTCTGACCTGGCGGTGTGAGAGCCGGGCAAGAGAGTGCACAAGTGGCTGTCAA	1375
QY	1380	1CAATGCCAACCCCAACTGAGCAACCTGATGGGGCTCAACCCGTTGTGCAATGGCCGTGGA	1435
Db	1380	1CAATGCCAACCCCAACTGAGCAACCTGATGGGGCTCAACCCGTTGTGCAATGGCCGTGGA	1435
QY	1440	1GAGGAGGGTGGGGGTGTGCTGTGAGCTCTGCTGGACGAGAAAGTCAATGTCAACGCCAA	1495
Db	1440	1GAGGAGGGTGGGGGTGTGCTGTGAGCTCTGCTGGACGAGAAAGTCAATGTCAACGCCAA	1495
QY	1500	1GGATGAGACCAAGTGGACAGCCCTTCACTTTTGACGCCACGAACGGGGATGAGTCTAGAC	1555
Db	1500	1GGATGAGACCAAGTGGACAGCCCTTCACTTTTGACGCCACGAACGGGGACAGTCTAGAC	1555
QY	1560	1ACGGCTGCTGTGGAGAGAAAGCCCTCGGTCAACGAGGTGCACTTTGAGGGCCGGACGC	1615
Db	1560	1ACGGCTGCTGTGGAGAGAAAGCCCTCGGTCAACGAGGTGCACTTTGAGGGCCGGACGC	1615
QY	1620	1CATGACGTGGCCCTGGCAGCAACGGCAGAGAAATATCGTGGCAATCTGTGTGCGCGAGG	1675
Db	1620	1CATGACGTGGCCCTGGCAGCAACGGCAGAGAAATATCGTGGCAATCTGTGTGCGCGAGG	1675
QY	1680	1CGTGAACGTGAGCCTGCAAGGGCAAGAGTCCCTGGCTGCACTGCATACGCTGCTGGCA	1735
Db	1680	1CGTGAACGTGAGCCTGCAAGGGCAAGAGTCCCTGGCTGCACTGCATACGCTGCTGGCA	1735
QY	1740	1GGGCAACCTGACCATGTCAAGACTGTGGCCAAAGCAAGCCGGGGGTGAGTGTGAACGCCCA	1795
Db	1740	1GGGCAACCTGACCATGTCAAGACTGTGGCCAAAGCAAGCCGGGGGTGAGTGTGAACGCCCA	1795
QY	1800	1GACGCTGGAATGGGAGAGAGCCATTGCACTGTGGCCGACAGGCCGGGCACTACCGGTGGC	1855
Db	1800	1GACGCTGGAATGGGAGAGAGCCATTGCACTGTGGCCGACAGGCCGGGCACTACCGGTGGC	1855
QY	1860	1CGGATCCTCAATCAACCTGTGTCCGAGGTCAAGCTTGCAAGCCGCTGGAGCAAGACCC	1915
Db	1860	1CGGATCCTCAATCAACCTGTGTCCGAGGTCAAGCTTGCAAGCCGCTGGAGCAAGACCC	1915
QY	1920	1CTGACCTGTGGCCGCGAGAGACGGGGCAACGAGCACTGACAGGCTTCTGTCAATCGGG	1975

QY	DB	Sequence	Score	DB	Length	Indels	Gaps
QY	1980	CGCTGGCAAGAGGCGCTGTA	98.7%	2324	2355	5	2
DB	1980	CGCTGGCAAGAGGCGCTGTA	99.7%	2324	2355	5	2
QY	2040	CGGACACCTGGGCACTGTCA	98.7%	2324	2355	5	2
DB	2040	CGGACACCTGGGCACTGTCA	99.7%	2324	2355	5	2
QY	2100	ACCCCTGAAACGAGGCGCTG	98.7%	2324	2355	5	2
DB	2100	ACCCCTGAAACGAGGCGCTG	99.7%	2324	2355	5	2
QY	2160	GGAGTGGTCAAGCGCGCAT	98.7%	2324	2355	5	2
DB	2160	GGAGTGGTCAAGCGCGCAT	99.7%	2324	2355	5	2
QY	2220	CCTGGCGGCCCAAGGCGCA	98.7%	2324	2355	5	2
DB	2220	CCTGGCGGCCCAAGGCGCA	99.7%	2324	2355	5	2
QY	2280	CATCAACCTGCAGAGCTCA	98.7%	2324	2355	5	2
DB	2280	CATCAACCTGCAGAGCTCA	99.7%	2324	2355	5	2
QY	2340	GGGAGCAAGACCTAG	98.7%	2324	2355	5	2
DB	2340	GGGAGCAAGACCTAG	99.7%	2324	2355	5	2

Db 241 ATCTGCTGTGTATGAGCATCTGCGGAAACCTGTCCGCTGTGATGAGTACATGAG 300
Qy 301 ACGGGCTCTCTGAAAAAGCTCTGAGCTTCCGAGCCATTGCGATCTCCGGTCCGA 360
Db 301 ACGGGCTCTCTGAAAAAGCTCTGAGCTTCCGAGCCATTGCGATCTCCGGTCCGA 360
Qy 361 ATCATCCAGGAGCGGCGGTGGGATGAACTTCCGTGACCTGCAATGAGCCCGGCACTCTG 420
Db 361 ATCATCCAGGAGCGGCGGTGGGATGAACTTCCGTGACCTGCAATGAGCCCGGCACTCTG 420
Qy 421 CACCTGACCTCAAGCCCGGAAACATCTGTGATGCGCCACTACAGTCAAGATTCT 480
Db 421 CACCTGACCTCAAGCCCGGAAACATCTGTGATGCGCCACTACAGTCAAGATTCT 480
Qy 481 GATTTTGTGTGCGCAAGTGCAAGGCGGTGTCCACTGCAATGAACTTCAGATGATGCG 540
Db 481 GATTTTGTGTGCGCAAGTGCAAGGCGGTGTCCACTGCAATGAACTTCAGATGATGCG 540
Qy 541 CTGTTTGGCAAAATCGCTTACCTCTCCAGAGCGCAATCAAGGAGAAAGCGGCTCTTC 600
Db 541 CTGTTTGGCAAAATCGCTTACCTCTCCAGAGCGCAATCAAGGAGAAAGCGGCTCTTC 600
Qy 601 GACACCAAGCAAGATGTATACAGCTTTCGATCGATCTGAGGCGTGTCAACAAGAG 660
Db 601 GACACCAAGCAAGATGTATACAGCTTTCGATCGATCTGAGGCGTGTCAACAAGAG 660
Qy 661 AAGCGTTTGGAGATGAGAAAGAACTCTGCAATCATGTGTGAAGGTGAGAGGCGAC 720
Db 661 AAGCGTTTGGAGATGAGAAAGAACTCTGCAATCATGTGTGAAGGTGAGAGGCGAC 720
Qy 721 CGCCCCGAGCTGCGCCCTGTGTGCAAGCCCGGCGCGGCTGTGAGCACTGTATAGC 780
Db 721 CGCCCCGAGCTGCGCCCTGTGTGCAAGCCCGGCGCGGCTGTGAGCACTGTATAGC 780
Qy 781 CTCAATGACGCGGTGTGCAAGGAGGAGTCCGCGAGTTAGGCGCACTTCCAGAAATTACT 840
Db 781 CTCAATGACGCGGTGTGCAAGGAGGAGTCCGCGAGTTAGGCGCACTTCCAGAAATTACT 840
Qy 841 TCTGAACCGAGAGACTGTGTGAAAAAGCTGTGAAGAGTGAAGAAAGAACTGTCTATGAT 900
Db 841 TCTGAACCGAGAGACTGTGTGAAAAAGCTGTGAAGAGTGAAGAAAGAACTGTCTATGAT 900
Qy 901 CTGGAATGTGAAAAAGCCCCCGAGGCCAGAGCGAGGTGTGCTGTGCAAGGCTCAAGCGG 960
Db 901 CTGGAATGTGAAAAAGCCCCCGAGGCCAGAGCGAGGTGTGCTGTGCAAGGCTCAAGCGG 960
Qy 961 GCGCTGTGCCCCCACTTGTGATGATACGATCAAGGCTCTCCAGGCTTCTCTCAAGCTGAGC 1020
Db 961 GCGCTGTGCCCCCACTTGTGATGATACGATCAAGGCTCTCCAGGCTTCTCTCAAGCTGAGC 1020
Qy 1021 TCTGAGTTTCCCAAGGCTGTGAGGAGCCCGAGAGACTCAAGCCGAGCTCTCTGAGTCC 1080
Db 1021 TCTGAGTTTCCCAAGGCTGTGAGGAGCCCGAGAGACTCAAGCCGAGCTCTCTGAGTCC 1080
Qy 1081 AAGCTGCAATGTCTCGGAGTGGGAAAGGCTCTCTCGGAGGTGTCTCTGAGTCACTCCGC 1140
Db 1081 AAGCTGCAATGTCTCGGAGTGGGAAAGGCTCTCTCGGAGGTGTCTCTGAGTCACTCCGC 1140
Qy 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTGTGAGCGGAGAACTTTCACACGCAATCTG 1200
Db 1141 TTCTCTTCCAGAGATCACTGTGCTGTCTTGTGAGCGGAGAACTTTCACACGCAATCTG 1200
Qy 1201 GGTACCAAGAAGCTTCAAGAAAGAAAGCTTGTGATGCAATGTGTCC-GGAGACAG 1259
Db 1201 GGTACCAAGAAGCTTCAAGAAAGAAAGCTTGTGATGCAATGTGTCC-GGAGACAG 1259
Qy 1260 CAAATCTGATGAAGATCTTCAAGCCGAGAGCTGTGACCTGTGAGCAAGGAGTCCAG 1319
Db 1260 CAAATCTGATGAAGATCTTCAAGCCGAGAGCTGTGACCTGTGAGCAAGGAGTCCAG 1319
Qy 1320 CTTGTGCACTGTGGCGGTGAGAGCGGCGCAAGAGAGTGCAGATGAGCTGTCTCA 1379
Db 1320 CTTGTGCACTGTGGCGGTGAGAGCGGCGCAAGAGAGTGCAGATGAGCTGTCTCA 1379

Qy 1380 CAATGCCAACCCGAACCTGAGCAACCGTAGGGCTCCACCCGTTGCAATGAGCCGTGGA 1439
Db 1380 CAATGCCAACCCGAACCTGAGCAACCGTAGGGCTCCACCCGTTGCAATGAGCCGTGGA 1439
Qy 1440 GAGAGGGGTGCGGGGTGTCTGTGAGCTCTGTGCGAGAGATCATGTGTCAACGCCAA 1499
Db 1440 GAGAGGGGTGCGGGGTGTCTGTGAGCTCTGTGCGAGAGATCATGTGTCAACGCCAA 1499
Qy 1500 GATGAGGAGCAATGAGCAAGCCCTTCCACTTTGCAAGCCCAAGCGGAGATGAGTATGAC 1559
Db 1500 GATGAGGAGCAATGAGCAAGCCCTTCCACTTTGCAAGCCCAAGCGGAGATGAGTATGAC 1559
Qy 1560 ACGGCTGTGTGAGAGAAAGCGCTGTGCAAGAGTGAAGCTTTGAGAGGCGGAGGCC 1619
Db 1560 ACGGCTGTGTGAGAGAAAGCGCTGTGCAAGAGTGAAGCTTTGAGAGGCGGAGGCC 1619
Qy 1620 CATGCACTGTGAGCTGCGAGCAAGGAGAGAAATATGTGCGCATCTGTGCGCGAGG 1679
Db 1620 CATGCACTGTGAGCTGCGAGCAAGGAGAGAAATATGTGCGCATCTGTGCGCGAGG 1679
Qy 1680 CGTGAAGTGAAGCTGTGAGGAGAGAGATGCTGTGCGCACTGCACTTACGCTGTGGA 1739
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Qy 1740 GGGCGAAGCTGCGCAATGTCAAGGCTGTGCGCAAGAGCGGAGGTGAGTGAAGCGCCA 1799
Db 1740 GGGCGAAGCTGCGCAATGTCAAGGCTGTGCGCAAGAGCGGAGGTGAGTGAAGCGCCA 1799
Qy 1800 GACGCTGATGAGGAGAGAGCGCAATGCACTGTGCGCAAGAGCGGAGCTTACCGGTGAGC 1859
Db 1800 GACGCTGATGAGGAGAGAGCGCAATGCACTGTGCGCAAGAGCGGAGCTTACCGGTGAGC 1859
Qy 1860 CCGCATCTCATGCACTGTGTCTCCAGCTTGAAGCTGTGCAAGCTGTGCGCAAGAGACC 1919
Db 1860 CCGCATCTCATGCACTGTGTCTCCAGCTTGAAGCTGTGCAAGCTGTGCGCAAGAGACC 1919
Qy 1920 CTTGCAAGTGTGCGGAGAGCGGAGGACAGAGACATGCGAGGCTGCTCTGCAATCGGAG 1979
Db 1920 CTTGCAAGTGTGCGGAGAGCGGAGGACAGAGACATGCGAGGCTGCTCTGCAATCGGAG 1979
Qy 1980 CGCTGAGAGAGAGCGCTGTGACCTTCAAGCGCTTACACCGCTGTGCACTGTGCGTCCGCA 2039
Db 1980 CGCTGAGAGAGAGCGCTGTGACCTTCAAGCGCTTACACCGCTGTGCACTGTGCGTCCGCA 2039
Qy 2040 CGAGCACTGTGCACTGTCAAGCTGTCTTGTGAGAGAGAGCGGATGTGCTGTGCGCGG 2099
Db 2040 CGAGCACTGTGCACTGTCAAGCTGTCTTGTGAGAGAGAGCGGATGTGCTGTGCGCGG 2099
Qy 2100 ACCCTTGAACCAAGCGGCGCTGCACTGTGCGCGCGCAAGGAGCTCGAGAGGTGTGGA 2159
Db 2100 ACCCTTGAACCAAGCGGCGCTGCACTGTGCGCGCGCAAGGAGCTCGAGAGGTGTGGA 2159
Qy 2160 GGAATGTGTGAGCGCCGATGTCAATTTGACTGTGTGAGAGAGAGAGGCTCAAGCGGCTGCA 2219
Db 2160 GGAATGTGTGAGCGCCGATGTCAATTTGACTGTGTGAGAGAGAGAGGCTCAAGCGGCTGCA 2219
Qy 2220 CTTGAGCGCGCCAGGAGCGGAGCGCAAGAGCGGTGAGACTTGTCTCAAGGATGAGGCCA 2279
Db 2220 CTTGAGCGCGCCAGGAGCGGAGCGCAAGAGCGGTGAGACTTGTCTCAAGGATGAGGCCA 2279
Qy 2280 CATCAACTGTGAGAGCTTCAAGTTTCCAGGAGCGGCAAGGCGCGCGCACTTCTGTG 2339
Db 2280 CATCAACTGTGAGAGCTTCAAGTTTCCAGGAGCGGCAAGGCGCGCGCACTTCTGTG 2339
Qy 2340 GCGAAGCAAGACTAG 2355
Db 2340 GCGAAGCAAGACTAG 2355

RESULT 15
US-10-128-174-21
; Sequence 21, Application US/10128174

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Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UN-06967
CURRENT APPLICATION NUMBER: US/10/128,174
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 2355
TYPE: DNA
ORGANISM: Homo sapiens
US-10-128-174-21

Query Match      98.7%; Score 2324; DB 16; Length 2355;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2349; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
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QY 1 ATGAGGGCGACGGCGGACCCCATGGCCCTGGCGCTGCTGCCACCTTGCAGCGGGC 60
DB 1 ATGAGGGCGACGGCGGACCCCATGGCCCTGGCGCTGCTGCCACCTTGCAGCGGGC 60
QY 61 GAGTTCA CGGGCTGGAGAAAGTGGGCTCGGGCGGCTTGGGGCAGGTGTACAAAGTGGC 120
DB 61 GAGTTCA CGGGCTGGAGAAAGTGGGCTCGGGCGGCTTGGGGCAGGTGTACAAAGTGGC 120
QY 121 CATGTCCA CTGGAAGACCTGGCTGGCCATCAAGTGTCTGCCAGCCTTGCAGCGAC 180
DB 121 CATGTCCA CTGGAAGACCTGGCTGGCCATCAAGTGTCTGCCAGCCTTGCAGCGAC 180
QY 181 AGGGAAGCGCATGGAGCTTTTGGAGAAAGCCAAAGAAAGTGAAGTGGCCAAAGTTTGGCTAC 240
DB 181 AGGGAAGCGCATGGAGCTTTTGGAGAAAGCCAAAGAAAGTGAAGTGGCCAAAGTTTGGCTAC 240
QY 241 ATCTGCTGTGTATGTGCATCTGCCGCGAACCTGTGGCCCTGTGCATAGAGTACATGAGAG 300
DB 241 ATCTGCTGTGTATGTGCATCTGCCGCGAACCTGTGGCCCTGTGCATAGAGTACATGAGAG 300
QY 301 ACGGGCTCTCCCTGGAAGAAAGCTGCTGGCTTGGAGCCATTTGCCATGTCTCGGTTCCGA 360
DB 301 ACGGGCTCTCCCTGGAAGAAAGCTGCTGGCTTGGAGCCATTTGCCATGTCTCGGTTCCGA 360
QY 361 ATCATCCACGAGACGGCGGTGGGSCATGAATTCCTGCACCTGCATAGGCCCGGCCACTCTCG 420
DB 361 ATCATCCACGAGACGGCGGTGGGSCATGAATTCCTGCACCTGCATAGGCCCGGCCACTCTCG 420
QY 421 CACCTGGA CTCAAGCCCGCGAACATCTGTGATGATGCCACTACAGCTCAAGATTTCT 480
DB 421 CACCTGGA CTCAAGCCCGCGAACATCTGTGATGATGCCACTACAGCTCAAGATTTCT 480
QY 481 GATTTTGTCTGGCCAAAGTGCACGGGCTGTCCCATCTGCATGACCTTCAGCATGAGATGGC 540
DB 481 GATTTTGTCTGGCCAAAGTGCACGGGCTGTCCCATCTGCATGACCTTCAGCATGAGATGGC 540
QY 541 CTGTTTGGCAAAATCGCTACCTCCCTCAGAGGCGCATCAAGAGAAAGCGGCTCTTC 600
DB 541 CTGTTTGGCAAAATCGCTACCTCCCTCAGAGGCGCATCAAGAGAAAGCGGCTCTTC 600
QY 601 GACACCAAGCAGATGTATACAGCTTTTGCATCTGATCTGAGGGGTGTGCACACAGAG 660
DB 601 GACACCAAGCAGATGTATACAGCTTTTGCATCTGATCTGAGGGGTGTGCACACAGAG 660
QY 661 AAGCGTTTGCAGATGAGAAAGACATCTTGCACATCATGTGAAAGTGTGAAGGGCCAC 720
DB 661 AAGCGTTTGCAGATGAGAAAGACATCTTGCACATCATGTGAAAGTGTGAAGGGCCAC 720
QY 721 CGCCCCGAGCTGGCGCGGTGTGGAGAGCCGGCGCGGCGCTGAGGCACTGATACG 780
DB 721 CGCCCCGAGCTGGCGCGGTGTGGAGAGCCGGCGCGGCGCTGAGGCACTGATACG 780
QY 781 CTCATGCAAGCGGTGTGGCAAGGGGAGTCGGCAATTAGGCCCACTTTCAGAAATTACT 840

DB 781 CTCATGCAAGCGGTGTGGCAAGGGGAGATCCGGCAATTAGGCCCACTTTCAGAAATTACT 840
QY 841 TCTGAAACCGAGGACCTGTGTGTGAAAAGCCTGATGACGAAGTGAAGAAATGCTCTATGAT 900
DB 841 TCTGAAACCGAGGACCTGTGTGTGAAAAGCCTGATGACGAAGTGAAGAAATGCTCTATGAT 900
QY 901 CTGAGGTGAAAAGCCCGCGAGCCGAGAGCGAGGTGTGCTGAGAGCTCAAGCGG 960
DB 901 CTGAGGTGAAAAGCCCGCGAGCCGAGAGCGAGGTGTGCTGAGAGCTCAAGCGG 960
QY 961 GCCTTGGCCCCCACTTTCATTAACGATACAGGCTTCTCGAGCTTCTCAAGCTTGGAC 1020
DB 961 GCCTTGGCCCCCACTTTCATTAACGATACAGGCTTCTCGAGCTTCTCAAGCTTGGAC 1020
QY 1021 TCTGAGATTTCCAGAGCTGTGAGGGCCCGAGAGACTCAGCCGAGCTCTGAGTCC 1080
DB 1021 TCTGAGATTTCCAGAGCTGTGAGGGCCCGAGAGACTCAGCCGAGCTCTGAGTCC 1080
QY 1081 AAGCTGCATCGATCCGGCAGTGGGAAAGAGGCTCTCGGGGGTGTCTCGGTGACTCGGC 1140
DB 1081 AAGCTGCATCGATCCGGCAGTGGGAAAGAGGCTCTCGGGGGTGTCTCGGTGACTCGGC 1140
QY 1141 TTCTTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAACCTTTCACACGATCTG 1200
DB 1141 TTCTTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAACCTTTCACACGATCTG 1200
QY 1201 GGTACCAAGAGATCCAGAGAAAGAAAGCTTGTGATGCCATGTGTTC -GGGACACGAG 1259
DB 1201 GGTACCAAGAGATCCAGAGAAAGAAAGCTTGTGATGCCATGTGTTC -GGGACACGAG 1259
QY 1260 CAAATGATGAATCCTGACGCGCAGAGAGCTTGGCACTGGCACTGGACAGCGGTGCA 1319
DB 1260 CAAATGATGAATCCTGACGCGCAGAGAGCTTGGCACTGGCACTGGACAGCGGTGCA 1319
QY 1320 CTGTGTGCACCTGCGGTGAGAGCCCGGCAAGAGAGTGGCCCAAGTGTCTGCTCAA 1379
DB 1320 CTGTGTGCACCTGCGGTGAGAGCCCGGCAAGAGAGTGGCCCAAGTGTCTGCTCAA 1379
QY 1380 CAATGCAACCCCAACCTGAGCAACGTTAGGGGCTCAACCCGTTGCACTAGGCGTGA 1439
DB 1380 CAATGCAACCCCAACCTGAGCAACGTTAGGGGCTCAACCCGTTGCACTAGGCGTGA 1439
QY 1440 GAGGAGGGTGCGGGGTGTCTGTGAGGCTCTGTGAGCAGAGAGATCATGTCAACGCGCA 1499
DB 1440 GAGGAGGGTGCGGGGTGTCTGTGAGGCTCTGTGAGCAGAGAGATCATGTCAACGCGCA 1499
QY 1500 GATGAGGACCAAGTGAACAGCCCTTCCACTTTGCAAGCCAGAACGGGATGATCTAGCAC 1559
DB 1500 GATGAGGACCAAGTGAACAGCCCTTCCACTTTGCAAGCCAGAACGGGATGATCTAGCAC 1559
QY 1560 ACGGCTGCTTGTGAGAAAGAACGCTTCGATCAACGAGTGAATTTGAGGGCGGAGCGCC 1619
DB 1560 ACGGCTGCTTGTGAGAAAGAACGCTTCGATCAACGAGTGAATTTGAGGGCGGAGCGCC 1619
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DB 1620 CATGCAAGTGGCTTGCAGAGACGGGCAAGAGATATGTGTGCACTCTGCGCGAGG 1679
QY 1680 CGTGAGCTGAGCCTGCAAGGCAAGATGCTGTGCTGCACTGCACTACCTGTGCGCA 1739
DB 1680 CGTGAGCTGAGCCTGCAAGGCAAGATGCTGTGCTGCACTGCACTACCTGTGCGCA 1739
QY 1740 GGGGCACTTGGCCCATGTGTCAAGGCTGTGAGCAAGGCGGGGGTGTGTAAGCGCCA 1799
DB 1740 GGGGCACTTGGCCCATGTGTCAAGGCTGTGAGCAAGGCGGGGGTGTGTAAGCGCCA 1799
QY 1800 GACGCTGATGAGGAGAGAGCGCATTTGCACTTGGCGGCAACAGCGGGCACTACCGCGTGGC 1859
DB 1800 GACGCTGATGAGGAGAGAGCGCATTTGCACTTGGCGGCAACAGCGGGCACTACCGCGTGGC 1859
QY 1860 CCGCATCTCATGACCTGTGTCTCCAGCTCAAGCTTGTGAGGCTGTGGCAAGACACC 1919

Db	1860	CCGCATCCTCATCGA	CTGTGTCCGAGCTCA	ACGTCTGACAGCTG	GGCAGACAC	1919
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Db	1920	CCTGCACTGGCCCGG	AGACGGGGCACA	CGACACTGCCAGCTG	CTCTTGCA	1979
QY	1980	CGCTGGCAAGAGCCCTG	AGCTTCAAGAGGCTA	CAACCGCTGCACTG	GGCCCGCA	2039
Db	1980	CGCTGGCAAGAGCCCTG	AGCTTCAAGAGGCTA	CAACCGCTGCACTG	GGCCCGCA	2039
QY	2040	CGGACACCTGGCCACTG	TCAAGCTGCTTGTCA	GAGAGGCGGATGTG	CTGACC	2099
Db	2040	CGGACACCTGGCCACTG	TCAAGCTGCTTGTCA	GAGAGGCGGATGTG	CTGACC	2099
QY	2100	ACCCCTGAACGAGACGGG	CGCTGACCTGCGCCCA	CGGGCACTCGAAGTGTGA		2159
Db	2100	ACCCCTGAACGAGACGGG	CGCTGACCTGCGCCCA	CGGGCACTCGAAGTGTGA		2159
QY	2160	GAGCTTGGTCAAGCGCCG	ATGTCATTGACCTG	TTCAGACGAGCGGGCT	CAAGCGCTGCA	2219
Db	2160	GAGCTTGGTCAAGCGCCG	ATGTCATTGACCTG	TTCAGACGAGCGGGCT	CAAGCGCTGCA	2219
QY	2220	CCTGGCCGCCAGGCGCGG	CAAGCAAGACGGTGA	GACTGTCAAGSCATG	GGGCCCA	2279
Db	2220	CCTGGCCGCCAGGCGCGG	CAAGCAAGACGGTGA	GACTGTCAAGSCATG	GGGCCCA	2279
QY	2280	CATCAACCTGCAAGACCT	CAAGTTCCAGGGCGGCAT	GGCCCCCGCCACA	CTCTTGG	2339
Db	2280	CATCAACCTGCAAGACCT	CAAGTTCCAGGGCGGCAT	GGCCCCCGCCACA	CTCTTGG	2339
QY	2340	GCGAAGCAAGACTT	AG	2355		
Db	2340	GCGAAGCAAGACTT	AG	2355		

Search completed: September 17, 2005, 02:19:15
Job time : 5370.39 secs

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Db      |||||
421  CACCTGGACCTCAAGCCCGGCAACATCTGTGATGAGCCCACTACCAAGTCAAGATTTCT 480
Qy      |||||
481  GATTTTGGTCTGGGCAATGACAGGGGTGTCCCACTGTGATGACCTTCAGATGAGATGAGC 540
Db      |||||
481  GATTTTGGTCTGGGCAATGACAGGGGTGTCCCACTGTGATGACCTTCAGATGAGATGAGC 540
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601  GACACCAAGCAGATGATATACAGCTTTGCGATTCGTATCTTGAGGCGGTGCTACACAGAG 660
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601  GACACCAAGCAGATGATATACAGCTTTGCGATTCGTATCTTGAGGCGGTGCTACACAGAG 660
Qy      |||||
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661  AAGCGCTTGGCAGATGAGAAAGAACATCTGCAATCATATGATGAGATGATGAGAGGCGAC 720
Qy      |||||
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Db      |||||
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Db      |||||
781  CTATGACAGCGGTGTGAGAGGAGATCCGAGATGAGGCCACCTTCAAGAAATTAATCT 840
Qy      |||||
841  TCTGAAACCGAGAGCCTGTGTGAAAGAGCTGATGACGAATGAAAGAAACGTCTCATGAT 900
Db      |||||
841  TCTGAAACCGAGAGCCTGTGTGAAAGAGCTGATGACGAATGAAAGAAACGTCTCATGAT 900
Qy      |||||
901  CTGAGCGTGAAGAACCCCGCGAGCCAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
Db      |||||
901  CTGAGCGTGAAGAACCCCGCGAGCCAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
Qy      |||||
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961  GCGCTGTGCGCCACCTTGTGATTAAGCATACAGCCTCTCCGAGCTTCTCTCAACAGCTGAC 1020
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Db      |||||
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Qy      |||||
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1681  GTGAGCGTGAAGCTGTGAGGGGCAAGATGCTGTGCTGCACTGCACTACGCTGCTGGCAG 1740
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1741  GGCACCTGCGCCATTCGTCAAGCTGTGAGGCAAGAGCGGGGATGATGAAAGCGCCAG 1800
Qy      |||||
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Db      |||||
1801  ACGCTGATGAGAGAGAGCCATTGCACTTGGCCGCAAGCGCGGCACTACCGGTGGCC 1860
Qy      |||||
1861  CGCATCTTCAATCGAATCTGTGTCTCGAAGTCAAGTCTGAGAGCTGTGTGAGCAAGACCC 1920
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Qy      |||||
1921  CTGCAAGTGTGCGCGAGAGACGGGGCAACAAGAGACTTGCAGGCTGTCTGCAATCGGAGG 1980
Db      |||||
1921  CTGCAAGTGTGCGCGAGAGACGGGGCAACAAGAGACTTGCAGGCTGTCTGCAATCGGAGG 1980
Qy      |||||
1981  GCTGTGAGAGAGGCGGTGACCTTGAACGAGCTACACGCTGTGCACTGTGCTGCGCAAC 2040
Db      |||||
1981  GCTGTGAGAGAGGCGGTGACCTTGAACGAGCTACACGCTGTGCACTGTGCTGCGCAAC 2040
Qy      |||||
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Db      |||||
2041  GAGACCTGTGCGCACTGTCAAGCTGTGTGTGAGAGAGAGGCGATGTGTCTGCGCGGAGA 2100
Qy      |||||
2101  CCCCTGAACAGAGCGGCGCTGCACTGTGCTGCGGCCAAGGCACTGTGAGGTGTGTAGAG 2160
Db      |||||
2101  CCCCTGAACAGAGCGGCGCTGCACTGTGCTGCGGCCAAGGCACTGTGAGGTGTGTAGAG 2160
Qy      |||||
2161  GAGTTGTGACGCGCCGATGTCAATTGAATCTGTGTGACGAGCAAGGAGGCTCAAGCGGCTGAC 2220
Db      |||||
2161  GAGTTGTGACGCGCCGATGTCAATTGAATCTGTGTGACGAGCAAGGAGGCTCAAGCGGCTGAC 2220
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2221  CTGCGCGCCCAAGGCGCGGCAAGCAAGAGCTGTGATGAGTGTCTCAAGGCAATGGGCGCCAC 2280
Db      |||||
2221  CTGCGCGCCCAAGGCGCGGCAAGCAAGAGCTGTGATGAGTGTCTCAAGGCAATGGGCGCCAC 2280
Qy      |||||
2281  ATCAACCTGAGAGGCTCAAGGTTCAAGGCGGCGCATGAGCCCGCGGCACTCTGCGG 2340
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Db      |||||
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RESULT 2
US-09-781-882-1
; Sequence 1, Application US/09781882
; Patent No. 663035
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 14171 Protein Kinase, a No. 663035e1 Human
; FILE REFERENCE: 035800-2090145800-6
; CURRENT APPLICATION NUMBER: US/09/781,882

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RESULT 3
US-09-949-016-1103
; Sequence 1103, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1103
; LENGTH: 3879
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1103

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QY 1 ATGAGAGGGCGAAGCGCGGGACCCCATATGGGCGCTCTGTGGGCACTTTGACAGCGGGG 60

Db 49 ATGAGAGGGCGAAGCGCGGGACCCCATATGGGCGCTCTGTGGGCACTTTGACAGCGGGG 108

QY 61 GAGTTCAACGGGCTGTGGAGAAAGGTGGGCTCGGGCGGCTTTCGGCAGGTGTATCAAGTGTGCG 120

Db 109 GAGTTCAACGGGCTGTGGAGAAAGGTGGGCTCGGGCGGCTTTCGGCAGGTGTATCAAGTGTGCG 168

QY	121	CATGTCAC	CTG3AAAGAC	CTGCGCTG	GCATCA	TAGTGTG	GCC	CAGCTTG	GCATG	TCGACGAC	180
Db	169	CATGTCAC	CTG3AAAGAC	CTTGCTG	GCATCA	TCAAGGTG	CTCGCC	CAGCTTG	GCATG	TCGACGAC	228
QY	181	AGGAGCG	GCATG3AG	CTTTTGG	AAAGAC	CAAGAAG	TGAGATG	GGCCAA	GTTCG	CTAC	240
Db	229	AGGAGCG	GCATG3AG	CTTTTGG	AAAGAC	CAAGAAG	TGAGATG	GGCCAA	GTTCG	CTAC	288
QY	241	ATCTG	CCCTGTG	TATG	ATG	CACTG	CCCG	GCATCTG	CGGCTGTG	ATGAGTACATG	300
Db	289	ATCTG	CCCTGTG	TATG	ATG	CACTG	CCCG	GCATCTG	CGGCTGTG	ATGAGTACATG	348
QY	301	ACGGG	CTCCCTG	GA	AAAGCTG	CTGG	CTTCCG	AGGCATTTG	GCATG	AGGATCTCCGGTTCCGA	360
Db	349	ACGGG	CTCCCTG	GA	AAAGCTG	CTGG	CTTCCG	AGGCATTTG	GCATG	AGGATCTTCGGTTCCGA	408
QY	361	ATCAT	CA	CGAGAC	CGCGCG	TGGG	GCATG	AACTTCTG	CACTG	CACTGACATG	420
Db	409	ATCAT	CA	CGAGAC	CGCGCG	TGGG	GCATG	AACTTCTG	CACTG	CACTGACATG	468
QY	421	CACCTG	GA	ACTTCA	AGCCCG	CG	GCATCTG	CTG	CGATG	CCCATCTAC	480
Db	469	CACCTG	GA	ACTTCA	AGCCCG	CG	GCATCTG	CTG	CGATG	CCCATCTAC	528
QY	481	GATTTT	GGCTG	GC	CAAGT	GTG	CA	CGGGCTG	CTCC	CACTG	540
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QY	541	CTGTTT	GG	CA	CAATG	CG	CTCA	CTTC	CTC	CA	600
Db	589	CTGTTT	GG	CA	CAATG	CG	CTCA	CTTC	CTC	CA	648
QY	601	GACAC	CA	AG	CA	CG	ATG	TATAC	AG	CG	660
Db	649	GACAC	CA	AG	CA	CG	ATG	TATAC	AG	CG	708
QY	661	AAGCG	TTT	GC	ATG	AG	AA	CA	CTCTG	CA	720
Db	709	AAGCG	TTT	GC	ATG	AG	AA	CA	CTCTG	CA	768
QY	721	CGCC	CCG	AG	CTG	CG	AG	CCCG	CG	CG	780
Db	769	CGCC	CCG	AG	CTG	CG	AG	CCCG	CG	CG	828
QY	781	CTCAT	G	CA	CG	CG	ATG	AG	CG	CG	840
Db	829	CTCAT	G	CA	CG	CG	ATG	AG	CG	CG	888
QY	841	TCTG	AA	CCG	AG	CA	CTG	TG	AA	AG	900
Db	889	TCTG	AA	CCG	AG	CA	CTG	TG	AA	AG	948
QY	901	CTG	CA	CG	AA	AA	AG	CCCG	CG	AG	960
Db	949	CTG	CA	CG	AA	AA	AG	CCCG	CG	AG	1008
QY	961	GCCT	TG	CC	CC	CA	CTT	GC	AT	AA	1020
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QY	1021	TCTG	AG	ATTTT	CC	CA	AG	CTG	TG	AA	1080
Db	1069	TCTG	AG	ATTTT	CC	CA	AG	CTG	TG	AA	1128
QY	1081	AAG	CTG	CA	ATG	CG	AG	CA	AG	CG	1140
Db	1129	AAG	CTG	CA	ATG	CG	AG	CA	AG	CG	1188
QY	1141	TTCT	TT	TC	CA	AG	AT	CA	CTG	TG	1200
Db	1189	TTCT	TT	TC	CA	AG	AT	CA	CTG	TG	1248

OY	1201	GGTACACAAACGGTCCGGAAGAAAGAACCTTGTGGATGCAATGCGTCC - GGACACACAG	1259
Db	1249	GGTACACAC - AAGACGTTCAGAAAGAAAGAACCTTGTGGATGCAATGCGTCCGGAACACAG	1307
OY	1260	CAAACTGATGAAAGATCCTGCACAGCCGCACAGACGTGACCTTGCACATGACACAGCGGTCCAG	1319
Db	1308	CAAACTGATGAAAGATCCTGCACAGCCGCACAGACGTGACCTTGCACATGACACAGCGGTCCAG	1367
OY	1320	CCTGCTGCACTTGGCGGTGGAGAGGCCGGGCAGAAGAGATGTCGCACAGTGGCTGTGCTTCA	1379
Db	1368	CCTGCTGCACTTGGCGGTGGAGAGGCCGGGCAGAAGAGATGTCGCACAGTGGCTGTGCTTCA	1427
OY	1380	CAATGCGCAACCCCAACCTGAGCAACCGTAAGGGGCTCCACCCTGTGCAATGACCGGTGGA	1439
Db	1428	CAATGCGCAACCCCAACCTGAGCAACCGTAAGGGGCTCCACCCTGTGCAATGACCGGTGGA	1487
OY	1440	GAGAGAGGTGGCGGGGTGTCTGTAGAGCTCTGTGCGACGGAAGATCACTGTCAACGCCAA	1499
Db	1488	GAGAGAGGTGGCGGGGTGTCTGTAGAGCTCTGTGCGACGGAAGATCACTGTCAACGCCAA	1547
OY	1500	GGATGAGGACCAATGAGCAAGCCCTTCACTTTGCAGCCCAAGACGGGGATAGATCTAGACAC	1555
Db	1548	GGATGAGGACCAATGAGCAAGCCCTTCACTTTGCAGCCCAAGACGGGGATAGATCTAGACAC	1607
OY	1560	ACGGCTGTCTGTTGGAGGAAGAACGCTCGGTCAACGAGGTGACCTTGAAGGGCCGACGCC	1619
Db	1608	ACGGCTGTCTGTTGGAGGAAGAACGCTCGGTCAACGAGGTGACCTTGAAGGGCCGACGCC	1667
OY	1620	CATGCACTGGGCTTCCACAGCACGGGCACGGAAGATATCGTGGCACTCTGCTGCGCGAGG	1679
Db	1668	CATGCACTGGGCTTCCACAGCACGGGCACGGAAGATATCGTGGCACTCTGCTGCGCGAGG	1727
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Db	1728	CGTGGACGTGAGCCTTGCAGAGGGCAAGATGCTGTGCTGCCACTGCACTAGCCTGCTTGGCA	1787
OY	1740	GGGCGCACTTGGCCATCTGCACAGCTCTGGCCAAAGACCGGGGGTGAATGGAAGGCCCA	1799
Db	1788	GGGCGCACTTGGCCATCTGCACAGCTCTGGCCAAAGACCGGGGGTGAATGGAAGGCCCA	1847
OY	1800	GACGCTGATGAGGAGACGCAATTGCACTGTGCGCACAGACCGGGGACCTAACCGGCTGAC	1855
Db	1848	GACGCTGATGAGGAGACGCAATTGCACTGTGCGCACAGACCGGGGACCTAACCGGCTGAC	1907
OY	1860	CCGCACTCTCATTCAGACTGTGTCTCCGACGTCAAGCTGTGCAGCTTGTGGCACACAGACC	1915
Db	1908	CCGCACTCTCATTCAGACTGTGTCTCCGACGTCAAGCTGTGCAGCTTGTGGCACACAGACC	1967
OY	1920	CCTGCACTGGTCCCGCGAGAGCGGGGCAACACAGCACTGCACAGCTGTCTTCTTCAATCGGG	1975
Db	1968	CCTGCACTGGTCCCGCGAGAGCGGGGCAACACAGCACTGCACAGCTGTCTTCTTCAATCGGG	2027
OY	1980	CGCTGGCAAGAGAGGCGCGTGAACCTCAAGACGGCTTCAACCGCTGTGCACCTTGGCTCGGCA	2035
Db	2028	CGCTGGCAAGAGAGGCGCGTGAACCTCAAGACGGCTTCAACCGCTGTGCACCTTGGCTCGGCA	2087
OY	2040	CGGACACTTGGCCACTGTCAAGCTGTCTTGTTCAGAGGAAGAGGCGATGTGCTGGGCCCGGG	2095
Db	2088	CGGACACTTGGCCACTGTCAAGCTGTCTTGTTCAGAGGAAGAGGCGATGTGCTGGGCCCGGG	2147
OY	2100	ACCCCTGAACACAGACCGGCGCTGCACCTGGCTGCCGCCACCGGGCACTCGGAAGTGTGGA	2155
Db	2148	ACCCCTGAACACAGACCGGCGCTGCACCTGGCTGCCGCCACCGGGCACTCGGAAGTGTGGA	2207
OY	2160	GGAGTTTGTCAAGGCGGATGTCAATTGACCTGTTTCAGACAGACAGGGGCTCAAGGCGCTGCA	2211
Db	2208	GGAGTTTGTCAAGGCGGATGTCAATTGACCTGTTTCAGACAGACAGGGGCTCAAGGCGCTGCA	2267
OY	2220	CCTGGCGCGCCAGAGGCGCGCACGCAACAGCTGTGAAGATCTTGTCAAGCATTGGGCCCA	2275
Db	2268	CCTGGCGCGCCAGAGGCGCGCACGCAACAGCTGTGTGAAGATCTTGTGTCAAGCATTGGGCCCA	2327
OY	2280	CATCAACTTGCAGAGCTTCAAGTTTCAGAGGCGGCAATGGCCCCCGGCCACACTCTGTGG	2333

DB	2328	2340	2388
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OY		GCGAAGCAAGACTTAG	2355
DB		GCGAAGCAAGACTTAG	2403

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1      RESULT 4
2      US-09-949-016-5205
3      ; Sequence 5205, Application US/09949016
4      ; Patent No. 6812319
5      ; GENERAL INFORMATION:
6      ; APPLICANT: VENTER, J. Craig et al.
7      ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
8      ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
9      ; FILE REFERENCE: CL001307
10     ; CURRENT APPLICATION NUMBER: US/09/949,016
11     ; CURRENT FILING DATE: 2000-04-14
12     ; PRIOR APPLICATION NUMBER: 60/241,755
13     ; PRIOR FILING DATE: 2000-10-20
14     ; PRIOR APPLICATION NUMBER: 60/237,768
15     ; PRIOR FILING DATE: 2000-10-03
16     ; PRIOR APPLICATION NUMBER: 60/231,498
17     ; PRIOR FILING DATE: 2000-09-08
18     ; NUMBER OF SEQ ID NOS: 207012
19     ; SOFTWARE: FASTSEQ for Windows Version 4.0
20     ; SEQ ID NO 5205
21     ; LENGTH: 3868
22     ; TYPE: DNA
23     ; ORGANISM: Human
24     US-09-949-016-5205

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Query Match	98.5%	Score 2320.8;	DB 4;	Length 3868;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 2347; Conservative	0;	Mismatches 7;	Indels 2;	Gaps 2

QY	1	ATGAGAGGGGAGACGGGCGGAGACCCCAATGGGACCTCGGCGCTGCTGCGACCTTGCACCGCGGC	50
Db	49	ATGGAGGGCGACGGGCGGAGACCCCAATGGGACCTCGGCGCTGCTGCGACCTTGCACCGCGGC	108
QY	61	GAGTTCAAGGGCTGGGAGAAAGTGGGCTCGGGCGGGCTTTCGGGCAAGTGTACAAAGGTGCGC	120
Db	109	GAGTTCAAGGGCTGGGAGAAAGTGGGCTCGGGCGGGCTTTCGGGCAAGTGTACAAAGTGTGCGC	168
QY	121	CATGTCCACTGGAGAACCTGGCTGGCCATCAAGTCTCGCCGACCTGCAAGTGCAGAC	180
Db	169	CATGTCCACTGGAGAACCTGGCTGGCCATCAAGTCTCGCCGACCTGCAAGTGCAGAC	228
QY	181	AGGAGGCGCATGGAGCTTTTGGAGAGAACCCAAAGAAATGGAGATGGCCAACTTTTGGCTAC	240
Db	229	AGGAGGCGCATGGAGCTTTTGGAGAGAACCCAAAGAAATGGAGATGGCCAACTTTTGGCTAC	288
QY	241	ATCCGCGCTGTGTATGGCATCGCGCGCAACCTGTGGGCTGTGATGAGATGATGGAG	300
Db	289	ATCCGCGCTGTGTATGGCATCGCGCGCAACCTGTGGGCTGTGATGAGATGATGGAG	348
QY	301	ACGGGCTCCCTGGAGAAAGCTGTGGCTTTCGAGCCATTTGCCATGGGATCTCCGATTCCGA	360
Db	349	ACGGGCTCCCTGGAGAAAGCTGTGGCTTTCGAGCCATTTGCCATGGGATCTCCGATTCCGC	408
QY	361	ATCATCCACGAGACGGGCGGTGGGCAATGAACTTCTGCACTGCATGGCCCCCGCACTCCTG	420
Db	409	ATCATCCACGAGAGCGGCGGTGGGCAATGAACTTCTGCACTGCATGGCCCCCGCACTCCTG	468
QY	421	CACCTGGACCTGAACCGCGCGCAACATCTGTGCTGATGCGCACTACCAAGTCAAGATTTCT	480
Db	469	CACCTGGACCTGAACCGCGCGCAACATCTGTGCTGATGCGCACTACCAAGTCAAGATTTCT	528
QY	481	GATTTTGGCTGGGCGCAAGTGCACGGGCGTGTCCCACTGCAGATGACCTCAGACATGATGGC	540
Db	529	GATTTTGGCTGGGCGCAAGTGCACGGGCGTGTCCCACTGCAGATGACCTCAGACATGATGGC	588

QY 541 CTGTTTGGCAACATGCGCTACCTCCCTCCAGAGCGCATCAGGGAGAAAGCCGGCTCTTC 600
Db 589 CTGTTTGGCAACATGCGCTACCTCCCTCCAGAGCGCATCAGGGAGAAAGCCGGCTCTTC 648
QY 601 GACACCAAGCAOGATGTATACAGCTTTGCGATCTGTCACTCTGCGGCGTGTCAACAGAG 660
Db 649 GACACCAAGCAOGATGTATACAGCTTTGCGATCTGTCACTCTGCGGCGTGTCAACAGAG 708
QY 661 AAGCGCTTTGCAAGATGAGAAAGACATCTGTCACTCATGTGTGAAGGTGTGAAGGGCCAC 720
Db 709 AAGCGCTTTGCAAGATGAGAAAGACATCTGTCACTCATGTGTGAAGGTGTGAAGGGCCAC 768
QY 721 CGCCCCGAGCTGCGCGCGCTGTGCGAGAGCCCGCGCGCGCTGTCAAGCCACTGATAGCG 780
Db 769 CGCCCCGAGCTGCGCGCGCTGTGCGAGAGCCCGCGCGCGCTGTCAAGCCACTGATAGCG 828
QY 781 CTATGCAAGCGGTGCTGCGAGAGGGAGATCGCGAGTTAGGCCACCTTTCAGAAATTAAT 840
Db 829 CTATGCAAGCGGTGCTGCGAGAGGGAGATCGCGAGTTAGGCCACCTTTCAGAAATTAAT 888
QY 841 TCTGAAACCGAGGACCTGTGTGAAAGAGCTGTATGACAGAGTGAAGAACTGTCTATGAT 900
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Db 949 CTGAGACGTGAAGAAAGCCCCCGAGAGCCAGAGCGAGGTGTGCTGTGCGAGGCTCAAGCGG 1008
QY 961 GCCTCTGCGCCCACTTGTGATTAACGATACAGCTCTTCGAGCTTCTGTCAACAGTGGAC 1020
Db 1009 GCCTCTGCGCCCACTTGTGATTAACGATACAGCTCTTCGAGCTTCTGTCAACAGTGGAC 1068
QY 1021 TCTGGAAGTTTCCAGGCGTGTGAGAGGGCCCCGAGAGGCTCAAGCCAGAGTCTCTGAGTCC 1080
Db 1069 TCTGGAAGTTTCCAGGCGTGTGAGAGGGCCCCGAGAGGCTCAAGCCAGAGTCTCTGAGTCC 1128
QY 1081 AAGCTGCATGATCGTCCGAGTGTGAGAGAGGCTCTCTGCGGGTGTCTCTCGTGAATCCGCC 1140
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QY 1141 TTCTCTTCCAGAGGATCACTGTCTGTCTCTTTGAGCGGAACTTTCACACGAGATGTG 1200
Db 1189 TTCTCTTCCAGAGGATCACTGTCTGTCTCTTTGAGCGGAACTTTCACACGAGATGTG 1248
QY 1201 GGTACCAAGAGAGCTTCCAGAGAGAGAGCTCTCTGCGGGTGTCTCTCGTGAATCCGCC 1259
Db 1249 GGTACCAAGAGAGCTTCCAGAGAGAGAGCTCTCTGCGGGTGTCTCTCGTGAATCCGCC 1307
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Db 1308 CAAACTGATGAAGATCTGTGAGCGCGAGAGAGTGTGAACCTTGGCACTGGACACGCGTGCAG 1367
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Db 1368 CCTGCTGCACTGTGCGGTGAGAGCGGGCAAGAGAGTGCSCCAAGTGGCTGTGTCA 1427
QY 1380 CAATGCCAACCCCAACCTGAGAGAACCTGTAAGGGGCTCCACCCCGTTGSCACATGGCCGTGGA 1439
Db 1428 CAATGCCAACCCCAACCTGAGAGAACCTGTAAGGGGCTCCACCCCGTTGSCACATGGCCGTGGA 1487
QY 1440 GAGGAGGTGTGCGGGGTGTGTGTGAGAGCTCTGTGCGAGCGAAGATCACTGTCAACGCCAA 1499
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QY 1500 GAGATGAGAGCAAGTGAAGAGCCCTTCACTTTGCAAGCCAGAAACGGGGATGAGTCTAGAC 1559
Db 1548 GAGATGAGAGCAAGTGAAGAGCCCTTCACTTTGCAAGCCAGAAACGGGGATGAGTCTAGAC 1607
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Db 1608 ACGGTGTGTGTGTGAGAGAGAGCTCTGTGTCAACGAGGTGGAATTTGAGGGCCGAGACGCC 1667
QY 1620 CATGCAAGTGGCGCTGCAAGACGGGCAAGAGAAATTCGTGCGCATCTGTGCGCGAGG 1679

Db 1668 CATGCAAGTGGCGCTGCAAGACGGGCAAGAGAAATATCTGTGCGCATCTGTGCGCGAGG 1727
QY 1680 CGTGAGAGTGAAGCTTGAAGGGCAAGAGATGCTGTGGCTGCCACTGTCACTATCGCTTCCGCA 1739
Db 1728 CGTGAGAGTGAAGCTTGAAGGGCAAGAGATGCTGTGGCTGCCACTGTCACTATCGCTTCCGCA 1787
QY 1740 GGGCCACCTGCGCATGCTGAAGCTGTGAGCGCAAGCGCCGGGGTGAAGTGAACGCCCA 1799
Db 1788 GGGCCACCTGCGCATGCTGAAGCTGTGAGCGCAAGCGCCGGGGTGAAGTGAACGCCCA 1847
QY 1800 GAGCGTGAATGAGAGAGACGCCATTGCACTGTGCGCGACAGCGCGGCACTAACCGGTGGC 1859
Db 1848 GAGCGTGAATGAGAGAGACGCCATTGCACTGTGCGCGACAGCGCGGCACTAACCGGTGGC 1907
QY 1860 CCGCATCTTATGACCTGTGTCTCCAGCGTCAACGTCTGAGCGCTGTGCGCAAGACACC 1919
Db 1908 CCGCATCTTATGACCTGTGTCTCCAGCGTCAACGTCTGAGCGCTGTGCGCAAGACACC 1967
QY 1920 CTTGCAAGTGGCGCGGAGACGGGGGACAGAGACATGCGCAGGCTGTCTGTGATCGAGG 1979
Db 1968 CTTGCAAGTGGCGCGGAGACGGGGGACAGAGACATGCGCAGGCTGTCTGTGATCGAGG 2027
QY 1980 CGCTGGCAAGAGAGCGCTGACCTTCAAGCGCTTCAACCGCTTGTCACTGTGCTGCCGCA 2039
Db 2028 CGCTGGCAAGAGAGCGCTGACCTTCAAGCGCTTGTGAGAGAGAGCGAGTGTGCGCGGG 2087
QY 2040 CGGACACCTTGGCCACTGTCAAGCTGTGTGAGAGAGAGCGAGTGTGCGCGGG 2099
Db 2088 CGGACACCTTGGCCACTGTCAAGCTGTGTGAGAGAGAGCGAGTGTGCGCGGG 2147
QY 2100 ACCCGTGAACCAAGCGCGCTGACCTGTGCGCGCCACGCGCACTCGAGGTGTGGA 2159
Db 2148 ACCCGTGAACCAAGCGCGCTGACCTGTGCGCGCCACGCGCACTCGAGGTGTGGA 2207
QY 2160 GAGATTGTGAGCGCGCGAGTCAATTGACTGTTCAGACAGAGAGGCTCAAGCGCGTGA 2219
Db 2208 GAGATTGTGAGCGCGCGAGTCAATTGACTGTTCAGACAGAGAGGCTCAAGCGCGTGA 2267
QY 2220 CTTGCGCGCCCAAGGCGCGGACCGCAACAGAGGTGAGAGCTCTGTCAAGAGATGGGGCCCA 2279
Db 2268 CTTGCGCGCCCAAGGCGCGGACCGCAACAGAGGTGAGAGCTCTGTCAAGAGATGGGGCCCA 2327
QY 2280 CATCAACTGACAGAGCTTCAAGTTTCCAGGCGGCGCATGTGCGCGCCCACTCTCTGCG 2339
Db 2328 CATCAACTGACAGAGCTTCAAGTTTCCAGGCGGCGCATGTGCGCGCGCCCACTCTCTGCG 2387
QY 2340 GCGAAGCAAGACCTTGA 2355
Db 2388 GCGAAGCAAGACCTTGA 2403

RESULT 5
US-09-799-451-905
Sequence 905, Application US/09799451
Patent No. 6783969
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Ma, Yungqing
APPLICANT: Yamazaki, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Duntui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom

APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 678369e1 Nucleic Acids and
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pc_fl_genes Version 2.0
SEQ ID NO 905
LENGTH: 3981
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(2496)
US-09-799-451-905

Query Match 92.1%; Score 2170; DB 4; Length 3981;
Best Local Similarity 94.0%; Pred. No. 0;
Matches 2349; Conservative 0; Mismatches 5; Indels 146; Gaps 3;

QY 1 ATGAGGCGGAGCGGCGGAGACCCATGAGGCGCTGCGGCTGCGGACCTTCGACGCGGCG 60
DB 1 ATGAGGCGGAGCGGCGGAGACCCATGAGGCGCTGCGGCTGCGGACCTTCGACGCGGCG 60
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DB 61 GAGTTCACGCGGCTGCGGAGAGGTGGGCTCGGCGGCTTCGCGCAGGTGTACAGGTGCGC 120
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DB 121 CATGTCCACTGGAACCTCTGCTGCGCATCAAGTGTCTGCGGCGGCTTCGCGCAGGTGTAC 180
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DB 181 AGGAGCGCATGAGCTTTTGGAGAGCGCAAGATGAGATGAGGAGGCTTTCGCTAC 240
QY 241 ATCTGCGCTGTGTATGCGCATCTGCGGAGACCTGTGCGCTGTGTATGAGATGATCAGTAC 300
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DB 421 CACTGGAACCTTCAGACCGCGGAGCATCTCTGCTGATGAGGCGCACTACAGTCAAGATTCT 480
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DB 601 GACACCAAGCAGATGTATACAGCTTTGCGATGTCATCTGGGGCGTGTCTCACAGAG 660
QY 661 AAGCGCTTTGCGATGAGAGAGCATCTCTGCAATATATGATGAGAGGTGTGAAGGCGCAC 720
DB 661 AAGCGCTTTGCGATGAGAGAGCATCTCTGCAATATATGATGAGAGGTGTGAAGGCGCAC 720
QY 721 GCGCCCGAGCTGCGCGGCTGTGAGAGCGCGGCGCGGCTGCGAGCGACCTGATACGC 780
DB 721 GCGCCCGAGCTGCGCGGCTGTGAGAGCGCGGCGCGGCTGCGAGCGACCTGATACGC 780

QY 781 CTGATGAGCGGCTGTGAGAGGAGATCCGCGATTAGGCCCACTTC----- 828
DB 781 CTGATGAGCGGCTGTGAGAGGAGATCCGCGATTAGGCCCACTTCGAGAGAGG 840
QY 829 ----- 828
DB 841 CTGAATGGGAGCTCATCCGCGAGGTCTGAGCTGTCTCCCTGTGATGCGAGGTGG 900
QY 829 ----- 828
DB 901 CGCTCCCGGAGAGGCTTCGCGCTTGAATCTGAATCATTCGAGTGAATGTC 960
QY 829 -----CAAGAAATTACTTTGAAACCGAGGACCTGTGTGAAAAGCTGATGAC 876
DB 961 CTTTCTTCCCAAGAAATTACTTTGAAACCGAGGACCTGTGTGAAAAGCTGATGAC 1020
QY 877 GAAGTGAAGAACTGTCTCATGATCTGGAAGTGAAGAGGCGCGAGGCCGAGAGCGAG 936
DB 1021 GAAGTGAAGAACTGTCTCATGATCTGGAAGTGAAGAGGCGCGAGGCCGAGAGCGAG 1080
QY 937 GTGTGCTCTGCGAGGCTTCAGCGGCGCTTGTCCCTTCATTAAGCTTACAGCTTC 996
DB 1081 GTGTGCTCTGCGAGGCTTCAGCGGCGCTTGTCCCTTCATTAAGCTTACAGCTTC 1140
QY 997 TCCGAGCTTCTTCAAGCTGGAATCTGAGATTCCAGGCTGTGAGGCGCGAGAG 1056
DB 1141 TCCGAGCTTCTTCAAGCTGGAATCTGAGATTTCAGGCTGTGAGGCGCGAGAG 1200
QY 1057 CTCAGCGCGAGCTTCTTGTGATTCAGGCTGATGTCGCGAGTGGAGAGAGGCTTCG 1116
DB 1201 CTCAGCGCGAGCTTCTTGTGATTCAGGCTGATGTCGCGAGTGGAGAGAGGCTTCG 1260
QY 1117 GGGGTGTCTGTGTGAGCTCGGCTTCTTCCAGAGATTCATCTGTGCTTCTTGGAG 1176
DB 1261 GGGGTGTCTGTGTGAGCTCGGCTTCTTCCAGAGATTCATCTGTGCTTCTTGGAG 1320
QY 1177 CCGGACCTTCAACAGAGATCTGAGTACCAAGAGCTTCAGAGAGAGAGCTTGTGGA 1236
DB 1321 CCGGACCTTCAACAGAGATCTGAGTACCAAGAGCTTCAGAGAGAGAGCTTGTGGA 1379
QY 1237 TGCCATGTGTCC-GGAGCAGCAGCAAGATGATGAGATCTTCGAGCGCGAGAGTGA 1295
DB 1380 TGCCATGTGTCCGGGAGCAGCAGCAAGATGATGAGATCTTCGAGCGCGAGAGTGA 1439
QY 1296 CTTGCACTGGAACGCGGTGCGAGCTGTGCACTTCGCGGTGAGAGGCTCGGCGAGAGGA 1355
DB 1440 CTTGCACTGGAACGCGGTGCGAGCTGTGCACTTCGCGGTGAGAGGCTCGGCGAGAGGA 1499
QY 1356 GTGCGCCAGAGGTGTGCTGCAACATTCGCAACCCCAACTGAGCAACGTTAGGGGCTC 1415
DB 1500 GTGCGCCAGAGGTGTGCTGCAACATTCGCAACCCCAACTGAGCAACGTTAGGGGCTC 1559
QY 1416 CACCCGTTTGCATATGCGCGGTGAGAGAGGAGGTGTGTGTGAGCTTCGTGGC 1475
DB 1560 CACCCGTTTGCATATGCGCGGTGAGAGAGGAGGTGTGTGTGAGCTTCGTGGC 1619
QY 1476 AGGAAATCAAGTGTCAACGCGCAAGATGAGAACGATGGAACAGCTTCCTTGCAGC 1535
DB 1620 AGGAAATCAAGTGTCAACGCGCAAGATGAGAACGATGGAACAGCTTCCTTGCAGC 1679
QY 1356 CCAAGACGGGATATAGTCTTACACACGCGCTGTGTGAGAGAGAGCGCTGCGTCAACGA 1595
DB 1680 CCAAGACGGGATATAGTCTTACACACGCGCTGTGTGAGAGAGAGCGCTGCGTCAACGA 1739
QY 1596 GATGACCTTTGAGGGCGGAGCGCCATGCAAGTGTGCTGCGCAGCAAGAGATAT 1655
DB 1740 GATGACCTTTGAGGGCGGAGCGCCATGCAAGTGTGCTGCGCAGCAAGAGATAT 1799
QY 1656 GTGTGCAATCTTGTGCGCGGAGGCGGTGAGAGTGTGAGCTTGTGAGGCAAGATGCTGCT 1715
DB 1800 GTGTGCAATCTTGTGCGCGGAGGCGGTGAGAGTGTGAGCTTGTGAGGCAAGATGCTGCT 1859

Qy	1716	GCCACTGCACTACGCTGCTCTGGGCAAGGGCCACTCTGCCCATGTGTAACTGCTGGCCAAAGA	1775
Db	1860	GCCACTGCACTACGCTCTCTGGGCAAGGGCCACTCTGCCCATGTGTAACTGCTGGCCAAAGA	1919
Qy	1776	GCCGAGGGGTGATGATGTGAACGCCCAAGACGCTGGAATGGGAAGGACGCAATTGCACTTGAGCGCG	1835
Db	1920	GCCGAGGGGTGATGATGTGAACGCCCAAGACGCTGGAATGGGAAGGACGCAATTGCACTTGAGCGCG	1979
Qy	1836	ACAGCGGGGCACTACCGCGTGGGCCCGCATCTCATTCGACTTGTGCTCGACGTCMAAGT	1895
Db	1980	ACAGCGGGGCACTACCGCGTGGGCCCGCATCTCATTCGACTTGTGCTCGACGTCMAAGT	2039
Qy	1896	CTGCAAGCTGTCTGGCAACAACCCCTGCACTGTGGCCGCGAGACGAGGCAACAAGACAC	1955
Db	2040	CTGCAAGCTGTCTGGCAACAACCCCTGCACTGTGGCCGCGAGACGAGGCAACAAGACAC	2099
Qy	1956	TGCGAAGCTGTCTCTGCATGGGGGCGTGGCAAGAGGCGGTGACCTTCAGAAGGCTTACAC	2015
Db	2100	TGCGAAGCTGTCTCTGCATGGGGGCGTGGCAAGAGGCGGTGACCTTCAGAAGGCTTACAC	2159
Qy	2016	CGCTCTGCACTGGCTGCTCCCGCAACGAGACACTGTGACACTGTGAAGCTGTGTGAGGA	2075
Db	2160	CGCTCTGCACTGGCTGCTCCCGCAACGAGACACTGTGACACTGTGAAGCTGTGTGAGGA	2219
Qy	2076	GAAAGCGGATGTGTGTGGCCCGGAGGACCCCTGAACAGAGCGGCGCTCACTGTGCTGGC	2135
Db	2220	GAAAGCGGATGTGTGTGGCCCGGAGGACCCCTGAACAGAGCGGCGCTCACTGTGCTGGC	2279
Qy	2136	CCACGGGCACTCGGAGGTGTGTGAGAGATTGTGTCAAGCGCGGATGTGACTTGTTCGA	2195
Db	2280	CCACGGGCACTCGGAGGTGTGTGAGAGATTGTGTCAAGCGCGGATGTGACTTGTTCGA	2339
Qy	2196	CGACCGAGGGGTGACGCGCGCTGCACCTGTGGCGCGCCAGAGGCGGCGCAAGACAGCGGTGA	2255
Db	2340	CGACCGAGGGGTGACGCGCGCTGCACCTGTGGCGCGCCAGAGGCGGCGCAAGACAGCGGTGA	2399
Qy	2256	GACTGTGCTCAGGATGGGGCCCAATCAACTGTGCAAGGCTCAAGTTCAGAGGCGGCGCA	2315
Db	2400	GACTGTGCTCAGGATGGGGCCCAATCAACTGTGCAAGGCTCAAGTTCAGAGGCGGCGCA	2459
Qy	2316	TGGCCCGCGCGCAACTCTGTGGCGGCAAGCAAGACTTAG	2355
Db	2460	TGGCCCGCGCGCAACTCTGTGGCGGCAAGCAAGACTTAG	2499
RESULT 6			
US-09-509-802-1			
; Sequence 1, Application US/09509802			
; Patent No. 6489130			
; GENERAL INFORMATION:			
; APPLICANT: Immunex Corp.			
; APPLICANT: Bird, Timothy			
; APPLICANT: Vitca, G.D.			
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR)			
; FILE REFERENCE: 2889-US			
; CURRENT APPLICATION NUMBER: US/09/509,802			
; CURRENT FILING DATE: 2000-06-02			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 1			
; LENGTH: 2370			
; TYPE: DNA			
; ORGANISM: Mus sp.			
US-09-509-802-1			

QY	62	AGTTCA	CGGGCTGGGAA	AAAGTGGGCTCGGGCGGCTTGGGGCAGGTATACAAGTGGGCC	122		
Db	71	AATTGCA	GAGGTGGGAA	AAAGTGGGCTCGGGCGGCTTGGGGCAGGTATACAAGTGGGCC	130		
QY	122	ATGTCCA	CTGGA	AAACCTGGCTGGCCATCAAGTCTCGCCAGCCTGCAAGTGCAGCA	181		
Db	131	ATGTGCA	CTGGA	AAACCTGGCTGGCCATCAAGTCTCGCCAGCCTGCAAGTGCAGCA	190		
QY	182	GGAGCG	CATGAG	CTTTTGGAA	AGCCAA	GAATGAGATGGCCAAGTTTGGCTACA	241
Db	191	GGGAAC	GAATGAG	ACTCTGGAGGA	AGCTAA	GAAGATGGCCAAAGTCTCGATACA	250
QY	242	TTCCTG	CTGTGT	ATAGGCATCTGCCGCGA	ACTGTGGGCTGTGTATAGAGTACA	TTGAGAGA	301
Db	251	TTCTA	ACCTGTGT	ATAGGCATCTGCCGCGA	ACTGTGGGCTGTGTATAGAGTACA	TTGAGAGA	310
QY	302	CGGGCT	CCCTTGGAA	AAAGTGTGCTGGCTTGGAGCCATTTGGCATGAGGATCTCGGTTCCGAA	361		
Db	311	CAGGCT	CCCTTGGAA	AAAGTGTGCTGGCTTGGAGCCATTTGGCATGAGGATCTCGGTTTCGCA	370		
QY	362	TCATCCA	CGA	ACGCGGTGGGCA	TGAATTTCTGCACTGCACTGATGGCCCGGCACTCTGTC	421	
Db	371	TGATGCA	CGA	ACGCGGTGGGCA	TGAATTTCTGCACTGCACTGATGGCCCGGCACTCTGTC	430	
QY	422	ACCTG	GAACCTTCA	AGCCCGGCAACATCTGTCTGATATGCCCACTACCAAGTCAAGATTTCTG	481		
Db	431	ACCTG	AGACCTTCA	AGCCCGGCAACATCTGTCTGATATGCCCACTACCAAGTCAAGATTTCTG	490		
QY	482	ATTTTGG	CTGSGCA	AGTGCAAAGGGGCTGTCCACTGCGATGACCTGAGCATGAGATGGCC	541		
Db	491	ACTTTGG	CTGSGCA	AGTGCAAAGGGGCTGTCCACTGCGATGACCTGAGCATGAGATGGCC	550		
QY	542	TGTTTGG	CACATG	CGCTTACCTTCCCTCCAGACCGCATCAAGGAGAAAGCCGCGCTCTTGC	601		
Db	551	TGTTTGG	CACATG	CGCTTACCTTCCCTCCAGACCGCATCAAGGAGAAAGCCGCGCTCTTGC	610		
QY	602	ACACCA	AGCA	CGATGTATACGCTTTGGCATCGTCACTCTGGGGGCTGTCTACACAGAGA	661		
Db	611	ACACCA	AGCA	CGATGTATACGCTTTGGCATCGTCACTCTGGGGGCTGTCTACACAGAGA	670		
QY	662	AGCG	TTTGG	CAGATGAGA	AGAAACATCTCTGCA	CATCATGTGTGAAGTGTGAAGGGCCACC	721
Db	671	AGCC	ATTGG	CAGATGAGA	AGAAACATCTCTGCA	CATCATGTGTGAAGTGTGAAGGGCCACC	730
QY	722	GCCCCG	AGCTG	CCGCCCGGTGTGCA	GAGCCCGCGCGCGCTTGACGCA	CCTGTATACGC	781
Db	731	GCCCCG	AGCTG	CCGCCCGGTGTGCA	GAGCCCGCGCGCGCTTGACGCA	CCTGTATACGC	790
QY	782	TCATG	CAGCGGTG	CTGAGGAGGAGATCCGCGATTTAGGCCCACTTCCAGAAATTA	CTT	841	
Db	791	TCATG	CAGCGGTG	CTGAGGAGGAGATCCGCGATTTAGGCCCACTTCCAGAAATTA	CTT	850	
QY	842	CTGA	AACCGG	AGATCTGTGTGTA	AAAAAGCTGATGACGAAGTGA	AGAAACGTGCTATGATC	901
Db	851	CTGA	AACCGG	AGATCTGTGTGTA	AAAAAGCTGATGACGAAGTGA	AGAAACGTGCTATGATC	910
QY	902	TG	AGCTGA	AAAGCCCCCGGAGCCACAGAGCAGAGTGTGTGCTG-----CGAGGCTCA	955		
Db	911	CAGG	GA	AAAGCCCCCGGAGCCACAGAGCAGAGTGTGTGCTG-----CGAGGCTCA	970		
QY	956	AGCG	GGCTCTG	CCCCCACTTGTGATACGATACAGCTTCTCGAGCTTCTCTACAGC	1015		
Db	971	AGCG	GGCTCTG	CCCCCACTTGTGATACGATACAGCTTCTCGAGCTTCTCTACAGC	1030		
QY	1016	TG	GAATCTG	GAAGTTTCCAGGCTGTGAGGGCCCCGAGAGACTCAAGCCGAGCTTCTG	1075		
Db	1031	TG	GAATCTG	GAAGTTTCCAGGCTGTGAGGGCCCCGAGAGACTCAAGCCGAGCTTCTG	1090		
QY	1076	AGTCA	ACATG	CAATCGTCCGAGCTGGGGAAGAGGCTCTCGGGGGGTGTCTCGGTGAGCT	1135		
Db	1091	ATGTA	ACATG	CAATCGTCCGAGCTGGGGAAGAGGCTCTCGGGGGGTGTCTCGGTGAGCT	1150		
QY	1136	CGG	CTTCTTCC	AGAGATCACTGTGCTGTCTCTTGTGACGGGAACTTTCACACAGC	1195		

[illegible]

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Db          2230  CTGCACCTGGGTGTGCATAGGGGAGGCATTCAACAAGCTGTGAGACACTGCTCAAAACATGGA 2289
QY          2275  GCCCAATCAATCACTGCGACAGAGCCTTAAGTTCCAGGCGCGCCATGGCCCCGGCCGACACTC 2334
Db          2290  GCACACATCAACTTGCACGAGTCTCAAGTTCCAAAGAGGAGCCAGAGACTGTGCTGCCACGTTG 2349
QY          2335  CTGCGCGCGAAGACGACCTAG 2355
Db          2350  CTCGACGCGACGAAAGACTTAG 2370

RESULT 7
US-09-188-930-257
; Sequence 257, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlson, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 1100.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 257
; LENGTH: 3516
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-257

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QY 542 TGTTCGCACAATGCGCTACCTCCCTCCAGAGCGCATCAGGAGAGAGAGCCGGCTTCG 601
Db 545 TGTTCGCACAATGCGCTACCTCCCTCCAGAGCGCATTCGAGAGAGCGCGCTTCGTTG 604
QY 602 ACACCAAGCAAGATGATATACAGCTTTGGATCGTCATCTGGGGGCTGCTCAACAGAGA 661
Db 605 ACACCAAGCAAGATGATATACAGCTTTGGATCGTCATCTGGGGGCTGCTTCACAGAGA 664
QY 662 AGCCGTTTGAGATGAGAGAAACATCTGCAATCATGATGAGAGTGTGAGAGGCCCA 721
Db 665 AGCCATTTGAGATGAGAGAAACATCTGCAATCATGATGAGAGTGTGAGAGGCCCA 724
QY 722 GCGCCGAGCTGCGCCCGCTGTCAGAGCGCGCGCGCGCTGCAAGCCACTGATAGGCC 781
Db 725 GCGCCGAGCTGCGCCCGCTGTCAGAGCGCGCGCGCGCTGTCAGAGCGCTGATAGGCC 784
QY 782 TCATGCAAGCGGTGCTGCGAGGGGATCCGCGAGTTAGGCCCACTTCCAGAGAAATTA 841
Db 785 TCATGCAAGCGGTGCTGCGATGCAAGCCCAAGTTCGCGCCCACTTCCAGAGAAATTA 844
QY 842 CTGAAACGAGAGACCTGTGTGAGAAAGCTGTATGACGAAAGTAAAGAACTGTCTAT 901
Db 845 CTGAAACGAGAGACCTTTGTGAGAAAGCTGTATGAGAGTGAAGAACTGTCTATGAGC 904
QY 902 TGGAGCTGAGAAAGCCCCCGGAGCCAGAGCGAGTGTGCTG-----CGAGGCTCA 955
Db 905 CAGGAGAGAAAGCTCTCTAGAGTCCAGAGTGAAGGCGAGCGCGAGTCTCAAGCTCA 964
QY 956 AGCGGCGCTGTCGCCCACTTCGATTAACGATACAGCTCTCGAGGCTTCTTCACAGC 1015
Db 965 AGCGGCGCTGTCGCCCTTCCCTTCGATTAACGATGAGTCTCTCGAGTTCGTCACAGT 1024
QY 1016 TGGACTGTGAGTTTCCAGGCTGTGAGGGCCCCGAGAGAGCTCAAGCTGCTCTG 1075
Db 1025 TGGACTGTGAGTTTCCAGAGCTCTTGAAGGCCCGGAGAGCTCAAGGCTCTCTG 1084
QY 1076 AGTCCAACTGCGCATTCGTCGCGAGTGGAGAGAGGCTCTCGGGGCTGCTCGGAGCT 1135
Db 1085 AATGCAACTGCTCCATGCTCCAGAGTGGAGAGAGGCTCTCGGGGCTGCTCGAGGAGCT 1144
QY 1136 CGGCTTCTCTTCCAGAGATCACTGTGCTGCTTTCGAGCGGAGACCTTCAACAGCG 1195
Db 1145 CAGCTTTTCTTCCAGAGATGCTGTCACTGTCTTTTGAAGCGGAGACCTTCAACAGCG 1204
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Db 1205 ACTGGGCCCCA-C-AGATCCAGAGAAAGAGCTATGATGCTATCAAGGGGAGC 1263
QY 1255 ACCAGCAATGATGAGATCCTGAGCGCGAGCGAGCTGAGACCTGAGCACTGAGCAAGCGGT 1314
Db 1264 ACCAGCAAGCTGATGAGATCCTGAGCGCGAGCGAGCTGAGTGTGCTTGAAGCAAGCT 1323
QY 1315 GCGAGCTGTCGACCTGCGGCTGAGAGCGCGGCAAGAGTGTGCGCAAGTGTGCTGCTG 1374
Db 1324 GCGAGCTGTCGACCTGCGTGTGAGAGCGCGGCAAGAGTGTGATGAGTGTGCTGCTG 1383
QY 1375 CTCAACATGCGCAATCCCACTTGAAGCAAGCTAGGGGCTTCAACCTGTCGATGAGCC 1434
Db 1384 CTTAACATGCGCAATCCCACTTGAAGCAAGAGGGGCTTCAACCTGTCATGAGCT 1443
QY 1435 GTTGAAGAGAGGTGCGGGGTGTGTCGAGCTCCGCTGAGCGAGAAATGATGATCAAC 1494
Db 1444 GTTGAAGAGAGAGGTGAGAAATGTCGATGATGAGTGTGAGTGTGAGTGTGAT 1503
QY 1495 GCGCAAGATGAGAGCAAGTGAAGAGCTTCACTTTCAGAGCCAGAGAGGGGATGATCT 1554
Db 1504 GCGCAAGATGAGAGCAAGTGAAGCTGCTGCTGCACTTTCAGAGCCAGAAATGAGGAGCC 1563
QY 1555 AGCAGACGAGCTGCTGTGAGAGAAAGCTTGTCAACGAGTGTGAGCTTTGAGGGCGG 1614
Db 1564 AGCAGACGAGCTGCTGTGAGAGAAAGTGTGCTTCAATGAGTGTGAGCTTTGAGGGCGG 1623

QY 1615 ACCGCAATGCAAGTGGCTTGCAGCAAGGAGAGAAATATCTGTGCGCATCTGCTGCGC 1674
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QY 1675 CGAGGCGTGAAGCTGAGCTGCAAGGCGAAGATGCTGCTGCTGCACTGACCTGCTGCC 1734
Db 1684 CGTGTGTGATGTGGGCTGCGAGGAGAAAGAGTGTGCTGCTGCACTATGCTGCC 1743
QY 1735 TGGCAGGAGCCACTTGCATTCGTCAGCTGCGGCAAGAGAGCGGGGGGAGATGGAAC 1794
Db 1744 TGGCAGGAGCCACTTGCATTTGTAAGCTGTAGCCAGAGAGCGCTGGAGTGAAT 1803
QY 1795 GCCCAGACGCTGATGAGAGAGAGCCCATGTCACCTGAGCCGACAGCGCGGCACTACCGC 1854
Db 1804 GCCCAGACATTAACGAGAGAGACCCCTGTCACCTGAGCTGTCTGAGAGGGGAGTACCGT 1863
QY 1855 GTGGCCCGCATCTCATGACCTGTGCTCCGAGCTCAACCTGTGACGCTGTGCGCAG 1914
Db 1864 GTGGCTGCAATCTCATGACCTGTGCTGTGATGTTAACATCTGACGCTTACAGGCAAG 1923
QY 1915 ACAACCCCTGACGTCGCGCGGAGAGCGGGGCAACAGAGCACTGAGCGGCTGCTCAT 1974
Db 1924 ACACCTGTGATGTCGTGAGAGAGCTGAGACATGATGATGTCGAGAGCTTCTGAT 1983
QY 1975 CGGGGCGCTGCGAAGAGAGCGCTGACCTCAGACGCTTACACCGCTGCACTGCTGCC 2034
Db 1984 CGTGTGCTGCGAAGAGAGCTTTGATGCTTCAAGAGGCTATCTGCTTTCAGCTGGAGCC 2043
QY 2035 CGCAACGAGACCTGAGCACTGTCAAGCTGCTGTGAGAGAAAGCTGATGCTGCTGCC 2094
Db 2044 CAGATGAGACCTGAGCTGTCAGAGCTGCTCATGAGAGAGAGCTGATGATGCTGCT 2103
QY 2095 CGGGGAGCCCTGAAACAGAGCGGGGCTGACCTGAGCTGCGCCAGCGGCACTCGAGGCT 2154
Db 2104 CGGGGCTCCCTGATGTCAGAGAGCTGACCTGAGCTGCTGCTGAGCACTCAGAGGCT 2163
QY 2155 GTGAGAGATGTTGTCAGAGCGCGGATGTCATTTGATGATGATGATGAGAGGAGCT 2214
Db 2164 GTAGAGAGCTGTGTCAGAGCTGTCAGCTTATGATGATGATGAGAGGAGCTTCAAGGCA 2223
QY 2215 CTGCACTGCGCGCCAGAGCGCGGAGCAAGAGCTGTGAGAGCTGCTGCTGAGAGGCT 2274
Db 2224 CTGCACTGCGCTGTCAGAGGAGGAGCTTCAAGAGCTGTGAGAGCACTGCTCAACATGAG 2283
QY 2275 GCCCAGATCAACCTGAGAGAGCTTCAAGTTCAGAGGAGGAGGAGGAGGAGGAGGAG 2334
Db 2284 GCAACATCAACCTTGCAGAGCTTCAAGTTCAGAGAGGAGGAGGAGGAGGAGGAGGAG 2343
QY 2335 CTGCGCGAAGCAAGACTAG 2355
Db 2344 CTCGAGCGAGCAAGACTAG 2364

RESULT 8
US-09-312-283C-257
Sequence 257, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011C2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 257
LENGTH: 3516

TYPE: DNA
ORGANISM: Mouse
US-09-312-283C-257

Query Match 74.1%; Score 1745.4; DB 4; Length 3516;
Best Local Similarity 84.6%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 356; Indels 8; Gaps 3;

QY 2 TGAAGGCGACGCGCGGAGCCCGCATGCGCTGCGCTGCGCACTTTCAGCGCGGCG 61
DB 5 TGAAGGCGAGGGCGCGGGCGCTGCGGCGCTGCGCTGCGCACTTTCAGCGCGGCG 64
QY 62 AGTTCACGGCGCTGGAGAAAGTGGGCTGCGGCGGCTTGGCGGAGGTGACAAAGTGGCGC 121
DB 65 AATTGCGAGGCTGGAGAAAGTGGGCTGCGGCGGCTTGGCGGAGGTGACAAAGTGGCGC 124
QY 122 ATGTCCACTGGAGAAGCTGGCTGGCCATTCAGATGTGCGCCAGCTGACGTGACGACA 181
DB 125 ATGTGCACTGGAGAAGCTGGCTGGCCATTCAGATGTGCGCCAGCTGACGTGACGACA 184
QY 182 GGGAGCGACATGAGGCTTTTGAAGAAAGCCAGAGAGATGAGATGGCCAAAGTTTGGCTACA 241
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DB 245 TTCTTACCTGTGTATGAGCATATGCGAGAACTGTGCGGCTGTGTATGAGATGAGAGA 304
QY 302 CGGGCTCCCTGGAAAGGCTGCGGCTTGGAGCAATGCGAGGATCTCGGGTTCCGAA 361
DB 305 CAGGCTCCCTGGAGAAAGCTGCGGCTTGGAGCAATGCGAGGATCTCGGGTTCCGCA 364
QY 362 TCATCCACGAGACGGCGGTGGCATGAATTCCTGCACTGCACTGCAATGGCCCGCATCTTGC 421
DB 365 TCGTCACGAGACAGCGCGGTGGCATGAATTCCTGCACTGCACTGCAATGGCCCGCATCTTGC 424
QY 422 AGCTGAGCCTCAAGCCCGGAAATCTGCTGGAGATGCCATCAACGCTCAAGATTTTCTG 481
DB 425 AGCTGAGCCTCAAGCGGAGCAATCTGCTGGAGATGCCATCAACGCTCAAGATTTTCTG 484
QY 482 ATTTTGTCTGCGCAAGTGCACAGGGCTGTCCCATCTGCAATGACCTCAAGCATGATGAGCC 541
DB 485 AGCTTGGGCTGGCGCAAGTGCATGAGCATGTCCCATCTGCAATGACCTCAAGCATGATGAGCC 544
QY 542 TGTTTGGCAATATCGCTCACTCCCTCCAGAGCGCATCAAGGAGAAAGCGGCTTTTGC 601
DB 545 TGTTTGGTATCATATCGCTCACTCCCTCCAGAGCGAATGTGAGAAAGCGGCTTTTGC 604
QY 602 ACAACGAGCATATGATATCAAGCTTTGGCATGTGATCTGGGCGGTGCTCAACAGAGAGA 661
DB 605 ACAACGAGCATATGATATCAAGCTTTGGCATGTGATCTGGGCGGTGCTTACACAGAGAGA 664
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DB 665 AGCCATTTGCATATGAGAGAAATCTGCGCATCATATGATGAGAGGTGAGAGGCGCAC 724
QY 722 GCCCGGAGCTGCGCGCGGTGTCAGAGCGCGCGCGCGCTGCAAGCCACTGATAGCGC 781
DB 725 GCCCGAGCTGCGCACCTCATCTGAGACCGCGCGCGCGGTGCTGTCAGAGCTGATAGGCGC 784
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DB 785 TCATGCAAGGTGTGTGCGAGGGGAGATCCGCGAGTTAGGCCCATTTCCAAAGAAATTAATT 844
QY 842 CTGAAGACGAGGACCTGTGTGAAGAAAGCTGATGACGAGTGAAGAAATGTGCTCATGATC 901
DB 845 CTGAAGACGAGGACCTTTTGTGAAGAGCTGATGAGAGGTGAAGAAATGTGCTCATGAGC 904
QY 902 TGAAGCTGAAGAAAGCCCGCGAGCCCGAGAGCGAGGTGTGCTG-----GAGGCTCA 955
DB 905 CAGGCGAGAGAAAGCTCTCTTAGAGTCCAGAGTGAAGGCGCGAGGTCTTCAACGCTCA 964
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DB 965 AGCGGCGCTCTGCTGCGCCCGCTTGATTAACGATGCAAGTCTCTCGAGGTGCTGTCAAGT 1024
QY 1016 TGAAGCTGAGATTTCCAGAGCTGTGAGAGGCCCGGAGAGCTTACGCGAGCTCTCTG 1075
DB 1025 TGAAGCTGAGATTTCCAGAGCTTGTGAAGGCCCGGAGAGCTTACGCGAGGTCTCTG 1084
QY 1076 AGTCAAGCTGCGCATGCTGCGGCGAGTGGAGAGGCTCTGCGGCGGTGCTCTGCTGAGACT 1135
DB 1085 AATCAAGCTTCCATGCTTCCAGAGTGGCAAGAGCTCTGCGGCGGTGCTCTGAGTGAAGCT 1144
QY 1136 CCGGCTTCTCTTCCAGAGATTCATGCTGCTGTCTTTTGAAGCGGAGAACTTCAACAGCG 1195
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DB 1205 AGCTGGCGCCGAC--AGACATTCAGAGAGAAAGAGTGTGATGCTATTCATCAAGGGAGC 1263
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DB 1264 ACCAGCAGCTGATGAAGATTCACAGCCCGAGATGTGACTTGTGTTTGAAGAGAGCT 1323
QY 1315 GCCAGCTGCTGCACTGCGCGGTGAGAGCGCGGAGAGAGATGCGCAAGTGGCTGCTG 1374
DB 1324 GCCAGCTGCTGCACTGCTGCTGTGAGAGCGGAGAGAGAGATGCTGCAAGTGGCTGCTG 1383
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DB 1384 CTTAACATGTCACCCCAACCTGAGCAACAGAGAGGCTTCAACCACTCATATATGCT 1443
QY 1435 GTGAGAGAGAGGTGCGGCGGTGTGTGAGAGCTGCTGCTGCGCAAGGAGATGAAGTCAAC 1494
DB 1444 GTGAGAGAGAGAGAGCTGAGATTTGTAGAGTACGTGAGCGGAGAGACAGATGTCAT 1503
QY 1495 GCCAAGATGAGAGACCAAGTGCAGAGCCCTCCACTTTCAGCGCCAGAAAGCGGAGTATGCT 1554
DB 1504 GCCAAGATGAGAGACAGATGAGAGCTGCTGCACTTTCAGCGCCAGAAAGGAGATGAGGCGC 1563
QY 1555 AGCAACAGCTGCTGTGAGAGAGAAAGCTGCTGCTGCAACAGAGTGTGACTTTGAGGCGCG 1614
DB 1564 AGCAACAGCTGCTGTGAGAGAGAAAGCTTGTCAATGAGGTGTGACTTTGAGGCGCGA 1623
QY 1615 AGCGCCATGCAACGCGGCTGCTGCAAGCGGAGAGAAATTCGCGCATCTGCTGCGC 1674
DB 1624 AGCGCCATGCAATGAGCTGCTGCAAGCGGAGAGAAATTCGCGCATCTGCTGCGC 1683
QY 1675 CGAGCGGTGAGAGTGAAGCTGTCAGAGGAGAGATGCTGCTGCTGCACTGACTGACTGCGC 1734
DB 1684 CGTGTGTGATGTGTGCGCTGTCAGAGGAGAGAGATGCTGCTGCTGCACTGACTGCGC 1743
QY 1735 TGGCAGGCGCACTGCGCATCTGTCAGAGCTGTGCGCAAGCAGCGGAGGTGATGTGAAC 1794
DB 1744 TGGCAGGCGCACTTCCCATTTTAAGCTGTACCAAGCAGCTGCGGAGGTGATGTGAAT 1803
QY 1795 GCCCAGAGCTGTGATGAGAGAGAGCGCATTTGCACTGTGCGCGAGCGCGGCACTAACCGC 1854
DB 1804 GCCCAGAGCATGAGAGGAGAGAGAGCGCGCATTTGCACTGTGCGCGAGCGGCACTTAACCGT 1863
QY 1855 GTGGCGGCGCATCTCATGAGCTGTGCTGCGAGCTGCAAGCTGTCAGAGCTGCTGCGCAG 1914
DB 1864 GTGGCTGCGCATCTCATGAGCTGTGCTGCGAGCTGTCATGATGATGATGAGAGCTTACAG 1923
QY 1915 ACAACCTGCAAGTGTGCGCGGAGAGAGAGGAGAGAGAGCTGCGAGCTGCTGCTGAT 1974
DB 1924 ACAACCTGCAATGTGTGCGAGAGAGCTGAGACACTGTGATGCGAGAGCTTCTGCTGAT 1983
QY 1975 CGGGCGCTGCGCAGAGAGAGCGGTGACCTTCAAGCGCTTACACCGCTGCGCACTGCGCGC 2034
DB 1984 CGTGTGTGCGCAGAGAGAGCTTTGACCTTCAAGAGGCTTATATGCTTGTGCACTGCGCAGCGC 2043
QY 2035 CGCAACGAGCACTGCGCACTGTCAAGCTGCTGTGCGAGAGAGAGCGGATGTGCTGCGC 2094

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1446 GTGAGAGCGGAAAGGAGCGTGAATTTGTGAGCTAGCCCGGAAAGACAGATGTCAAT 1505
1495 GCCAAGATGAGACCAATGAGCAAGCCCTTCCATTGTGAGGCCGAAACGGGGATGAGCT 1554
1506 GCCAAGATGAGACCAATGAGCAAGCCCTTCCATTGTGAGGCCGAAATGGAGAGCC 1565
1555 AGCACAAGGCTGCTGTGAGAGAAAGCCTCGGTCAAGAGATGAGCTTTGAGGGCCGG 1614
1566 AGCACAAGGCTGCTGTGAGAGAAATCTTGTCAATGAGTGAATTTGAGGGCCGA 1625
1615 AGCACAAGGCTGCTGTGAGAGAAATCTTGTCAATGAGTGAATTTGAGGGCCGG 1674
1626 AACACCATGATGTAGCTGCTGCAAGATGAGCAAGAGAAATTTGTGAGCTGCTGCGC 1685
1675 CGAGCGGTGAGAGTGAAGCTTGAAGGCGAAGATGCTGCGCACTGCACTAGCGTGC 1734
1686 CGTGTGTGAGATGTGAGGCTGCGAGGAAAGATGCTGCTGCTGCACTAGCTGCC 1745
1735 TGGCAGGGCCACCTGCGCATGTCAGACT 1763
1746 TGGCAGGGCCACCTTCCCATTTGTAAGCT 1774

RESULT 10
US-09-188-930-66
Sequence 66, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murlson, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PaedSeq For Windows Version 3.0
SEQ ID NO 66
LENGTH: 1888
TYPE: DNA
ORGANISM: mouse
FEATURE:
NAME/KEY: unsure
LOCATION: (1690)...(1690)
NAME/KEY: unsure
LOCATION: (1755)...(1755)
NAME/KEY: unsure
LOCATION: (1864)...(1864)
US-09-188-930-66

Query Match 54.5%; Score 1284; DB 3; Length 1888;
Best Local Similarity 83.1%; Pred. No. 1.5e-287;
Matches 1572; Conservative 0; Mismatches 298; Indels 21; Gaps 9;

2 TGGAGGCGACAGCGCGGAGCCCAATGAGCCCTGCGCTGCTGCGACCTTTGACGCGGGCG 61
5 TGGAGGCGAGGCGCGGGCCCGGTGCGCTCTGCGGCTGCTGCGACCTTTGACGCGGGCG 64
62 AGTTCAAGGCTGCGGAGAGAGTGGGCTCGGGCGGCTTGGGGCAGGTGACAGAGTGGCG 121
65 AATTTGCGAGCTGCGAGAGAGTGGGCTCGGGCGGCTTGGGGCAGGTGACAGAGTGGCG 124
122 ATGTCACTGAGAGACCTGCGCTGCGCATCAAGTCTCGCCAGCCTGCACTGCAAGAGCA 181
125 ATGTGACCTGAGAGAGCTGCTGCGCATCAAGTCTCGCCAGTCTGCACTGCAAGAGCA 184
182 GGGAGCGCATGAGCTTTTGGAAAGAAAGCAAGAGATGAGATGGCCAAAGTTTGGCTACA 241

185 GGGAGAGATGAGAGCTCTGAGAGAGCTAAAGAAATGAGATGGCCAAAGTCCGATACA 244
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245 TTCTACCTGTGTATGAGCATTTGCCCGGACCTGTGGCTGTGTATGAGATTAATGAGAGA 304
302 CGGGCTTCCGAGAGAGCTGTGGCTTGGAGCATTTGCCCGGACCTGTGGCTGTGTATGAG 361
305 CAGGCTTCCGAGAGAGCTGTGGCTTGGAGCATTTGCCCGGACCTGTGGCTGTGTATGAG 364
362 TCATCCAGAGAGCGCGGTGGAGATGAATCTTCTGCACTGCAATGAGCCCGGACCTGTGC 421
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422 ACTGAGACTGAGAGCGCGGTGGAGATGAATCTTCTGCACTGCAATGAGCCCGGACCTGTGC 479
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480 -TGAATTTGGATGAGAGCGCGGTGGAGATGAATCTTCTGCACTGCAATGAGCCCGGACCTGTGC 538
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539 GCTGTTTGGAGCGCGGTGGAGATGAATCTTCTGCACTGCAATGAGCCCGGACCTGTGC 598
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659 AGAAGCGGTGGAGAGCGCGGTGGAGATGAATCTTCTGCACTGCAATGAGCCCGGACCTGTGC 718
665 ATTAATCAATTTGGAGAGCGCGGTGGAGATGAATCTTCTGCACTGCAATGAGCCCGGACCTGTGC 724
719 ACCGCGCGAGAGCGCGGTGGAGATGAATCTTCTGCACTGCAATGAGCCCGGACCTGTGC 778
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1205 CAGGAGAGCGCGGTGGAGATGAATCTTCTGCACTGCAATGAGCCCGGACCTGTGC 1263
1249 CGGAGAGAGCGCGGTGGAGATGAATCTTCTGCACTGCAATGAGCCCGGACCTGTGC 1308

Db	1264	GGGGACACCAAGAGCTGATGAAATCTCTACAGCCCCCAAAATGTGACTTGTCTTAAGAC	1323
Qy	1309	AGCGATCCAGACCTGCTGCACTTGGCGGTGAGGCCGGGCAAGAGAGTGCCTCAAGTGG	1368
Db	1324	AGCAGTCCAGACCTGCTGCACTTGGCGGTGAGGCCGGGCAAGAGAGTGTCTCAAGTGG	1383
Qy	1369	CTGTGCTTCAACATATGCAACCCCAACCTTGAAGCAACCTTGAAGGCTTCCACCCCGTTGCAC	1428
Db	1384	CTGTGCTTCAACATATGCAACCCCAACCTTGAAGCAACCTTGAAGGCTTCCACCACTGCAAT	1443
Qy	1429	ATGCGCTGAGAGAGAGGTGCGGGGTGTGCTGAGAGCTCTGCTGGGCAAGAGATCAAT	1488
Db	1444	ATGCTGTGAGAGCGGAGAGGAGCGTGAATTTGTGAAGTTACTGTGAGCCCGGAGACCAAGT	1503
Qy	1489	GTCACCGCAAGATGAGAGCAAGTGAACAGCCCTCCACTTTTGACCCCAAGCCGGGAT	1548
Db	1504	GTCATGCTCAAGATGAGAGCAAGTGAACAGCTGCTGCACTTTGCAAGCCCAAAATGGGAGT	1563
Qy	1549	G-AATCTAAGCAACGGCTGCTGTGTAAGAAAGACGCTTGCTCAACGAGGTGAACCTTTGA	1607
Db	1564	GAAGGCCAGCAAGAGGCTGCTGTGAAGAAAGATCTTGTCAATGAGGTGAACCTTTGA	1623
Qy	1608	GGGCGGAGCGCCATGACAGTGGCGCTCCAGACAGGCGAGAGAAATATCTGCGCAATCTT	1667
Db	1624	GGGCGGAGCAACCTATGCAATGTAGCTCTCCAGCAATGACAGAGAACTTTGTGGCAACCTT	1683
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Qy	1728	CGTGTCTGAGAGGGCCCACTGCTCCATCTGTCAAGCTCTGTGGCCAAAGAGCCGGGGTGAAG	1787
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Qy	1788	TGTGAAGCGCCAGAGCGTGAATGGAGAGAGCGCAATGCACTGGCCGCAAGCGCGGCA	1847
Db	1803	TGTGAATGCCAGACACTAAGGAGAGACACCTGACCTGTGTTCAA-----GGGGCA	1857
Qy	1848	CTACCGCGTGGCCCGCATCTCATGACCTTG	1878
Db	1858	TTTACAGGTGCTGCAATTTCTCAATTAACCTTG	1888
RESULT 11			
US-09-312-283C-66			
Sequence 66, Application US/09312283C			
Patent No. 6573095			
GENERAL INFORMATION:			
APPLICANT: Watson, James D.			
APPLICANT: Strachan, Lorna			
APPLICANT: Sleeman, Matthew			
APPLICANT: Onrust, Rene			
APPLICANT: Murison, James G.			
APPLICANT: Kumble, Krishanand D.			
TITLE OF INVENTION: Compositions and Methods for Their Use			
FILE REFERENCE: 11000.1011c2			
CURRENT APPLICATION NUMBER: US/09/312,283C			
CURRENT FILING DATE: 1999-05-14			
NUMBER OF SEQ ID NOS: 425			
SOFTWARE: FastSeq For Windows Version 4.0			
SEQ ID NO 66			
LENGTH: 1888			
TYPE: DNA			
ORGANISM: Mouse			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: (1)...(1888)			
OTHER INFORMATION: n = A,T,C or G			
US-09-312-283C-66			
Query Match	54.5%	Score 1284;	DB 4; Length 1888;
Best Local Similarity	83.1%;	Pred. No. 1,5e+287;	

QY 2094 CCGGGGACCCCTGGAACGAGCGCTGCACTGCGTGGCCGCCCAAGGCT 2153
DB 27994 CCGGGGACCCCTGGAACGAGCGCTGCACTGCGTGGCCGCCCAAGGCT 28053
QY 2154 GGTGAGAGATTGTGTCAGCGCGATGTATGACCTGTTCACGACGAGGGCTCAGCGC 2213
DB 28054 GGTGAGAGATTGTGTCAGCGCGATGTATGACCTGTTCACGACGAGGGCTCAGCGC 28113
QY 2214 GCTGCACTGCGCGCCCGGCGGCGACGACGACGCTGTGAGACTGTCTCAGGATGG 2273
DB 28114 GCTGCACTGCGCGCGCGGCGGCGACGACGCTGTGAGACTGTCTCAGGATGG 28173
QY 2274 GGGCCACATCAACCTGCAAGCTCTCAAGTTCAGGGCGGCGACATGGCCCGCCACACT 2333
DB 28174 GGGCCACATCAACCTGCAAGCTCTCAAGTTCAGGGCGGCGACATGGCCCGCCACACT 28233
QY 2334 CCTGCGCGAAGCAAGACTAG 2355
DB 28234 CCTGCGCGAAGCAAGACTAG 28255

RESULT 13
US-09-949-016-16947
; Sequence 16947, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16947
; LENGTH: 31720
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16947

Query Match 48.1%; Score 1131.6; DB 4; Length 31720;
Best Local Similarity 99.5%; Pred. No. 8-2e-252;
Matches 1156; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
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DB 27334 GGTGAGAGAGAGGCGGGGCTGTGAGAGCTCTGCTGCAAGAGATCAATGTCAA 27393
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QY 1794 CGCCCAAGCTGGAATGAGAGAGCGCAATGCACTGAGCGGCAAGCGGCGGCACTACCG 1853
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QY 1914 GACACCCCTGCAAGTGGCCCGGAGAGAGGGGCAACGAGACCTGCGAGGCTGCTGCA 1973
DB 27814 GACACCCCTGCAAGTGGCCCGGAGAGAGGGGCAACGAGACCTGCGAGGCTGCTGCA 27873
QY 1974 TCGGGGCGCTGGAAGAGGCGGCTGACCTGACGAGCTACACCGCTTGTGCACTGAGCTGC 2033
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DB 28234 CCTGCGCGAAGCAAGACTAG 28255

RESULT 14
US-09-949-016-39628/c
; Sequence 39628, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

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: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0.
: SEQ ID NO 39628
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Human
: OS-03-949-016-39628

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Query Match	23.6%	Score 555.4;	DB 4;	Length 601;
Best Local Similarity	99.1%;	Pred. No. 5e-119;		
Matches 578; Conservative	1;	Mismatches 2;	Indels 2;	Gaps 2;

OY	1195	GATCTGGGTACACAAAGACGTCCAGAAAGAAAGCTTGTGATGTCATCGTGTCC	-GGGA	125
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OY	1254	CACCAAGCAATGTATGAAGATCTTGACGCCGACGACCTTGACCTTGACCTTGAC	CAAGCG	131
Db	523	CACCAAGCAATGTATGAAGATCTTGACGCCGACGACCTTGACCTTGACCTTGAC	CAAGCG	464
OY	1314	TGCCAGCCTGCTGACCTTGCGCGTGTGAAGCGCGGGAAGAAGATGTACCAATGCTGT		137
Db	463	TGCCAGCCTGCTGACCTTGCGCGTGTGAAGCGCGGGAAGAAGATGTACCAATGCTGT		404
OY	1374	GCTCAACAAATGCCAACCCCAACCTTGACCAACCTGTAGGGCTCAACCCCGTGTCAATGGC		143
Db	403	GCTCAACAAATGCCAACCCCAACCTTGACCAACCTGTAGGGCTCAACCCCGTGTCAATGGC		344
OY	1434	CGTGAAGAGAGGGGTGCAGGGGTGTCTGTGAGGCTCTCTGTGACAGGAAGATCATGTGTCAA		149
Db	343	CGTGAAGAGAGGGGTGCAGGGGTGTCTGTGAGGCTCTCTGTGACAGGAAGATCATGTGTCAA		284
OY	1494	CGCCAAAGATGAGAACCAATGTGACAGCCCTCCACTTTGACGCCAGAAACGGGATGAGTCC		155
Db	283	CGCCAAAGATGAGAACCAATGTGACAGCCCTCCACTTTGACGCCAGAAACGGGATGAGTCC		224
OY	1554	TAGCAACAGGCTGCTGTTTGAAGAAGAACGCTCCGCTCAACAGAGTGAACCTTTGAGGGCCG		161
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OY	1614	GACGCCCATGTCACTGTGCGCTTGCCACGACCGGGACAGGAATATCTGTGCATCTGTCTCG		167
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RESULT 15
US-09-949-016-181231/c
; Sequence 181231, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PaStSeq for Windows Version 4.0
; SEQ ID NO: 181231
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
DS-09-949-016-181231

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Query Match	23.6%	Score 555.4;	DB 4;	Length 601;
Best Local Similarity	99.1%	Pred. No. 5e-119;		
Matches 578;	Conservative 1;	Mismatches 2;	Indels 2;	Gaps 2

OY	1195	GATCTGGGTTCACAAAGACGTTCAGGAAGAAAGACTTGTGATATCCATCGTGTCC-AGGA	1253
Db	582	GATCTGGGCACAC-AGACGTCCAGAGAAAGAAAGACTTGTGATATCCATCGTGTCCGGGGA	524
OY	1254	CACCAAGCAAACTGATGTAAGATCTTCAGACCGCAGAGACGTGACCTTGGCACTGACACACCG	1313
Db	523	CACCAAGCAAACTGATGTAAGATCTTCAGACCGCAGAGACGTGACCTTGGCACTGACACACCG	464
OY	1314	TGCCAGCTCGTGTGACCTCGCGGTGAGAGGCGCCAGAGAGTGGCGCAAGTGGTCT	1373
Db	463	TGCCAGCTCGTGTGACCTCGCGGTGAGAGGCGCCAGAGAGTGGCGCAAGTGGTCT	404
OY	1374	GCTCAACAATGCCAACCCCAACCTGAGCAACCTGTAGGGGCTCCACCCCGTTGCAATGGC	1433
Db	403	GCTCAACAATGCCAACCCCAACCTGAGCAACCTGTAGGGGCTCCACCCCGTTGCAATGGC	344
OY	1434	CGTGAAGAGAGGGTGCGGGGTGTCTGTAGACTCTCTGCTGGCACGGAAGATCAGTTCAA	1493
Db	343	CGTGAAGAGAGGGTGCGGGGTGTCTGTAGACTCTCTGCTGGCAGGAAGATCAAGTTCAA	284
OY	1494	CGCCCAAGATAGAGAACCAATGTGGAACAGCCCTCACTTTGACGCCAGAACGGGGAGTTAGTTC	1553
Db	283	CGCCCAAGATAGAGAACCAATGTGGAACAGCCCTCACTTTGACGCCAGAACGGGGAGTTC	224
OY	1554	TAGCAACACGGCTGTGTGTGAGAGAAACGCTCGGTCAACAGAGTGTGACTTTGAGGGCCG	1613
Db	223	TAGCAACACGGCTGTGTGTGAGAGAAACGCTCGGTCAACAGAGTGTGACTTTGAGGGCCG	164
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OY	1674	CCGAGGCGTGTGACGTGTGACCTTCGACGGGCAAGAGATGCTGTGGCACTGACCTTACGCTGG	1733
Db	103	CCGAGGCGTGTGACGTGTGACCTTCGACGGGCAAGAGATGCTGTGGCACTGACCTTACGCTGG	44
OY	1734	CTGGCAGGGCCACCTGGCCATGTCAAGCTCTGGCCAAAGCAG	1776
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genomic survey sequence.
ACCESSION AY419491
VERSION AY419491.1 GI:39775448
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
AUTHORS 1 (bases 1 to 1901)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trios
TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
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ORIGIN
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Best Local Similarity 86.7%; Pred. No. 0;
Matches 1648; Conservative 0; Mismatches 253; Indels 0; Gaps 0;
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DB 61 CTGCTGCTGTATGATCTGCGCGAAGCTGTGCGCTGTGTCAATGATGATGAGAGC 120
QY 303 GGGCTCTCTGAGAAAGCTGCTGCTGAGGCGATTCGATGAGATCTTCGCTTCGAAT 362
DB 121 GGGCTCTCTGAGAAAGCTGCTGCTGAGGCGATTCGATGAGATCTTCGCTTCGAAT 180
QY 363 CATTCACGAGAGCGGCGGTGGGATGAACTTCTGACATGACATGAGCCCGCGCATCTCTGCA 422
DB 181 CATTCACGAGAGCGGCGGTGGGATGAACTTCTGACATGACATGAGCCCGCGCATCTCTGCA 240
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DB 301 TTTTGGTCTGGCCAAAGTGAAGCGGCTGTCCATCTGCAATGACCTTCAGATGATGAGCTT 360
QY 543 GTTTGGCAATCGCTACCTCCCTCAGAGGCGATCAGGAGAGAGCGGCTCTTGA 602
DB 361 GTTTGGCAATCGCTACCTCCCTCAGAGGCGATCAGGAGAGAGCGGCTCTTGA 420

QY 603 CACCAAGCAGATGATATACGCTTTCGATGTCATCTGAGGCGTGTCTACACAGAGAA 662
DB 421 CACCAAGCAGATGATATACGCTTTCGATGTCATCTGAGGCGTGTCTACACAGAGAA 480
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DB 481 GCCCTTTCAGATGAGAGAAACATCTTCGACATCATGATGAGAGGTGTAAGGCCACCG 540
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DB 541 CCCCAGCTGCGCCCGTGTGACAGATCCCGGCGGCGCTGACGCCACCTGATACGCT 600
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DB 601 CATCAGCGGTGCTGGAGAGGGGATCCGCGATTAAGGCCCACTTCAAGAAATTACTTC 660
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 1
 Carninci, P., and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
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 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
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 3
 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, U., Nishi, K., Kitamura, T., Tashiro, H., Itoh, M.,
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 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
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 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
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 5
 The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
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 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3741)
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 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
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 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M., and Hayashizaki, Y.
 Direct Submission
 Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

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CONSRTM	TITLE				
JOURNAL					
COMMENT					

FEATURES

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ORGANISM Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 1119)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@db-remail.nih.gov
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cDNA Library Preparation: Life Technologies, Inc.
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 35.8%; Score 843.4; DB 5; Length 1119;
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DB	912	ATGATCTTGGACGGGAAAAGCCCCCGGAGATCCGAGAACCAAGGTGTGGCTGGAG	971
QY	951	GCTCAGCGGGGCTCTGGCCCCA--CCTTGATTAACAAGTACAGCTCTCC--GAGCT	1004
DB	972	GCTCAGGGGGGCCCTTGGCCCCCAGCTTGAAGAACATTAAGGCTTTTCGAAGTTGT	1031
QY	1005	TCTCTCAGAGCTGAGCTCTGGAGTTTCCC	1033
DB	1032	TCTTAAGATTGGACTCTGGAGTTTCC	1060
RESULT 7			
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DEFINITION	17000424186811 GRN_EB Homo sapiens CDNA 5', mRNA sequence.		
ACCESSION	CN308493		
VERSION	CN308493.1	GI:47324907	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukariyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 731)		
AUTHORS	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandelam, R., Lebkowski, J. and Statton, L. M. Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation		
JOURNAL	Contr. Biotechnol. 22 (6), 707-716 (2004)		
COMMENT	Contact: Brandenberger R Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@geron.com Insert Length: 731 Std Error: 0.00.		
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source	1..731 Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" /clone_lib="GRN_EB" /note="Oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."		
ORIGIN			
Query Match	29.4%;	Score 691.6;	DB 7; Length 731;
Best Local Similarity	99.2%;	Pred. No. 7.1e-138;	
Matches	716;	Conservative	0; Mismatches 4; Indels 2; Gaps 2;
QY	681	GAACTCTTGGCACTATCATGTGTGAAGTGTGAAGGGCCACCGCCCGAGCTGGCGGCGGT	740
DB	11	GGAAATCTTGGCACTATCATGTGTGAAGTGTGAAGGCCACCGCCCGAGCTGGCGGCGGT	70
QY	741	GTGCGAGAGCCGCGCGCGCGCTGGAGCACTGATAGCGCTCATGCAAGCGGTGTCTGCA	800
DB	71	GTGCGAGAGCCGCGCGCGCGCTGGAGCACTGATAGCGCTCATGCAAGCGGTGTCTGCA	130
QY	801	GGGGGATCCGCGAGTTTAGGCCCACTTCCAGAAATTAATTCTTGAACCGAGACCTGTG	860
DB	131	GGGGGATCCGCGAGTTTAGGCCCACTTCCAGAAATTAATTCTTGAACCGAGACCTGTG	190
QY	861	TGAAAGCCTGATTAAGCAAGTGAAGAAATCTCTCATATGATCTGAGCGTGAAGAGCCCCC	920
DB	191	TGAAAGCCTGATTAAGCAAGTGAAGAAATCTCTCATATGATCTGAGCGTGAAGAGCCCCC	250

Qy	921	GGAGCCGAGGAGGAGGTGTGCTGTGGAGAGCTTCAAGCCGGGCTCTTGCCTCCATCTTTCGA	980
Db	251	GGAGCCGAGGAGGAGGTGTGCTGTGGAGAGCTTCAAGCCGGGCTCTTGCCTCCATCTTTCGA	310
Qy	981	TTAAGCATTAAGAGCTCTCCAGAGCTTCTCTCAAGCTTGAATCTTGAAGTTTCCAGAGCTGT	1040
Db	311	TTAAGCATTAAGAGCTCTCCAGAGCTCTCTCAAGCTTGAATCTTGAAGTTTCCAGAGCTGT	370
Qy	1041	CGAGGGGCTCCGAGGAGCTCAAGCCGAGCTCTCTGAATCCAGCTGCTGCATCTGTCCGGCAG	1100
Db	371	CGAGGGGCTCCGAGGAGCTCAAGCCGAGCTCTCTGAATCCAGCTGCTGCATCTGTCCGGCAG	430
Qy	1101	TGGGAAAGAAGCTCTCCGGGGGTGTCTCTCGGTGGAATCCGCGCTTCTCTTCAAGAGGATAGCT	1160
Db	431	TGGGAAAGAAGCTCTCCGGGGGTGTCTCTCGGTGGAATCCGCGCTTCTCTTCAAGAGGATAGCT	490
Qy	1161	GTGCTGTGCTCTTGGAGGGGAGAACCTTCAGACAGGAGATCTGGGTACACAGAGCTCCAGA	1220
Db	491	GTGCTGTGCTCTTGGAGGGGAGAACCTTCAGACAGGAGATCTGGGACACAGAGCTCCAGA	549
Qy	1221	AGAGAAGACTTGTGATGTGCATCGTGTCC-GGAGCAGCAGCAAACTGATGAAGATCTCTGC	1279
Db	550	AGAGAAGACTTGTGATGTGCATCGTGTCCGGGGGACACAGCAAACTGATGAAGATCTCTGC	609
Qy	1280	AGCGCGAGAGCTGTGAATCTTGAGCATGGAACAGCGGTGTCAGCTCTGTGCACTCTGGCGGTGG	1339
Db	610	AGCGCGAGAGCTGTGAATCTTGAGCATGGAACAGCGGTGTCAGCTCTGTGCACTCTGGCGGTGG	669
Qy	1340	AGGCGCGGCGCAAGAGATGTGGCGCAAGTGGGCTGTCTCAACAAATGGCAATCCCAACTGA	1399
Db	670	AGGCGCGGCGCAAGAGATGTGGCGCAAGTGGGCTGTCTCAACAAATGGCAATCCCAACTGA	729
Qy	1400	GC 1401	
Db	730	GC 731	

RESULT	8
BG031653	
LOCUS	
DEFINITION	BG031653 830 bp mRNA linear EST 24-JAN-2001 602300806F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4402320 5' , mRNA sequence.
ACCESSION	BG031653
VERSION	BG031653.1 GI:12422155
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 830) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LHAM1010 row: 1 column: 01 High quality sequence stop: 646.
FEATURES	Location/Qualifiers
SOURCE	1..830 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4402320" /tissue_type="mammary adenocarcinoma, cell line" /lab_host="DH10B (phage-resistant)" /clone_id="NIH_MGC_87"

/note="Organ: breast; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 27.7%; Score 651.2; DB 4; Length 830;
 Best Local Similarity 93.8%; Pred. No. 3.5e-129;
 Matches 765; Conservative 0; Mismatches 43; Indels 8; Gaps 8;

OY 1239 CCATCGTGTCCGGGACACCAAGAACTGATGAAGTCTTGACGCGCAGAGAGCTGACCT 1238
 DB 1 CCAATGCTGTCCGGGACACCAAGAACTGATGAAGTCTTGACGCGCAGAGAGCTGACCT 60

OY 1299 GGCACCTGGACA-GCGGTGCCAGCTCTGTCACCTTGCGGTGAGAGCGCGGCAAGAGAGT 1357
 DB 61 GGCACCTGGACAGCGCGGTGCCAGCTCTGTCACCTTGCGGTGAGAGCGCGGCAAGAGAGT 120

OY 1358 GCGGCAAGTGGCTGCTGCTCAACAAATGCAACCCCACTGAGCAACCGTAGGGGCTCA 1417
 DB 121 GCGGCAAGTGGCTGCTGCTCAACAAATGCAACCCCACTGAGCAACCGTAGGGGCTCA 180

OY 1418 CCCCCTTGACATGAGCGCTGAGAGAGAGGGGTGTGCTGAGAGCTCTGCTGAGCAC 1477
 DB 181 CCCCCTTGACATGAGCGCTGAGAGAGAGGGGTGTGCTGAGAGCTCTGCTGAGCGC 240

OY 1478 GGAAGATGATGTCAACGCCAAGATGAGAGCAAGCTGAGCAAGCCTTCCACTTTGAGCCC 1537
 DB 241 GGAAGATGATGTCAACGCCAAGATGAGAGCAAGCTGAGCAAGCCTTCCACTTTGAGCCC 300

OY 1538 AGAAGCGGGATGAGTCTGACACAGCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1597
 DB 301 AGAAGCGGGATGAGTCTGACACAGCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 360

OY 1598 TGGAATTGAGGGGCGGAGCGCCATGACAGTGGCTGCGCAGCAGCGGAGAGAGATATCG 1657
 DB 361 TGGAATTGAGGGGCGGAGCGCCATGACAGTGGCTGCGCAGCAGCGGAGAGAGATATCG 420

OY 1658 TGCGCATCTCTGCTGCGCGGAGAGCGCTGAGAGCTGAGAGAGAGAGAGAGAGAG 1717
 DB 421 TGCGCATCTCTGCTGCGCGGAGAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

OY 1718 CACTGCATGAGCGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1777
 DB 481 CACTGCATGAGCGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 538

OY 1778 CCGGGGTGAGTGTGAACGCCAGAGCGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAG 1836
 DB 539 CCGGGGTGAGTGTGAACGCCAGAGCGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAG 598

OY 1837 CAGCGCGGAGCACTACCGCGTGGCGGAGCTGATGACCTGTGTCTCGGAGCTCAAGCTC 1896
 DB 599 CAGCGCGGAGCACTACCGCGTGGCGGAGCTGATGACCTGTGTCTCGGAGCTCAAGCTC 657

OY 1897 -TGAGCGCTGCTGGG-CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1953
 DB 658 TTGAGCGTGTGAG 717

OY 1954 ACTGCGAGAGTGTCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2013
 DB 718 ACTGCGAGAGTGTCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777

OY 2014 ACCGCTGTGACCTTGGCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2049
 DB 778 ACCGCTGTGAGCTTGGCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 813

RESULT 9
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 LOCUS BUI51784
 DEFINITION AGENCOURT 8753255 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6394286
 5', mRNA sequence.

ACCESSION BUI51784
 VERSION BUI51784.1 GI:22665316
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 924)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED (1999)
 CONTACT: Robert Straubeberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Mark Macdonald, Ph.D. and Nancy L. Freeman, Ph.D.
 CDNA Library Preparation: ResGen, Invitrogen Corp
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
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 High quality sequence stop: 649.
 Location/Qualifiers
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 /clone_11b="NIH MGC 130"
 /note="Organ: olocyats; Vector: PCMV-SPORT6.1; Site 1: EcoRV, Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 27.5%; Score 647.2; DB 5; Length 924;
 Best Local Similarity 85.3%; Pred. No. 2.5e-128;
 Matches 733; Conservative 0; Mismatches 124; Indels 2; Gaps 1;

OY 10 GAGCGCGGAGAGCCCATGAGGCGCTGAGCGCTGAGCACTTCAAGCGGAGAGTTCACG 69
 DB 1 GAGCGCGGAGAGCGGTGGGCTGAGGCGCTGAGCGCTGAGCACTTCAAGCGGAGAGTTCACG 60

OY 70 GCGTGGAGAGAGTGGGCTGAGGCGCTGAGGCGAGGTGACAGAGTTCAGATGCTCAC 129
 DB 61 GCGTGGAGAGAGTGGGCTGAGGCGCTGAGGCGAGGTGACAGAGTTCAGATGCTCAC 120

OY 130 TGGAAGACTGGGCTGAGGCAATGAGTGCAGCCAGCGTGGACGAGAGAGAGAGAGAG 189
 DB 121 TGGAAGAGTGGGCTGAGGCAATGAGTGCAGCCAGCTGAGCGAGAGAGAGAGAGAG 180

OY 190 ATGAGGCTTTTGAAGAGAGCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 249
 DB 181 ATGAGGCTTTTGAAGAGAGCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

OY 250 GTGTATGAGCATCTGCGCGGAGAGCTGTGCGCTGTGTATGAGAGTACATGAGAGAGAG 309
 DB 241 GTGTATGAGCATCTGCGCGGAGAGAGCTGTGCGCTGTGTATGAGAGTACATGAGAGAG 300

OY 310 CTGGAAG 369
 DB 301 CTGGAAG 360

OY 370 GAGAGCGGAG 429
 DB 361 GAGAGCGGAG 420

OY 430 CTGAAGCCGCGAG 489
 DB 421 CTGAAGCCGCGAG 480

AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
TITLE Mizushima-Sugano,J., Nakai,K. and Sugano,S.
JOURNAL Sequence comparison of human and mouse genes reveals a homologous
COMMENT block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/clone="OPR0893"
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Query Match 23.1%; Score 545; DB 5; Length 583;
Best Local Similarity 100.0%; Pred. No. 2.2e-106;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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39 ATGAGAGGCGGACCGGCGGACCCCATGAGCCCTGCGGCTGCTGCGACCTTTCGACGCGGCG 98
61 GAGTTACGCGGCTGCGGAGAGGTGGGCTCGGCGCGCTTCGAGGAGGTATACAGGTGGCG 120
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121 CATGTCCATGGAAGACCTGGCTGGCATCAAGTCTGCGCCAGCTTCAGTCGACGAC 180
159 CATGTCCATGGAAGACCTGGCTGGCATCAAGTCTGCGCCAGCTTCAGTCGACGAC 218
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219 AGGAGCGCATGAGACTTTTGGAGAGAGCCAAAGAGATGAGATGGCCAAAGTTTCGCTAC 278
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399 ATCATCCACGAGACGGCGGCTGGGCGATGAACTTCTGCGACCTGATGAGCCCGCGCATCTCG 458
421 CACCTGAGACTCAAGCCCGCGAACAATCTGTGCTGATGCGCCACTACACAGTCAAGATTCT 480
459 CACCTGAGACTCAAGCCCGCGAACAATCTGTGCTGATGCGCCACTACACAGTCAAGATTCT 518
481 GATTTGGTCTGGCCAAAGTGAACGGGCTGTCCACTCGCATGACCTTCAAGCATGAGATGGC 540
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541 CTGTT 545
579 CTGTT 583

RESULT 12
BP248960
LOCUS BP248960 Sugano cDNA library, embryo kidney Homo sapiens cDNA clone
DEFINITION HKR12328, mRNA sequence.
ACCESSION BP248960

VERSION BP248960.1 GI:52131239
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
TITLE Mizushima-Sugano,J., Nakai,K. and Sugano,S.
JOURNAL Sequence comparison of human and mouse genes reveals a homologous
COMMENT block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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1..583
/organism="Homo sapiens"
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/clone="HKR12328"
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ORIGIN
Query Match 23.1%; Score 544; DB 5; Length 583;
Best Local Similarity 99.8%; Pred. No. 3.6e-106;
Matches 544; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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99 GAGTTACGCGGCTGCGGAGAGGTGGGCTCGGCGCGCTTCGAGGAGGTATACAGGTGGCG 158
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459 CACCTGAGACTCAAGCCCGCGAACAATCTGTGCTGATGCGCCACTACACAGTCAAGATTCT 518
481 GATTTGGTCTGGCCAAAGTGAACGGGCTGTCCACTCGCATGACCTTCAAGCATGAGATGGC 540
519 GATTTGGTCTGGCCAAAGTGAACGGGCTGTCCACTCGCATGACCTTCAAGCATGAGATGGC 578
541 CTGTT 545
579 CTGTT 583

RESULT 13
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LOCUS BP314864 Sugano cDNA library, mammary gland OCB-F Homo sapiens
DEFINITION cDNA clone OCB07268, mRNA sequence.
ACCESSION BP314864
VERSION BP314864.1 GI:52243839
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OPR07268"
/tissue_type="mammary gland"
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/note="mammary gland tumor"

ORIGIN
Query Match 23.1%; Score 543.4; DB 5; Length 583;
Best Local Similarity 99.8%; Pred. No. 4.9e-106;
Matches 544; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGAGGGGCGACGGGGGACCCCATGGGGCCCTGGGCGCTGCGACCTTCGACGCGGGC 60
|||
39 ATGGAGGGGCGACGGGGGACCCCATGGGGCCCTGGGCGCTGCGACCTTCGACGCGGGC 98
61 GAGTTCACGGGCTGGGAGAGAGTGAGCTCGGGCGCTTCGGGCAAGGTGTACAGGTGCGC 120
99 GAGTTCACGGGCTGGGAGAGAGTGAGCTCGGGCGCTTCGGGCAAGGTGTACAGGTGCGC 158
121 CATGTCCACTGGAAGACCTGCTGGCATCAAGTGTGCGCCAGCTGCACTGCAAGAC 180
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361 ATCTCCACGAGAGCGGGGATGAGACTTCTGCACTGAGATGAGCCCGGCACTCTG 420
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459 CACTGGAAGCTCAAGCCCGGCAAGCATCTGCTGAGATGCCACTACCAAGTCAAGATTCT 518
481 GATTTTGTCTGGCCAAAGTGAAGAGGCTGTCCCACTGCAATGACTCAAGCATGATGAGC 540

RESULT 14
BP248808 582 bp mRNA linear EST 15-SEP-2004
LOCUS BP248808 Sugano cDNA library, embryo kidney Homo sapiens cDNA clone
DEFINITION BP248808 Sugano cDNA library, embryo kidney Homo sapiens cDNA clone
ACCESSION BP248808
VERSION BP248808.1 GI:52131087
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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Query Match 23.0%; Score 542.4; DB 5; Length 582;
Best Local Similarity 99.8%; Pred. No. 8e-106;
Matches 543; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||
39 ATGGAGGGGCGACGGGGGACCCCATGGGGCCCTGGGCGCTGCGACCTTCGACGCGGGC 98
61 GAGTTCACGGGCTGGGAGAGAGTGAGCTCGGGCGCTTCGGGCAAGGTGTACAGGTGCGC 120
99 GAGTTCACGGGCTGGGAGAGAGTGAGCTCGGGCGCTTCGGGCAAGGTGTACAGGTGCGC 158
121 CATGTCCACTGGAAGACCTGCTGGCATCAAGTGTGCGCCAGCTGCACTGCAAGAC 180
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339 ACGGGCTCCCTGGAAGAGCTGCTGGCTTGGAGCCATTGCGCATGGGATTCGGGTTCCGA 398
361 ATCTCCACGAGAGCGGGGATGAGACTTCTGCACTGAGATGAGCCCGGCACTCTG 420

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Db      399 ATCATCCAGAGAGCGGCGTGGCATGAACCTTCCTGCACCTGCGCCCGCACTCCTG 458
Qy      421 CACCTGGACTCAAGCCCGGCAATCTCTGTGATGCGCCACTACCACTCAAGATTCT 480
Db      459 CACCTGGACTCAAGCCCGGCAATCTCTGTGATGCGCCACTACCACTCAAGATTCT 518
Qy      481 GATTTGCTCTGGGCAAGTGAACGGGCTGTCCACTGCACTGACCTCAGCATGAGATGGC 540
Db      519 GATTTGCTCTGGGCAAGTGAACGGGCTGTCCACTGCACTGACCTCAGCATGAGATGGC 578
Qy      541 CTGT 544
Db      579 CTGT 582

RESULT 15
BP277059          580 bp      mRNA      linear      EST 16-SEP-2004
LOCUS             BP277059 Sugano cDNA library, kidney Homo sapiens cDNA clone
DEFINITION        KDN07909, mRNA sequence.
ACCESSION         BP277059
VERSION           BP277059.1 GI:52190791
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE         1 (bases 1 to 580)
AUTHORS          Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
                  Mizushima-Sugano,J., Nakai,K. and Sugano,S.
                  Sequence comparison of human and mouse genes reveals a homologous
                  block structure in the promoter regions
                  Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL           Contact: Yutaka Suzuki
COMMENT           Department of Virology
                  Institute of Medical Science, University of Tokyo
                  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                  Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES          location/Qualifiers
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                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="KDN07909"
                   /tissue_type="kidney"
                   /clone_id="Sugano cDNA library, kidney"

ORIGIN
Query Match      22.8%; Score 537.6; DB 5; Length 580;
Best Local Similarity 96.0%; Pred. No. 8.5e-105;
Matches 546; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy      1 ATGGAGGCGACGCGGCGGACCCCATGGGCGCTGCGCATGCGCACCTTCGACGCGGCG 60
Db      12 ATGGAGGCGGACGCGGCGGACCCCATGGGCGCTGCGCATGCGCACCTTCGACGCGGCG 71
Qy      61 GAGTTCAAGGCGTGGGAGAAAGTGGGCTCGGCGGCTTCGGGCAAGGTGACAAAGTGGCG 120
Db      72 GAGTTCAAGGCGTGGGAGAAAGTGGGCTCGGCGGCTTCGGGCAAGGTGACAAAGTGGCG 131
Qy      121 CATGTCCACTGGAGAACCTGGGCTGGGCAATCAAGTCTGCCCGACGCTGCGACGAC 180
Db      132 CATGTCCACTGGAGAACCTGGGCTGGGCAATCAAGTCTGCCCGACGCTGCGACGAC 191
Qy      181 AGGAGCGCATGAGACTTTTGGAGAGACCAAGAGATGAGATGGCCAGTTTGGCTAC 240
Db      192 AGGAGCGCATGAGACTTTTGGAGAGACCAAGAGATGAGATGGCCAGTTTGGCTAC 251
Qy      241 ATCTGCTCTGTGTATGGCATCTGCCGGAACCTGTGGGCTGGTATGAGATGATGAG 300
Db      252 ATCTGCTCTGTGTATGGCATCTGCCGGAACCTGTGGGCTGGTATGAGATGATGAG 311
Qy      301 ACGGCTCCCTGGAAAGCTGTGGCTTCGAGACATTGCAATGGGATCTCGGTTCCGA 360

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Db      312 ACGGCTCCCTGGAAAGCTGTGGCTTGGAGACANTGGCATGGGATCTCCGGTTCGA 371
Qy      361 ATCATCCAGAGAGCGGCGTGGGCAATGAACTTCTGTGCACTGCAATGAGCCCGCACTCTG 420
Db      372 ATCATCCAGAGAGCGGCGTGGGCAATGAACTTCTGTGCACTGCAATGAGCCCGCACTCTG 431
Qy      421 CACCTGGACTCAAGCCCGGGAACATCTGTGCTGGAATGCCACTACCACTCAAGATTCT 480
Db      432 CACCTGGACTCAAGCCCGGGAACATCTGTGGAATGCCACTACCACTCAAGATTCT 491
Qy      481 GATTTGCTCTGGGCAAGTGAACGGGCTGTCCACTGCACTGACCTCAGCATGAGATGGC 540
Db      492 GATTTGCTCTGGGCAAGTGAACGGGCTGTCCACTGCACTGACCTCAGCATGAGATGGC 551
Qy      541 CTGTTTGGCAAAATCGCTCACTCTCC 569
Db      552 CTGTTTGGCAAAATCGCTCACTCTCC 580

Search completed: September 16, 2005, 06:26:00
Job time : 6738.33 secs

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PT New 14171 human protein kinase and nucleic acids encoding the protein,
PT useful for treating viral infections, cellular growth related disorders,
PT cancers, disorders related with programmed cell death, or autoimmune
PT disorders.

XX Claim 1; SEQ ID NO 3; 50pp; English.

CC This invention relates to a novel isolated nucleic acid sequence and the
CC novel kinase protein encoded by it. Protein kinases play critical roles
CC in the regulation of biochemical and morphological changes associated
CC with cellular growth and division. The sequences of the invention may be
CC useful for gene therapy. The protein kinase or the nucleic acid encoding
CC the protein is useful for modulating cellular growth, differentiation
CC and/or development, and for modulating cellular metabolic pathways,
CC particularly for regulating one or more proteins involved in growth and
CC metabolism. The invention may also be useful for development of
CC therapeutics for the treatment of viral infections (for example hepatitis
CC B), cellular growth related disorders (for example heart failure,
CC hypertension, atrial fibrillation, dilated and idiopathic cardiomyopathy
CC or angina), proliferative or differentiative disorders such as cancer
CC (for example liver, melanoma, prostate, cervical, breast, colon or
CC sarcoma), disorders related with programmed cell death (for example
CC Alzheimer's disease, Parkinson's disease or epilepsy), or autoimmune
CC disorders (for example systemic lupus erythematosus). The present
CC sequence is the novel human kinase protein 14171 gene coding sequence of
CC the invention.

XX Sequence 2355 BP; 464 A; 738 C; 759 G; 394 T; 0 U; 0 Other;

Query Match 100.0%; Score 2355; DB 10; Length 2355;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGGCGACCGGGGACCCCAATGGGCGCTGGGCGTCCGCACTTTGACGCGGCG 60
DB 1 ATGAGAGGCGACCGGGGACCCCAATGGGCGCTGGGCGTCCGCACTTTGACGCGGCG 60
QY 61 GAGTTCAGGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTCGAGGAGGTGAACAAGTGGCG 120
DB 61 GAGTTCAGGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTCGAGGAGGTGAACAAGTGGCG 120
QY 121 CATGTCCACTGGAAGACCTGGCTGGCATCAAGTCTGCCGCAAGCTTCAGCTGACGAC 180
DB 121 CATGTCCACTGGAAGACCTGGCTGGCATCAAGTCTGCCGCAAGCTTCAGCTGACGAC 180
QY 181 AGGAGCGCATGGAGCTTTTGGAGAACCAAGAGATGGAGTGGCCAAAGTTTCGCTAC 240
DB 181 AGGAGCGCATGGAGCTTTTGGAGAACCAAGAGATGGAGTGGCCAAAGTTTCGCTAC 240
QY 241 ATTCGCTGTGTATGGCATCTGCCGCAACTGTCTGGCTGTGTATGATGATCAAGAG 300
DB 241 ATTCGCTGTGTATGGCATCTGCCGCAACTGTCTGGCTGTGTATGATGATCAAGAG 300
QY 301 ACGGAGCTCCCTGGAAGAACTGTCTGGCTTCGAGAGCAATTCAGTGGATCTCCGTTCCGA 360
DB 301 ACGGAGCTCCCTGGAAGAACTGTCTGGCTTCGAGAGCAATTCAGTGGATCTCCGTTCCGA 360
QY 361 ATTCATCCAGAGACCGCGGTGGGCGATGAACCTTCGCACTGCATGAGCCCCGCACTCTG 420
DB 361 ATTCATCCAGAGACCGCGGTGGGCGATGAACCTTCGCACTGCATGAGCCCCGCACTCTG 420
QY 421 CACCTGACCTCAAGCCCGCGAACAATCTGTGCTGATGCGCACTACAGTGAAGATTCT 480
DB 421 CACCTGACCTCAAGCCCGCGAACAATCTGTGCTGATGCGCACTACAGTGAAGATTCT 480
QY 481 GATTTGTGTGGCCAAATGCAACGAGGCTGTCCCACTTCGCAATGACCTTCAGATGATGGC 540
DB 481 GATTTGTGTGGCCAAATGCAACGAGGCTGTCCCACTTCGCAATGACCTTCAGATGATGGC 540
QY 541 CTGTTTGGCAATATGCTTACTCTCTCAGAGCGCATCAGGAGAAAGCGGCTCTTC 600
DB 541 CTGTTTGGCAATATGCTTACTCTCTCAGAGCGCATCAGGAGAAAGCGGCTCTTC 600

QY 601 GACACCAAGACAGATGTATACAGTTTGCAATCTGATGGGCGTGTCAACAGAAAG 660
DB 601 GACACCAAGACAGATGTATACAGTTTGCAATCTGATGGGCGTGTCAACAGAAAG 660
QY 661 AAGCGTTTGCAGATGAGAAAGACATCTTGCAATCATGTGAAGTGTGAAGGCGCAC 720
DB 661 AAGCGTTTGCAGATGAGAAAGACATCTTGCAATCATGTGAAGTGTGAAGGCGCAC 720
QY 721 CGCCCGAGCTGCCCGCGGTGTGAGAGCCCGCGCGCGCTGACCACTGATAGCG 780
DB 721 CGCCCGAGCTGCCCGCGGTGTGAGAGCCCGCGCGCGCTGACCACTGATAGCG 780
QY 781 CTATGACAGCGGTGTCTGGCAGGGGAGATCCGAGGTATGGCCCACTTCCAAGAAATTACT 840
DB 781 CTATGACAGCGGTGTCTGGCAGGGGAGATCCGAGGTATGGCCCACTTCCAAGAAATTACT 840
QY 841 TGTGAACCGAGAGACTGTGTGAAGACCTGATGACGAAGTGAAGAAATGCTCATGAT 900
DB 841 TGTGAACCGAGAGACTGTGTGAAGACCTGATGACGAAGTGAAGAAATGCTCATGAT 900
QY 901 CTGGAAGTGAAGAACCCCGCGAGCCGAGAGCGAGGATGCTGCGAGGCTCAAGCGG 960
DB 901 CTGGAAGTGAAGAACCCCGCGAGCCGAGAGCGAGGATGCTGCGAGGCTCAAGCGG 960
QY 961 GCTCTGCGCCCACTTCGATTAACGACTAAGCTTCGAGGCTTCTCAACAGCTGAGC 1020
DB 961 GCTCTGCGCCCACTTCGATTAACGACTAAGCTTCGAGGCTTCTCAACAGCTGAGC 1020
QY 1021 TCTGAAGTTTCCAGGCTGTGTGAGAGGCTCCGAGAGGCTCAAGCGGCTCTTGAATCC 1080
DB 1021 TCTGAAGTTTCCAGGCTGTGTGAGAGGCTCCGAGAGGCTCAAGCGGCTCTTGAATCC 1080
QY 1081 AAGCTGCAATCTTCGCGCAGTGGGAGAGGCTCTCGGGGATGCTCGGTGAGTCTCGGC 1140
DB 1081 AAGCTGCAATCTTCGCGCAGTGGGAGAGGCTCTCGGGGATGCTCGGTGAGTCTCGGC 1140
QY 1141 TTCTCTTCCAGAGGATCACTGTCTGTCTCTTTGAAGCGGGAACCTTCAACAGCATCTG 1200
DB 1141 TTCTCTTCCAGAGGATCACTGTCTGTCTCTTTGAAGCGGGAACCTTCAACAGCATCTG 1200
QY 1201 GGTACCAAGAGCTTCAAGAAAGAAAGTGTGTGATGCCATGTGTCTCGGAGACCAAGC 1260
DB 1201 GGTACCAAGAGCTTCAAGAAAGAAAGTGTGTGATGCCATGTGTCTCGGAGACCAAGC 1260
QY 1261 AAATGATGAAGATCTTCGAGCGCGCAGAGAGTGAACCTGCACTGCAAGCGGTGCCAGC 1320
DB 1261 AAATGATGAAGATCTTCGAGCGCGCAGAGAGTGAACCTGCACTGCAAGCGGTGCCAGC 1320
QY 1321 CTGCTGACCTGGCGGTGTGAGAGGCTCGGCAAGAGAGTGGCTGCTGCTCAAC 1380
DB 1321 CTGCTGACCTGGCGGTGTGAGAGGCTCGGCAAGAGAGTGGCTGCTGCTCAAC 1380
QY 1381 AATGCCAACCCCAACTGAGCAACCTGAGGGGCTTCACCCGTTTGCATAGGCGCTGAGAG 1440
DB 1381 AATGCCAACCCCAACTGAGCAACCTGAGGGGCTTCACCCGTTTGCATAGGCGCTGAGAG 1440
QY 1441 AGAGGGGTGGGGGTGTGTGTGAGCTCTGCTGGCAAGAAAGATCAAGTCAACGCAAG 1500
DB 1441 AGAGGGGTGGGGGTGTGTGTGAGCTCTGCTGGCAAGAAAGATCAAGTCAACGCAAG 1500
QY 1501 GATGAGGACAGTGAAGAGCCCTTCACTTTGCAAGCCCAAGAACGGGATGAGTGAAGACA 1560
DB 1501 GATGAGGACAGTGAAGAGCCCTTCACTTTGCAAGCCCAAGAACGGGATGAGTGAAGACA 1560
QY 1561 CGGCTGTGTGAGAAAGAAAGCTTCGATCAACAGGTGACCTTTGAGGGCCGAGCGCC 1620
DB 1561 CGGCTGTGTGAGAAAGAAAGCTTCGATCAACAGGTGACCTTTGAGGGCCGAGCGCC 1620
QY 1621 ATGACGTGGCTTCGCGAGCAGCGGCAAGGAATATCTGTGCAATCTCTGCTGCGCGAGGC 1680
DB 1621 ATGACGTGGCTTCGCGAGCAGCGGCAAGGAATATCTGTGCAATCTCTGCTGCGCGAGGC 1680
QY 1681 GTGACGTGAGCTGCAAGGCGCAAGGAATGCTGTGCTGCCACTGCACTACGCTGCTGGCAG 1740


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Db      541  CTGTTGGCACAATCGCTTACCTCCCTCCAGAGCGCATCAAGGAGAAAGCCGAGCTTTC
Qy      601  GACACCAAGCAGCATGTATACAGCTTTGCGATTCGTATCTGGGCGGTCTCAACACAGAG
Db      601  GACACCAAGCAGCATGTATACAGCTTTGCGATTCGTATCTGGGCGGTCTCAACACAGAG
Qy      661  AAGCGTTTGAAGATGAAGAAGACATCTGACATCATGTGAAGGTGAAGGAGCAG
Db      661  AAGCGTTTGAAGATGAAGAAGACATCTGACATCATGTGAAGGTGAAGGAGCAG
Qy      721  CGCCCGAGCTGCGCGCCGTGTGACAGAGCCGCGCGCGCTGAGCCACCTGAATAGC
Db      721  CGCCCGAGCTGCGCGCCGTGTGACAGAGCCGCGCGCGCTGAGCCACCTGAATAGC
Qy      781  CTCAATGACGCGGTGTGACAGAGGAGATCCGCGAGTTAAGGCCACTTTCAGAAATTAAT
Db      781  CTCAATGACGCGGTGTGACAGAGGAGATCCGCGAGTTAAGGCCACTTTCAGAAATTAAT
Qy      841  TCTGAAACGAGAGACCTGTGTGAAGAAAGCTGATGACGAAGTGAAGAAATGCTCATGAT
Db      841  TCTGAAACGAGAGACCTGTGTGAAGAAAGCTGATGACGAAGTGAAGAAATGCTCATGAT
Qy      901  CTGACATGTAAGAAAGCCCGCGAGCCCAAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG
Db      901  CTGACATGTAAGAAAGCCCGCGAGCCCAAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG
Qy      961  GCTCTGCGCCCACTTTGATTAACAATCAAGCTCTCCAGCTTCTTCAAGCTGAGAC
Db      961  GCTCTGCGCCCACTTTGATTAACAATCAAGCTCTCCAGCTTCTTCAAGCTGAGAC
Qy      1021  TCTGAGTTTCCAGAGCTGTGAGAGGAGCCCGAGAGAGCTCAAGCGAGCTCCCTGAGTGC
Db      1021  TCTGAGTTTCCAGAGCTGTGAGAGGAGCCCGAGAGAGCTCAAGCGAGCTCCCTGAGTGC
Qy      1081  AAGCTGCATCGTCCGCGAGTGGAGAGAGCTCTTCGCGGGGTGTCTCGGTGAGACTCCGC
Db      1081  AAGCTGCATCGTCCGCGAGTGGAGAGAGCTCTTCGCGGGGTGTCTCGGTGAGACTCCGC
Qy      1141  TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAACCTTCAACAGAGATTTG
Db      1141  TTCTCTTCCAGAGATCACTGTGCTGTCTTTGAGCGGGAACCTTCAACAGAGATTTG
Qy      1201  GGTACCAAGAGCGTCCAGAGAGAGAGAGCTTGTGATGCACTGTGTCGCGGACACAGC
Db      1201  GGTACCAAGAGCGTCCAGAGAGAGAGAGAGCTTGTGATGCACTGTGTCGCGGACACAGC
Qy      1261  AAACTGATGAAGATCTGCAAGCCGCGAGAGCTGGAAGCTGGAAGAGCGGTGCGAGC
Db      1261  AAACTGATGAAGATCTGCAAGCCGCGAGAGCTGGAAGCTGGAAGAGCGGTGCGAGC
Qy      1321  CTGCTGCACTGTGCGGTGAGAGCCCGGCAAGAGAGGTGCGCAAGTGTGCTGTCAAC
Db      1321  CTGCTGCACTGTGCGGTGAGAGCCCGGCAAGAGAGGTGCGCAAGTGTGCTGTCAAC
Qy      1381  AATGCCAACCCCAACTGAGCAACCGTGAAGGCTCCACCCGTTGACATGAGCGGTGAG
Db      1381  AATGCCAACCCCAACTGAGCAACCGTGAAGGCTCCACCCGTTGACATGAGCGGTGAG
Qy      1441  AGAGAGGTGCGGGGTGTGTGAGAGCTCTGTGCGACAGGAAGATCATGTCAAGCGCAAG
Db      1441  AGAGAGGTGCGGGGTGTGTGAGAGCTCTGTGCGACAGGAAGATCATGTCAAGCGCAAG
Qy      1501  GATGAGAGCAAGTGAAGAGCCCTTCACTTTGAGCGCCAGAAAGGAGATGAATCTAGCA
Db      1501  GATGAGAGCAAGTGAAGAGCCCTTCACTTTGAGCGCCAGAAAGGAGATGAATCTAGCA
Qy      1561  CGGCTGCTGTGAGAGAGAGAGCCCTCGGTCAAGAGGTGAGCTTTGAGGCGCGAGCGCC
Db      1561  CGGCTGCTGTGAGAGAGAGAGCCCTCGGTCAAGAGGTGAGCTTTGAGGCGCGAGCGCC
Qy      1621  ATGCACTGTGCTGCGAGCAGCGGAGAGAAATATGTCGCACTCTGCGCGAGGCG

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Db      1621  ATGCACTGTGCTGCGAGCAGCGGAGAGAAATATGTCGCACTCTGCTGCGCGAGGCG
Qy      1681  GTGAGCGTGAAGCTGTGAGAGGAGAGAGATGCTGAGCTGCACTGAATAGCTGCGAG
Db      1681  GTGAGCGTGAAGCTGTGAGAGGAGAGAGATGCTGAGCTGCACTGAATAGCTGCGAG
Qy      1741  GGCACCTGCGCACTGTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      1741  GGCACCTGCGCACTGTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      1801  ACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      1801  ACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      1861  CGCATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      1861  CGCATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      1921  CTGACAGTGGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      1921  CTGACAGTGGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      1981  GCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      1981  GCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      2041  GGAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      2041  GGAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      2101  CCCCTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      2101  CCCCTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      2161  GAGTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      2161  GAGTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      2221  CTGCGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      2221  CTGCGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      2281  ATCAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      2281  ATCAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      2341  CGAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
Db      2341  CGAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

RESULT 3
ADL67197
ID      ADL67197 standard; cDNA; 3860 BP.
XX      ADL67197;
XX      03-JUN-2004 (first entry)
XX      Human 14171 protein kinase cDNA.
XX      DE
XX      KW      Human ; 14171 protein kinase; cancer; immunological disorder;
XX      inflammation; heart failure; hypertension; atrial fibrillation;
XX      viral disorder; apoptotic disorder; chromosome mapping; tissue typing;
XX      KW      predictive medicine; forensic biology ; gene; ss.
XX      OS      Homo sapiens.
XX      FH      Key
XX      FT      CDS
XX      FT      17.2371
XX      FT      /product= "Human 14171 protein kinase"
XX      FT      XX

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US2004048305-A1.
11-MAR-2004.
10-SEP-2003; 2003US-00658904.
11-FEB-2000; 2000US-0182096P.
12-FEB-2001; 2001US-00781882.
(MILL-) MILLENNIUM PHARM INC.
Kapeller-Libermann R;
WPI; 2004-226195/21.
P-Psdb; ADL67198.
New 14171 protein kinase and nucleic acid, useful for diagnosing or treating diseases with aberrant expression of the 14171 protein kinase, such as cancer, an immunological disorder, inflammation, heart failure and hypertension.
Claim 1; SEQ ID NO 1; 62bp; English.
The invention provides novel human 14171 protein kinase polypeptides and polynucleotides. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of a 14171 protein kinase such as cancer, immunological disorder, inflammation, heart failure, hypertension, atrial fibrillation, viral disorder and apoptotic disorder. The invention can also be used in chromosome mapping, tissue typing, predictive medicine, forensic biology and prognostic assays. The present sequence is human 14171 protein kinase cDNA.

Sequence 3860 BP; 810 A; 1066 C; 1167 G; 816 T; 0 U; 1 Other;

Query Match 100.0%; Score 2355; DB 12; Length 3860;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGAGGCGACGCGGACCCCATGAGCCCTGAGCGCTGCGACCTTCGACGCGAGC 60
17 ATGAGAGGCGACGCGGACCCCATGAGCCCTGAGCGCTGCGACCTTCGACGCGAGC 76
61 GAGTTCACGCGCTGAGAGAGGTGAGCTGCGCGGCTTCGCGCAGGTGTACAGGTGCGC 120
77 GAGTTCACGCGCTGAGAGAGGTGAGCTGCGCGGCTTCGCGCAGGTGTACAGGTGCGC 136
121 CATGTCCTCATGAGAGAGCTGCGCTGCGCATCAAGTCTGCCAGCTGCACTGACGAGC 180
137 CATGTCCTCATGAGAGAGCTGCGCTGCGCATCAAGTCTGCCAGCTGCACTGACGAGC 196
181 AGGAGAGCGATGAGAGCTTTTGAAGAAGCAAGAGATGAGATGAGCCAAAGTTTGGCTAC 240
197 AGGAGAGCGATGAGAGCTTTTGAAGAAGCAAGAGATGAGATGAGCCAAAGTTTGGCTAC 256
241 ATCTGCTCTGTGATGAGCATCTGCGCGCAACTGTGCGCTGTGATGAGATGAGATGAG 300
257 ATCTGCTCTGTGATGAGCATCTGCGCGCAACTGTGCGCTGTGATGAGATGAGATGAG 316
301 AGGAGAGCGATGAGAGAGCTGCTGCTGAGAGCAATGAGATGAGATGAGATGAGATGAG 360
317 AGGAGAGCGATGAGAGAGCTGCTGCTGAGAGCAATGAGATGAGATGAGATGAGATGAG 376
361 ATCATCACAAGAGAGCGAGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 420
377 ATCATCACAAGAGAGCGAGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 436
421 CACCTGGAAGCTCAAGCCCGGAAACATCTGCTGAGATGAGATGAGATGAGATGAGATGAG 480
437 CACCTGGAAGCTCAAGCCCGGAAACATCTGCTGAGATGAGATGAGATGAGATGAGATGAG 496
481 GATTTGGTCTGGCGCAAGTGAAGAGCGAGCTGTCCCACTGAGATGAGATGAGATGAGATGAG 540

497 GATTTGGTCTGGCGCAAGTGAAGAGCGAGCTGTCCCACTGAGATGAGATGAGATGAGATGAG 556
541 CTGTTTGGCAATCGGCTTACCTTCCAGAGGCAATGAGAGAGAGCGGCTTCC 600
557 CTGTTTGGCAATCGGCTTACCTTCCAGAGGCAATGAGAGAGAGCGGCTTCC 616
601 GACACCAAGAGAGAGTGAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 660
617 GACACCAAGAGAGAGTGAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 676
661 AAGCGTTTGAATGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 720
677 AAGCGTTTGAATGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 736
721 CGCCCCAGAGCTGCGCGGCTGAG 780
737 CGCCCCAGAGCTGCGCGGCTGAG 796
781 CTGATGAG 840
797 CTGATGAG 856
841 TCTGAAACCGAG 900
857 TCTGAAACCGAG 916
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961 GCGCTGCGCGCGAG 1020
977 GCGCTGCGCGCGAG 1036
1021 TCTGAGAGTTCGAG 1080
1037 TCTGAGAGTTCGAG 1096
1081 AAGCTGCGATGAG 1140
1097 AAGCTGCGATGAG 1156
1141 TTCTCTTCCAGAGATGAG 1200
1157 TTCTCTTCCAGAGATGAG 1216
1201 GGTACCAAG 1260
1217 GGTACCAAG 1276
1261 AATGATGAG 1320
1277 AATGATGAG 1336
1321 CTGCTGAG 1380
1337 CTGCTGAG 1396
1381 AATGCAACCCCAACCTGAG 1440
1397 AATGCAACCCCAACCTGAG 1456
1441 AG 1500
1457 AG 1516
1501 GATGAG 1560
1517 GATGAG 1576
1561 CGGCTGCTGTTGAG 1620
1577 CGGCTGCTGTTGAG 1636

Key	Location/Qualifiers
QY	1621 ATGCACTGGCCTGGCACAACGGGAGGAAATATCGGGCCATCTCGCTGGCGCAAGGC 1680
Db	1637 ATGCACGTGGCCTGGCACACCGGACGAGAAATATCGGGCATCTCTGGCCGAGGC 1696
QY	1681 GTGACAGTGAAGCTTCAGAGGGCAAGGATGCTGGCTGCCACTACGCTGCTGGCAG 1740
Db	1697 GTGGACGTGAAGCTTCAGAGGGCAAGGATGCTGGCTGCCACTACGCTGCTGGCAG 1756
QY	1741 GGCCACCTGGCCATGTGTCAAGCTTGTGGCAAGCAGCCGGGGGTGAAGTGTGAAGCCCAAG 1800
Db	1757 GGCCACCTGGCCCATGTGTCAAGCTTGTGGCAAGCAGCCGGGGGTGAAGTGTGAAGCCCAAG 1816
QY	1801 AGCGTAGATGGAGGAGCGCATTTGACCTGGCCGACAGCGCGGGCACTACCGCGTGGCC 1860
Db	1817 AGCGTAGATGGAGGAGCGCATTTGACCTGGCCGACAGCGCGGGCACTACCGCGTGGCC 1876
QY	1861 CGCATCTTCATCGACTGTGTCTCCGACGTCAACGTCTGACGCTTGGTGGCAACAGACCC 1920
Db	1877 CGCATCTTCATCGACTGTGTCTCCGACGTCAACGTCTGACGCTTGGTGGCAACAGACCC 1936
QY	1921 CTGCACGTGGCCGGGAGACGGGGGACACAGACACTGGCAGGCTGCTGATGCGGGC 1980
Db	1937 CTGCACGTGGCCGGGAGACGGGGGACACAGACACTGGCAGGCTGCTGATGCGGGC 1996
QY	1981 GCTGGCAAGAGAGGCGGTGACTCAGACGGCTACACCGCTCTGACCTTGGCTGCCCAAC 2040
Db	1997 GCTGGCAAGAGAGGCGGTGACTCAGACGGCTACACCGCTCTGACCTTGGCTGCCCAAC 2056
QY	2041 GGAACCTGGCACTGTCAAGCTGTTGTGAGAGAAAGCGATGTGCTGGCCCGGGGA 2100
Db	2057 GGAACCTGGCACTGTCAAGCTGTTGTGAGAGAAAGCGATGTGCTGGCCCGGGGA 2116
QY	2101 CCCCTGAACACAACGGCGCTGACCTGGCTGGCCGCCACCTCGAAGGTGTGTAG 2160
Db	2117 CCCCTGAACACAACGGCGCTGACCTGGCTGGCCGCCACCTCGAAGGTGTGTAG 2176
QY	2161 GAGTTGGTCAAGCGCCGATGTCAATTGACCTGTTCAAGACAGAGGGCTGACGCGCTGAC 2220
Db	2177 GAGTTGGTCAAGCGCCGATGTCAATTGACCTGTTCAAGACAGAGGGCTGACGCGCTGAC 2236
QY	2221 CTGGCCGCCACAGGGCCGGCAACGACAGCGTGGAGACTTGTCTCAAGGATGGGGCCAC 2288
Db	2237 CTGGCCGCCACAGGGCCGGCAACGACAGCGTGGAGACTTGTCTCAAGGATGGGGCCAC 2296
QY	2281 ATCAACCTGACAGGCTCAAGTTCCAGGGCGGCAATGGCCCGCGCCACACTCTCGCGG 2340
Db	2297 ATCAACCTGACAGGCTCAAGTTCCAGGGCGGCAATGGCCCGCGCCACACTCTCGCGG 2356
QY	2341 CGAAGCAAGACTTAA 2355
Db	2357 CGAAGCAAGACTTAA 2371
RESULT 4	
AD38376	
ID	AD38376 standard; DNA; 3860 BP.
XX	
AC	AD38376;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Human protein 14171 gene sequence.
XX	
KW	tumorigenic disorder; angiogenic disorder; aberrant gene expression;
KW	aberrant protein activity; cytostatic; antithyroid; antidiabetic;
KW	ophthalmological; cancer; breast cancer; colon cancer; lung cancer;
KW	prostatic cancer; Grave's disease; diabetic retinopathy; gene; ds;
XX	protein 14171.
XX	
OS	Homo sapiens.
XX	
FH	

FT	CDS		14.._2371	
FT			/**tag= a	
XX			/product= "Human protein 14171"	
FN	WO2003065006-A2.			
PD	07-AUG-2003.			
XX				
FP	30-JUN-2003; 2003WO-US002588.			
XX				
PR	31-JAN-2002; 2002US-0353600P.			
PR	15-MAR-2002; 2002US-0364517P.			
PR	09-APR-2002; 2002US-0371075P.			
PR	10-APR-2002; 2002US-0371507P.			
PR	16-APR-2002; 2002US-0372984P.			
PR	19-APR-2002; 2002US-0374194P.			
PR	24-MAY-2002; 2002US-0382959P.			
PR	31-MAY-2002; 2002US-0385023P.			
PR	14-JUN-2002; 2002US-0388853P.			
PR	17-JUN-2002; 2002US-0389395P.			
PR	25-JUN-2002; 2002US-0391324P.			
PR	15-JUL-2002; 2002US-0395944P.			
PR	22-JUL-2002; 2002US-0397726P.			
PR	13-AUG-2002; 2002US-0403046P.			
PR	22-AUG-2002; 2002US-0405155P.			
PR	27-AUG-2002; 2002US-0406361P.			
PR	25-OCT-2002; 2002US-0421195P.			
PR	12-NOV-2002; 2002US-0425456P.			
PR	19-NOV-2002; 2002US-0427626P.			
PR	10-DEC-2002; 2002US-0432122P.			
XX				
PA	(MILL-) MILLENNIUM PHARM INC.			
XX				
PI	Hunter JJ, Macbeth KJ, Tsai F, Leeson A, Lightcap ES,			
PI	Williamson MW, Rudolph-Owen LA;			
DR	WPI; 2003-646176/61.			
XX	P-PDB; ADE38377.			
PT	Treating subject having tumorigenic disorder or angiogenic disorder caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic acid, by administering a modulator.			
PT				
PS	Disclosure; SEQ ID NO 37; 454pp; English.			
XX				
CC	This invention relates to a novel method of creating a human subject having a tumorigenic disorder or angiogenic disorder, caused by aberrant gene expression or activity of an isolated protein, by administering a modulator. The modulator may have cytosratic, antithyroid, antidiabetic or ophthalmological activity. The method is useful for treating a subject having a tumorigenic or angiogenic disorder, in particular for treating cancer (for example breast cancer, colon cancer, lung cancer or prostate cancer) and, for example, Grave's disease and diabetic retinopathy. The present sequence is a DNA sequence which encodes the novel isolated human protein 14171 of the invention.			
CC				
XX				
SQ	Sequence 3860 BP; 809 A; 1066 C; 1169 G; 816 T; 0 U; 0 Other;			
Query Match	99.0%; Score 2332; DB 10; Length 3860;			
Best Local Similarity	99.9%; Pred. No. 0;			
Matches 2354; Conservative	0; Mismatches 0; Indels 2; Gaps 2			
OY	1 ATGAGAGCGACGCGCGAGACCCTCATGGGCCCTTGCGCTGTGGCACCCTTGCAGCGGGC 60			
Db	17 ATGAGAGCGCGACGCGCGAGACCCTCATGGGCCCTTGCGCTGTGGCACCCTTGCAGCGGGC 76			
OY	GAGTTTCAGGGCTGGGAGAAGGTGGGCTCGGGCGGCTTCGGGCAGGTGTCAAAAGTGGCC 120			
Db	77 GAGTTTCAGGGCTGGGAGAAGGTGGGCTCGGGCGGCTTCGGGCAGGTGTCAAAAGTGGCC 136			
OY	CATGTCCACTGGANAACCTGGCTGGCCANTCAAGTGTGGCCAGGCTGCACCTGCAGCAC 180			
Db	137 CATGTCCACTGGANAACCTGGCTGGCCANTCAAGTGTGGCCAGGCTGCACCTGCAGCAC 196			

Db	1308	CAACTGATGAAGATTCCTGCACGCCGACGAGAGTGGAACCTGCACTGGACACAGCGGTGCAAG	1367
QY	1320	CTCTCTGCACCTGGCGGTGGAGGCGCGGCAAGAGAGTGCGCCAAAGTGAGCTGTGCTCAA	1379
Db	1368	CTGTGTGCACCTGGGTGGAGGCGCGGCAAGAGAGTGCGCCAAAGTGAGCTGTGCTCAA	1427
QY	1380	CAATGCCAAACCCCAACCTGAGCAACCGTAGGGGCTCCACCCCGTTGCAATAGGCGTGA	1439
Db	1428	CAATGCCAAACCCCAACCTGAGCAACCGTAGGGGCTCCACCCCGTTGCAATAGGCGTGA	1487
QY	1440	GAGAGGGGTGCGGGGTGTCTGTGAGACTCTGTGTGCACGAAAGTCAATGTCCACGCCAA	1499
Db	1488	GAGAGGGGTGCGGGGTGTCTGTGAGACTCTGTGTGCACGAAAGTCAATGTCCACGCCAA	1547
QY	1500	GGAATGAGGACCAATGAGCAAGCCCTCCATTGTGACGCCCAAGAACGGGGATGAGTATAGAC	1559
Db	1548	GGAATGAGGACCAATGAGCAAGCCCTCCATTGTGACGCCCAAGAACGGGGATGAGTATAGAC	1607
QY	1560	ACGGCTGTGTGGAGAGAAACGCTCGGTCAACGAGGTGACCTTGAAGGCGCGAACGCC	1619
Db	1608	ACGGCTGTGTGGAGAGAAACGCTCGGTCAACGAGGTGACCTTGAAGGCGCGAACGCC	1667
QY	1620	CATGCACTGTGACCTGCGCAACCGGCAAGAAATATGCTGGCATCTGTGCGCGAAG	1679
Db	1668	CATGCACTGTGACCTGCGCAACCGGCAAGAAATATGCTGGCATCTGTGCGCGCGAAG	1727
QY	1680	CGTGAACGTGAGCCCTGCGAAGGCAAGAGACCTGGCTGCACTGCACATACGCTGCTGGCA	1739
Db	1728	CGTGAACGTGAGCCCTGCGAAGGCAAGAGACCTGGCTGCACTGCACATACGCTGCTGGCA	1787
QY	1740	GGGCCACCTGCGCATCTGCTCAAGCTCTGAGCAAGCAAGCGCGGAGTGAATGAAACGCCA	1799
Db	1788	GGGCCACCTGCGCATCTGCTCAAGCTCTGAGCAAGCAAGCGCGGAGTGAATGAAACGCCA	1847
QY	1800	GACGCTGATGGAGAGAGCCATTGCACTTGCACTTGCCGCGCAACGCGCGGCACTAACCGCTGAGC	1859
Db	1848	GACGCTGATGGAGAGAGCCATTGCACTTGCACTTGCCGCGCAACGCGCGGCACTAACCGCTGAGC	1907
QY	1860	CGGCATCTCTCAATCGACCTGTGCTCGAAGTCAACGCTGACGCGCTGCGGACAGACAC	1919
Db	1908	CGGCATCTCTCAATCGACCTGTGCTCGAAGTCAACGCTGACGCGCTGCGGACAGACAC	1967
QY	1920	CTGTGACGTGGCGCGGAGAACGGGCAACAGACACTGCGAGGCTGTCTGTCAATCGGG	1979
Db	1968	CTGTGACGTGGCGCGGAGAACGGGCAACAGACACTGCGAGGCTGTCTGTCAATCGGG	2027
QY	1980	CGCTGGCAAGAGAGCGCTGACCTTCAAGCGGCTACACGCTGTGCACTGTGCGCGCGAA	2039
Db	2028	CGCTGGCAAGAGAGCGCTGACCTTCAAGCGGCTACACGCTGTGCACTGTGCGCGCGAA	2087
QY	2040	CGGACACTGCGGCACTGTCAAGCTGCTGTGAGAGAAAGCCGATGTGCTGGCGCGGG	2099
Db	2088	CGGACACTGCGGCACTGTGTCAAGCTGCTGTGAGAGAAAGCCGATGTGCTGGCGCGGG	2147
QY	2100	ACCCCTGAACCAAGACGAGCGCTGCACTGTGCTGCGCCACCGGCACTGTGAGTGTGGA	2159
Db	2148	ACCCCTGAACCAAGACGAGCGCTGCACTGTGCTGCGCCACCGGCACTGTGAGTGTGGA	2207
QY	2160	GGAATTTGTCAACGCGCGATGTCAATTGACCTGTGTGACAGACGAGGCTTCAAGCGGCTGCA	2219
Db	2208	GGAATTTGTCAACGCGCGCGATGTCAATTGACCTGTGTGACAGACGAGGCTTCAAGCGGCTGCA	2267
QY	2220	CTTGGCGCGCCAGGGCGCGGCAAGCAAGCGTTGAGACTGTGCTCAAGCAATGGGGCCCA	2279
Db	2268	CTTGGCGCGCCAGGGCGCGGCAAGCAAGCGTTGAGACTGTGCTCAAGCAATGGGGCCCA	2327
QY	2280	CATCAACCTGCAAGAGCTTCAAGTTTCAAGGAGGCGCATGGCCCGCGGCCACTCTGCG	2339
Db	2328	CATCAACCTGCAAGAGCTTCAAGTTTCAAGGAGGCGCATGGCCCGCGGCCACTCTCTCG	2387
QY	2340	GCGAAGCAAGACCTAG 2355	

DB	2388	GCGAAGCAAGACTTAG	2403
XX	RESULT 6		
XX	ADR25979		
XX	ADR25979 standard; DNA; 3879 BP.		
XX	ADR25979;		
XX	21-OCT-2004 (first entry)		
XX	Breast cancer prognosis marker #1840.		
XX	ds; breast cancer; prognosis; gene expression; diagnosis.		
XX	Homo sapiens.		
XX	WO2004065545-A2.		
XX	05-AUG-2004.		
XX	15-JAN-2004; 2004WO-US001100.		
XX	15-JAN-2003; 2003US-00342887.		
XX	(ROSE-) ROSETTA INPHARMATICS LLC.		
XX	(NECA-) NETHERLANDS CANCER INST.		
XX	Van't Veer LJ, He Y;		
XX	WPI; 2004-593473/57.		
XX	Classifying a breast cancer patient according to prognosis comprises		
XX	determining the similarity between the level of expression of each of		
XX	five genes in a cell sample taken from patient, to control levels.		
XX	Disclosure; SEQ ID NO 1840; 226bp; English.		
XX	The invention relates to a method of classifying a breast cancer patient		
XX	according to prognosis by determining the similarity between the level of		
XX	expression of each of five genes for which markers are listed in the		
XX	specification, in a cell sample taken from the breast cancer patient, to		
XX	control levels of expression for each respective five genes to obtain a		
XX	patient similarity value. The methods are useful for classifying a breast		
XX	cancer patient according to prognosis. Kits and computer program products		
XX	are useful for data analysis using the diagnostic, prognostic and		
XX	statistical methods of the invention. This sequence corresponds to a		
XX	marker used in the method of the invention.		
XX	Sequence 3879 BP; 807 A; 1074 C; 1178 G; 820 T; 0 U; 0 Other;		
XX	Query Match 99.0%; Score 2330.4; DB 13; Length 3879;		
XX	Best Local Similarity 99.9%; Pred. No. 0;		
XX	Matches 2353; Conservative 0; Mismatches 1; Indels 2; Gaps 2		
QY	1 ATGAGAGGCGAAGCGGGAACCCATGAGGCGCTGCGCTGCGCACTTGCAGCGGCGC 60		
DB	49 ATGAGAGGCGAAGCGGGAACCCATGAGGCGCTGCGCTGCGCACTTGCAGCGGCGC 108		
QY	61 GAGTTCAAGGCGTGGGAGAAAGTGGGCTCGGGCGGCTTCGGCAAGTGAACAAGGCGGC 120		
DB	109 GAGTTCAAGGCGTGGGAGAAAGTGGGCTCGGGCGGCTTCGGCAAGTGAACAAGGCGGC 168		
QY	121 CATGTCACGTGAAGACCTGCGGCACTCAAGTCTCGGCCAGGCTGCACTGCAAGCAG 180		
DB	169 CATGTCACGTGAAGACCTGCGGCACTCAAGTCTCGGCCAGGCTGCACTGCAAGCAG 228		
QY	181 AGGAGAGCGATGAGACTTTTGGAGAAGCGCAAGAAATGAGATGCGCAAGTTGGCTAC 240		
DB	229 AGGAGAGCGATGAGACTTTTGGAGAAGCGCAAGAAATGAGATGCGCAAGTTGGCTAC 288		
QY	241 ATCTGCTGCTGTATGGAATCTGCGCGAAGCTGTGCGGCTGATATGAGATCAATGAG 300		

Db	289	ATCTGCTGTGTATGGAATCTGCCGGAACCTGTGCGCTGTGTCATGAACTGAG	348
Qy	301	ACGGGCTCTCTGAAAAGCTGTGGCTTCGAGCCATTGGCCATGGAATCTCGGTTCCGA	360
Db	349	ACGGGCTCTCTGAAAAGCTGTGGCTTCGAGCCATTGGCCATGGAATCTCGGTTCCGA	408
Qy	361	ATCATTCACAGAACGGCGGTGGGCATGAACTTCTTGCACTGCATGGCCCCGCACTCTG	420
Db	409	ATCATTCACAGAACGGCGGTGGGCATGAACTTCTTGCACTGCATGGCCCCGCACTCTG	468
Qy	421	CACCTGGAACCTGAAGCCCGGAAACCTCGCTGGAATGCCACCTACAGCTCAAGATTCT	480
Db	469	CACCTGGAACCTGAAGCCCGGAAACCTCGCTGGAATGCCACCTACAGCTCAAGATTCT	528
Qy	481	GATTTTGGTCTGGCCAGTGCACCGGCTGTCCCACTCGCATGACCTCAGCATGGATGGC	540
Db	529	GATTTTGGTCTGGCCAGTGCACCGGCTGTCCCACTCGCATGACCTCAGCATGGATGGC	588
Qy	541	CTGTTTGGCAATATGCGCTTACTCCCTTCAGAGCGCATCAGGAGAAAGCCGCTCTTC	600
Db	589	CTGTTTGGCAATATGCGCTTACTCCCTTCAGAGCGCATCAGGAGAAAGCCGCTCTTC	648
Qy	601	GACACCAAGCAAGATGTAATACGCTTTGGATTCGTATCTGGGGGTGTCTACACAGAG	660
Db	649	GACACCAAGCAAGATGTAATACGCTTTGGATTCGTATCTGGGGGTGTCTACACAGAG	708
Qy	661	AGCCGTTTGACAGATGAGAAAGAACTCTGCACATCATATGATGAAAGTGTGAAGGCAC	720
Db	709	AGCCGTTTGACAGATGAGAAAGAACTCTGCACATCATATGATGAAAGTGTGAAGGCAC	768
Qy	721	CGCCCTGAGCTGCCGCCGTGTGCAGAGCCCGGCGCGCTGCAGCCACTGTATACG	780
Db	769	CGCCCTGAGCTGCCGCCGTGTGCAGAGCCCGGCGCGCTGCAGCCACTGTATACG	828
Qy	781	CTCATGACGGGTGTGTCGAGAGGGGGAATCCGGAAGTTAAGGCCCACTTCAGAAATTACT	840
Db	829	CTCATGACGGGTGTGTCGAGAGGGGGAATCCGGAAGTTAAGGCCCACTTCAGAAATTACT	888
Qy	841	TCTGAAACCGAGAACCTGTGTGTAAGAAAGCTGTATGACGAAGTGAAGAAACTGCTCATAT	900
Db	889	TCTGAAACCGAGAACCTGTGTGTAAGAAAGCTGTATGACGAAGTGAAGAAACTGCTCATAT	948
Qy	901	CTGGAAGTGAAGAACCCGCCGAGCCCGAGACGAGAGTGTGTCTGCAAGCTCAAGCGG	960
Db	949	CTGGAAGTGAAGAACCCGCCGAGCCCGAGACGAGAGTGTGTCTGCAAGCTCAAGCGG	1008
Qy	961	GGCTCTGCCCCCACTTCGTGATTAAGACATACGCTCTCGAGCTTCTTCAACGCTGAGC	1020
Db	1009	GGCTCTGCCCCCACTTCGTGATTAAGACATACGCTCTCGAGCTTCTTCAACGCTGAGC	1068
Qy	1021	TCTGGAATTTCCAGAGCTGTGAGAGGCCCGAGAGAGCTCAGCCGAGCTCTCTGAGTCC	1080
Db	1069	TCTGGAATTTCCAGAGCTGTGAGAGGCCCGAGAGAGCTCAGCCGAGCTCTCTGAGTCC	1128
Qy	1081	AACTTGCATTCGTCCGCGAGTGGGAAAGAGCTCTCGGGGGTGTCTCGGTGACTCGGCC	1140
Db	1129	AACTTGCATTCGTCCGCGAGTGGGAAAGAGCTCTCGGGGGTGTCTCGGTGACTCGGCC	1188
Qy	1141	TTCTCTTCCAGAGGATCACTGTGCTGTCTTTGAGCGGAACTTTCAACAGAGCATTTG	1200
Db	1189	TTCTCTTCCAGAGGATCACTGTGCTGTCTTTGAGCGGAACTTTCAACAGAGCATTTG	1248
Qy	1201	GGTACCAAGAGCGTCCAGAAAGAGCTTGTGATGCATCGATGCC - GGACACAG	1252
Db	1249	GGTACCAAGAGCGTCCAGAAAGAGCTTGTGATGCATCGATGCC - GGACACAG	1307
Qy	1260	CAAACTGATGAAGATCTTGACGCGCAGGACCTGGAACCTGGCACTGGAACAGCGGTGCC	1319
Db	1308	CAAACTGATGAAGATCTTGACGCGCAGGACCTGGAACCTGGCACTGGAACAGCGGTGCC	1367
Qy	1320	CCTGCTGCACCTGGCGGTGGAAGCGCGGCAAGAGATGCGCAAGTGTCTGCTCA	1379
Db	1368	CCTGCTGCACCTGGCGGTGGAAGCGCGGCAAGAGATGCGCAAGTGTCTGCTCA	1427

Qy	1360	CAATGCCAA	CCCCCAACCTTGAGCAA	CCGTAGGGGCTCCACCCTTGTTGCA	CATGACCTGTGGA	1439
Db	1428	CAATGCCAA	CCCCCAACCTTGAGCAA	CCGTAGGGGCTCCACCCTTGTTGCA	CATGACCTGTGGA	1487
Qy	1440	GAGGAGGGGTGGGGGGTGTGCTGTGGAGCTCTCTGTGTGGCA	CCGAAAGATCA	AGTGCAAACGCCCAA		1499
Db	1488	GAGGAGGGGTGGGGGGTGTGCTGTGGAGCTCTCTGTGTGGCA	CCGAAAGATCA	AGTGCAAACGCCCAA		1547
Qy	1500	GGATGAGGACCAAGTGGACAGACCCCTTCCA	CTTTTGACGCCCAAGAACCGGGATGAGTCTAGCAC			1559
Db	1548	GGATGAGGACCAAGTGGACAGACCCCTTCCA	CTTTTGACGCCCAAGAACCGGGATGAGTCTAGCAC			1607
Qy	1560	ACGGCTGCTGTTGGAGAAAGAACCCCTTGCTCA	CGAGAGTGAACCTTTGAGGGCCCGAAGCC			1619
Db	1608	ACGGCTGCTGTTGGAGAAAGAACCCCTTGCTCA	CGAGAGTGAACCTTTGAGGGCCCGAAGCC			1667
Qy	1620	CATGCACTGTGGCTCTGGCAAGCA	CCGGGCAAGAAATATGTGTGGCATCTCTGCTGCGCCGAGG			1679
Db	1668	CATGCACTGTGGCTCTGGCAAGCA	CCGGGCAAGAAATATGTGTGGCATCTCTGCTGCGCCGAGG			1727
Qy	1680	CGTGGACGTGAGCTGTCAGGGGCAAGAGATGCTGTGGCTGCAC	CTGCACTACGCTGTGCTGGCA			1739
Db	1728	CGTGGACGTGAGCTGTCAGGGGCAAGAGATGCTGTGGCTGCAC	CTGCACTACGCTGTGCTGGCA			1787
Qy	1740	GGGGCCACTGTCGCCCATCGTCAAGCTGTGACCAAGAC	CCGGGGGTGAGTGTGAACGCCCA			1799
Db	1788	GGGGCCACTGTCGCCCATCGTCAAGCTGTGACCAAGAC	CCGGGGGTGAGTGTGAACGCCCA			1847
Qy	1800	GACGCTGGATGGGAGAGACGCCATTGGCA	CTGTGGCCGCCCAAGCCGGGGCATATCCGCGTGTGC			1859
Db	1848	GACGCTGGATGGGAGAGACGCCATTGGCA	CTGTGGCCGCCCAAGCCGGGGCATATCCGCGTGTGC			1907
Qy	1860	CCGCACTCTCATCGACCTGTGCTCCGACGTCAC	AGTCAAGCTGTGACGCTGTGTGGCA	CAGACACC		1919
Db	1908	CCGCACTCTCATCGACCTGTGCTCCGACGTCAC	AGTCAAGCTGTGTGGCA	CAGACACC		1967
Qy	1920	CTTGCAACGTGGCCCGCGGAGACGGGGGCA	CGAGCACTGCCAGGCTGTCTCTGCATCGGGG			1979
Db	1968	CTTGCAACGTGGCCCGCGGAGACGGGGGCA	CGAGCACTGCCAGGCTGTCTCTGCATCGGGG			2027
Qy	1980	CGCTGTGGCAAGAGGCGCTGTGACCTCA	GACACGGCTTACACCGCTTGTGCA	CCCTGGCTGTGCCGCCCA		2039
Db	2028	CGCTGTGGCAAGAGGCGCTGTGACCTCA	GACACGGCTTACACCGCTTGTGCA	CCCTGGCTGTGCCGCCCA		2087
Qy	2040	CGGACACTGTGGCACTGTCAAGCTGTGTGTCA	GGAAGAAAGGCGCATGTGCTGTGGCCGGGG			2099
Db	2088	CGGACACTGTGGCACTGTGTCAAGCTGTGTGTCA	GGAAGAAAGGCGCATGTGCTGTGGCCGGGG			2147
Qy	2100	AACCCCTGAACCAAGACGGGCGTGCAC	CTTGACCTGCCGCCCA	CGGGGCACTCGAGAGTGTGGA		2159
Db	2148	AACCCCTGAACCAAGACGGGCGTGCAC	CTTGACCTGCCGCCCA	CGGGGCACTCGAGAGTGTGGA		2207
Qy	2160	GGAAGTTGGTCAAGCCCGCATGTTCATTGAC	CTGTTTGAGAGAGAGGGGGCTCA	AGCCGGCTGTGCA		2219
Db	2208	GGAAGTTGGTCAAGCCCGCATGTTCATTGAC	CTGTTTGAGAGAGAGGGGGCTCA	AGCCGGCTGTGCA		2267
Qy	2220	CGTGGCGGCCCAAGGGGCGGGCA	CGGCAAGACGGTGAAGCTTGTGTCAGGCA	GGCAATGGGGGCCA		2279
Db	2268	CGTGGCGGCCCAAGGGGCGGGCA	CGGCAAGACGGTGAAGCTTGTGTCAGGCA	GGCAATGGGGGCCA		2327
Qy	2280	CATCAACCTGCAAGAGCCCTCAAGTTTCA	AGGGCGGGCCATATGGCCCGGCCCA	CTTCTGTGCG		2339
Db	2328	CATCAACCTGCAAGAGCCCTCAAGTTTCA	AGGGCGGGCCATATGGCCCGGCCCA	CTTCTGTGCG		2387
Qy	2340	GGGAAGCAAGACCTTAG	2355			
Db	2388	GGGAAGCAAGACCTTAG	2403			

RESULT 7
AAD64343
ID AAD64343 standard; DNA; 2355 BP.

XX AD64343;
AC 12-FEB-2004 (first entry)
XX Human protein kinase C-associated kinase (PKK) variant DNA #5.
DE Human protein kinase C-associated kinase (PKK) variant DNA #5.
XX Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
XX Homo sapiens.
OS US2003199462-A1.
XX PD 23-OCT-2003.
XX PF 23-APR-2002; 2002US-00128174.
XX PR 23-APR-2002; 2002US-00128174.
XX (NUNEZ/) NUNEZ G.
XX (INOH/) INOHARA N.
XX (MUTO/) MUTO A.
XX PI Nunez G, Inohara N, Muto A;
XX WPI, 2003-852808/79.
XX New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKK induced NF-KB activation for treating hyperglycemia.
XX Disclosure; SEQ ID NO 18; Opp; English.
XX The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC encoding such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKK induced NF-kappaB activation for treating hyperglycemia.
CC The invention is also used in gene therapy. The present sequence is human
CC PKK variant DNA
XX
XX
SQ Sequence 2355 BP; 463 A; 740 C; 761 G; 391 T; 0 U; 0 Other;
Query Match 98.8%; Score 2337.2; DB 10; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY 1 ATGAGAGGCGAGCGCGGAGCCCATAGGCGCTGCGGCTGCGCACTTTCAGACGCGGCG 60
DB 1 ATGAGAGGCGAGCGCGGAGCCCATAGGCGCTGCGGCTGCGCACTTTCAGACGCGGCG 60
QY 61 GAGTTCAAGGCGCTGCGGAGAGAGTGGGCTGGGCGGCTTGGGCAAGTGTACAAAGTGGCG 120
DB 61 GAGTTCAAGGCGCTGCGGAGAGAGTGGGCTGGGCGGCTTGGGCAAGTGTACAAAGTGGCG 120
QY 121 CATGTCCATGGAAGACTGCGTGGCATCAAGTGTCCGCCAGCTGCACTTCAGACGAC 180
DB 121 CATGTCCATGGAAGACTGCGTGGCATCAAGTGTCCGCCAGCTGCACTTCAGACGAC 180
QY 181 AGGAGCGCATGAGAGCTTTTGGAGAGGCAAGAGATGAGATGAGCCAAAGTTTCGTAC 240
DB 181 AGGAGCGCATGAGAGCTTTTGGAGAGGCAAGAGATGAGATGAGCCAAAGTTTCGTAC 240
QY 241 ATCTTCCTGTGTATGAGCATCTGCCGGAACCTGTGGCTGGTCAATGAGTACATGAG 300
DB 241 ATCTTCCTGTGTATGAGCATCTGCCGGAACCTGTGGCTGGTCAATGAGTACATGAG 300
QY 301 ACGGAGCTCCCTGGAAGAGCTGCTGCGCTTGGAGCCATTCGATGGAATCTCCGGTTCCGA 360
DB 301 ACGGAGCTCCCTGGAAGAGCTGCTGCGCTTGGAGCCATTCGATGGAATCTCCGGTTCCGA 360

QY 361 ATCATCCAGAGAGCGGCGGTGGCATGAATCTTCGTCATGTCATGAGCCGCCCATCTCTG 420
DB 361 ATCATCCAGAGAGCGGCGGTGGCATGAATCTTCGTCATGTCATGAGCCGCCCATCTCTG 420
QY 421 CACCTGAGACCTCAAGCCCGGGAACATCTGCTGATGCCCATCACTCAAGTCAATTTCT 480
DB 421 CACCTGAGACCTCAAGCCCGGGAACATCTGCTGATGCCCATCACTCAAGTCAATTTCT 480
QY 481 GATTTTGTCTGCGCAAGTGCACAGGCGCTGCCCATCTGCAATGAGCCAGATGAGTGGC 540
DB 481 GATTTTGTCTGCGCAAGTGCACAGGCGCTGCCCATCTGCAATGAGCCAGATGAGTGGC 540
QY 541 CTGTTTGGCAAAATCGCTACCTCCCTCCAGAGGCGCATCAAGGAGAGAGCGCGCTTC 600
DB 541 CTGTTTGGCAAAATCGCTACCTCCCTCCAGAGGCGCATCAAGGAGAGAGCGCGCTTC 600
QY 601 GACACCAAGCAGATGATACAGCTTTGCGATCGATCTTGGGCGTGTCAACAGAG 660
DB 601 GACACCAAGCAGATGATACAGCTTTGCGATCGATCTTGGGCGTGTCAACAGAG 660
QY 661 AAGCGTTTGCAGATGAGAGAAACATCTCTGCACTCATGATGAGTGTGAAGGGCCAC 720
DB 661 AAGCGTTTGCAGATGAGAGAAACATCTCTGCACTCATGATGAGTGTGAAGGGCCAC 720
QY 721 CGCCCGAGCTGCGCGCGGTGTCAGAGCGCGCGCGCGCTGCAAGCATCTGATACGC 780
DB 721 CGCCCGAGCTGCGCGCGGTGTCAGAGCGCGCGCGCGCTGCAAGCATCTGATACGC 780
QY 781 CTGATGAGCGGTCTGTCAGAGGCGGATCCGGAATTAGGCCACCTTTCAGAAATTAAT 840
DB 781 CTGATGAGCGGTCTGTCAGAGGCGGATCCGGAATTAGGCCACCTTTCAGAAATTAAT 840
QY 841 TCTGAACCGAGACCTGTGTGAAGAGCTGTATGACCAAGTGAAGAAACCTGTCATAT 900
DB 841 TCTGAACCGAGACCTGTGTGAAGAGCTGTATGACCAAGTGAAGAAACCTGTCATAT 900
QY 901 CTGAGCGTGAAGAGCG 960
DB 901 CTGAGCGTGAAGAGCG 960
QY 961 GCTCTGCG 1020
DB 961 GCTCTGCG 1020
QY 1021 TCTGAGATTTTCCAGAGCTGTGAGAGGCGCGCGAGAGCTCAAGCCGACTCTTGAATCC 1080
DB 1021 TCTGAGATTTTCCAGAGCTGTGAGAGGCGCGCGAGAGCTCAAGCCGACTCTTGAATCC 1080
QY 1081 AAGCTGCCATGCTCCGAGTGGAGAGAGGCTCTCGGCGGTGCTCTGAGTGAATCCGCC 1140
DB 1081 AAGCTGCCATGCTCCGAGTGGAGAGAGGCTCTCGGCGGTGCTCTGAGTGAATCCGCC 1140
QY 1141 TTCTCTTCAGAGATCACTGTGCTGCTTTTGAAGCGGGAACCTTCAACAGCATCTG 1200
DB 1141 TTCTCTTCAGAGATCACTGTGCTGCTTTTGAAGCGGGAACCTTCAACAGCATCTG 1200
QY 1201 GGTACCAAGACCTTCCAGAGAGAGAGCTTGTGATGCTCATGTGTCC -GGAGACAG 1259
DB 1201 GGTACCAAGACCTTCCAGAGAGAGAGCTTGTGATGCTCATGTGTCC -GGAGACAG 1259
QY 1260 GGCACCAAC -AGACGTCCAGAGAGAGAGAGCTTGTGATGCTCATGTGTCCGGAGACAG 1259
DB 1260 GGCACCAAC -AGACGTCCAGAGAGAGAGAGCTTGTGATGCTCATGTGTCCGGAGACAG 1259
QY 1320 CCGTGTGACCTGCGGAGTGGAGGCGCGCGCAAGAGAGTGCACAGTGGCTGTCTCA 1379
DB 1320 CCGTGTGACCTGCGGAGTGGAGGCGCGCGCAAGAGAGTGCACAGTGGCTGTCTCA 1379
QY 1380 CAATCCAAACCCCAACCTGAGCAACCTGAGGAGCTTCCACCCGTTTGCATAGGCGGTG 1439
DB 1380 CAATCCAAACCCCAACCTGAGCAACCTGAGGAGCTTCCACCCGTTTGCATAGGCGGTG 1439
QY 1440 GAGAGGGTGGGCGGTGTGTGAGAGCTCTGTCGCAAGAGATCAATGTCAACGCCAA 1499
DB 1440 GAGAGGGTGGGCGGTGTGTGAGAGCTCTGTCGCAAGAGATCAATGTCAACGCCAA 1499

Db 1440 GAGGAGGTTGCGGGGTGCTGAGAGCTCTCTGCGACAGAGAGTCAAGTTCAGACGCCAA 1499
Qy 1500 GGATGAGGACCAAGTGAAGAGCCCTTCACTTTGCAAGCCAGAAAGGAGATGAGTCTAGCAC 1559
Db 1500 GGATGAGGACCAAGTGAAGAGCCCTTCACTTTGCAAGCCAGAAAGGAGATGAGTCTAGCAC 1559
Qy 1560 ACCGCTGCTGTTGAGAGAGAACGCTCGGTCAACAGAGTGAACCTTTGAGGGCCGAGCC 1619
Db 1560 ACCGCTGCTGTTGAGAGAGAACGCTCGGTCAACAGAGTGAACCTTTGAGGGCCGAGCC 1619
Qy 1620 CATGCACTGAGCCTGCGACAGAGCAAGAGATATCTGCGCACTCTGCGCCGAGAG 1679
Db 1620 CATGCACTGAGCCTGCGACAGAGCAAGAGATATCTGCGCACTCTGCGCCGAGAG 1679
Qy 1680 CGTGAAGCTGAGACCTGAGAGGCAAGAGATGCTGCTGCTGCACTGCACTACGCTGCTGCA 1739
Db 1680 CGTGAAGCTGAGACCTGAGAGGCAAGAGATGCTGCTGCTGCACTGCACTACGCTGCTGCA 1739
Qy 1740 GGGGCACTGCGCCATCGTCAAGCTGCTGCGCAAGAGCGGGGGTGAAGTGAAGCCCA 1799
Db 1740 GGGGCACTGCGCCATCGTCAAGCTGCTGCGCAAGAGCGGGGGTGAAGTGAAGCCCA 1799
Qy 1800 GACGCTGATGAGAGAGAGCCATTGCACTGCGCGCAAGAGCGCGGCACTACCGGCTGGC 1859
Db 1800 GACGCTGATGAGAGAGAGCCATTGCACTGCGCGCAAGAGCGCGGCACTACCGGCTGGC 1859
Qy 1860 CCGCATCTCTCATCGACCTGCTGCTCGAGCTCAACCTTTCAGAGCTGCGGACAGACACC 1919
Db 1860 CCGCATCTCTCATCGACCTGCTGCTCGAGCTCAACCTTTCAGAGCTGCGGACAGACACC 1919
Qy 1920 CCGTGAAGTGGCGCGGAGAGAGGAGACAGAGCACTGCGCGCTGCGCATCGGAG 1979
Db 1920 CCGTGAAGTGGCGCGGAGAGAGGAGACAGAGCACTGCGCGCTGCGCATCGGAG 1979
Qy 1980 CGCTGGCAAGAGAGCGCTGAGCTTGAAGAGCTTGAAGAGAGAGCGCTGAGCGGCA 2039
Db 1980 CGCTGGCAAGAGAGCGCTGAGCTTGAAGAGCTTGAAGAGAGAGCGCTGAGCGGCA 2039
Qy 2040 CGAGACCTGCGCCATCTGCAAGCTGCTTTCGAGAGAGAGAGCGCTGAGCGGCGG 2099
Db 2040 CGAGACCTGCGCCATCTGCAAGCTGCTTTCGAGAGAGAGAGCGCTGAGCGGCGG 2099
Qy 2100 ACCCTGAAACAGAGAGGCTGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2159
Db 2100 ACCCTGAAACAGAGAGGCTGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2159
Qy 2160 GAGTGTGTCAGAGCGCGCATGTCATTGACCTGTCAGAGAGAGGCTGAGCGCTGCA 2219
Db 2160 GAGTGTGTCAGAGCGCGCATGTCATTGACCTGTCAGAGAGAGGCTGAGCGCTGCA 2219
Qy 2220 CCGTGGCG 2279
Db 2220 CCGTGGCG 2279
Qy 2280 CATCAACCTGAGAGAGCTCAAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2339
Db 2280 CATCAACCTGAGAGAGCTCAAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2339
Qy 2340 GCGAAGCAAGACTAG 2355
Db 2340 GCGAAGCAAGACTAG 2355

RESULT 8
ID AAD64340 standard; DNA; 2355 BP.
AC AAD64340;
XX 12-FEB-2004 (first entry)
DT
XX Human protein kinase C-associated kinase (PKK) variant DNA #2.
DE

XX Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
KM RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
OS Homo sapiens.
XX US2003199462-A1.
XX 23-OCT-2003.
XX 23-APR-2002; 2002US-00128174.
XX 23-APR-2002; 2002US-00128174.
XX 23-APR-2002; 2002US-00128174.
XX (NINE/) NUNEZ G.
XX (INOH/) INOHARA N.
XX (MUTO/) MUTO A.
XX Nunez G, Inohara N, Muto A;
XX WPI; 2003-852808/79.
XX New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKK induced NF-KB activation for treating hyperglycemia.
XX Disclosure; SEQ ID NO 15; Opp; English.
XX The invention relates to methods and compositions for modulating cellular
XX signalling. In particular the present invention relates to protein kinase
XX C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
XX encoding such proteins. The invention further relates to the use of PKK
XX and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
XX molecules of the invention are useful in preparing a composition for
XX inhibiting PKK induced NF-kappaB activation for treating hyperglycaemia.
XX The invention is also used in gene therapy. The present sequence is human
XX PKK variant DNA
XX
SQ Sequence 2355 BP; 462 A; 740 C; 761 G; 392 T; 0 U; 0 Other;
Query Match 98.8%; Score 2327.2; DB 10; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
Qy 1 ATGAGAGGCGAGCGGCGGAGACCCCATGAGGCGCTGCGTGGCGACCTTCAAGCGGCG 60
Db 1 ATGAGAGGCGAGCGGCGGAGACCCCATGAGGCGCTGCGTGGCGACCTTCAAGCGGCG 60
Qy 61 GAGTTCAAGGAGCTGGAGAGAGTGGCTCGAGCGGCTTTCGAGGAGATGAAGAGTGGC 120
Db 61 GAGTTCAAGGAGCTGGAGAGAGTGGCTCGAGCGGCTTTCGAGGAGATGAAGAGTGGC 120
Qy 121 CATTCACATGGAAGAGCTGCTGCGCATCAAGTCTGCGCCAGAGCTGCAAGTGAAGAC 180
Db 121 CATTCACATGGAAGAGCTGCTGCGCATCAAGTCTGCGCCAGAGCTGCAAGTGAAGAC 180
Qy 121 CATTCACATGGAAGAGCTGCTGCGCATCAAGTCTGCGCCAGAGCTGCAAGTGAAGAC 180
Db 121 CATTCACATGGAAGAGCTGCTGCGCATCAAGTCTGCGCCAGAGCTGCAAGTGAAGAC 180
Qy 181 AGGAGAGCGATGAGAGCTTTTGAAGAGAGCAAGAGATGAGAGTGGCAAGTTTCGTAC 240
Db 181 AGGAGAGCGATGAGAGCTTTTGAAGAGAGCAAGAGATGAGAGTGGCAAGTTTCGTAC 240
Qy 241 ATCTGCTGTGTATGAGCATCTGCGCGAACTGTGCGGCTGTGATGAGAGTATGAGAG 300
Db 241 ATCTGCTGTGTATGAGCATCTGCGCGAACTGTGCGGCTGTGATGAGAGTATGAGAG 300
Qy 301 ACGGAGCTCCCTGGAAGAGCTGCTGCGAGCATTTGCCATGAGATTCCTGGTTCCGA 360
Db 301 ACGGAGCTCCCTGGAAGAGCTGCTGCGAGCATTTGCCATGAGATTCCTGGTTCCGA 360
Qy 361 ATCATCAAGAGAGAGAGAGTGGAGATGAGATTCCTGCAAGTATGAGAGCGCGCGCATCTTG 420
Db 361 ATCATCAAGAGAGAGAGAGTGGAGATGAGATTCCTGCAAGTATGAGAGCGCGCGCATCTTG 420
Qy 421 CACCTGAGCTCAAGCCCGGAAATCTCTGATGAGCCCACTACAGAGTCAAGATTCT 480

Db 421 CACCTGACCTCAAGCCCGGAAACATCTGCTGATAGCCCACTACAGTCAAGATTCT 480
 Oy 481 GATTTGGTCTGGCCAGATGCAACGGGCTGTCCACTCGCATGACCTGACATGATGGC 540
 Db 481 GATTTGGTCTGGCCAGATGCAACGGGCTGTCCACTCGCATGACCTGACATGATGGC 540
 Oy 541 CTGTTGGCAATGCGCTTACTCTCCAGAGCGGATCAAGGANAAGCGGCTTTC 600
 Db 541 CTGTTGGCAATGCGCTTACTCTCCAGAGCGGATCAAGGANAAGCGGCTTTC 600
 Oy 601 GACCAAGCAAGATGATATACAGCTTTGCGATGTCATCTGGGGGCTGTCTCAACAGAG 660
 Db 601 GACCAAGCAAGATGATATACAGCTTTGCGATGTCATCTGGGGGCTGTCTCAACAGAG 660
 Oy 661 AAGCGTTTGACAGATGAGAAACATCTGCACATCATGTGAGGTGTGAAAGGCGAC 720
 Db 661 AAGCGTTTGACAGATGAGAAACATCTGCACATCATGTGAGGTGTGAAAGGCGAC 720
 Oy 721 CGCCCGAGCTGCGCCGCTGTGCAAGCCCGCGCGCTGTGAGGCACTGTATAGC 780
 Db 721 CGCCCGAGCTGCGCCGCTGTGCAAGCCCGCGCGCTGTGAGGCACTGTATAGC 780
 Oy 781 CTGATGACGGGTGCTGGAGGGGATCGCGAGTTAGGCGCCACTTCAAGAAATTACT 840
 Db 781 CTGATGACGGGTGCTGGAGGGGATCGCGAGTTAGGCGCCACTTCAAGAAATTACT 840
 Oy 841 TCTGAACCGAGGACCTGTGTGAAAAAGCTGATGACGAAGTGAAGAACTGTCTATAT 900
 Db 841 TCTGAACCGAGGACCTGTGTGAAAAAGCTGATGACGAAGTGAAGAACTGTCTATAT 900
 Oy 901 CTGAGACGTGAAAAAGCCCCCGAGGCCAGAGACGAGGTGTGCTGCGAGGCTCAAGGG 960
 Db 901 CTGAGACGTGAAAAAGCCCCCGAGGCCAGAGACGAGGTGTGCTGCGAGGCTCAAGGG 960
 Oy 961 GCTCTGCGCCCACTTGTGATACGATACAGCTCTCTCGAGCTTCTCAAGCTGAGC 1020
 Db 961 GCTCTGCGCCCACTTGTGATACGATACAGCTCTCTCGAGCTTCTCAAGCTGAGC 1020
 Oy 1021 TCTGAGTTTCCAGGCTGTGAGGGCCCGAGAGCTTCAAGCGAGCTCTGATGTC 1080
 Db 1021 TCTGAGTTTCCAGGCTGTGAGGGCCCGAGAGCTTCAAGCGAGCTCTGATGTC 1080
 Oy 1081 AAGCTGCACTGTCTGCGGAGTGGGAAAGGCTCTCGGGGTGTCTCTGCTGAGCTCGGC 1140
 Db 1081 AAGCTGCACTGTCTGCGGAGTGGGAAAGGCTCTCGGGGTGTCTCTGCTGAGCTCGGC 1140
 Oy 1141 TTCTCTTCCAGAGGATCACTGTGCTGTCTTGTGAGCGGAACTTCAACAGCGATCTG 1200
 Db 1141 TTCTCTTCCAGAGGATCACTGTGCTGTCTTGTGAGCGGAACTTCAACAGCGATCTG 1200
 Oy 1201 GGTACCAAGAGCTTCCAGAGAGAGAGCTTGTGATGTCATGTGTCC-GGAGACAG 1259
 Db 1201 GGTACCAAGAGCTTCCAGAGAGAGAGCTTGTGATGTCATGTGTCC-GGAGACAG 1259
 Oy 1260 CAAACTGATGAAAGATCTTCAAGCCGAGAGCTGTGACCTGTGCACTGTGACAGGGGTCCAG 1319
 Db 1260 CAAACTGATGAAAGATCTTCAAGCCGAGAGCTGTGACCTGTGCACTGTGACAGGGGTCCAG 1319
 Oy 1320 CCGTGTGACCTGGCGGTGAGAGCGGGAGAGAGAGTGGCAAGTGGCTGTGCTCA 1379
 Db 1320 CCGTGTGACCTGGCGGTGAGAGCGGGAGAGAGAGTGGCAAGTGGCTGTGCTCA 1379
 Oy 1380 CAATGCAACCCCAACCTGAGGAACTGTAGGGGCTTCAACCCGTTGCAATGAGCGGTGGA 1439
 Db 1380 CAATGCAACCCCAACCTGAGGAACTGTAGGGGCTTCAACCCGTTGCAATGAGCGGTGGA 1439
 Oy 1440 GAGGAGGGTGGCGGGGTGTGTGTGAGCTCTGTGCTGTGAGAGAGATGAGTGTAAAGCCCA 1499
 Db 1440 GAGGAGGGTGGCGGGGTGTGTGTGAGCTCTGTGCTGTGAGAGAGATGAGTGTAAAGCCCA 1499
 Oy 1500 GATGAGGACCAAGTGAACAGCTCTCACTTTGCAAGCCAGAAAGGGGAGAGATGTAGCAC 1559
 Db 1500 GATGAGGACCAAGTGAACAGCTCTCACTTTGCAAGCCAGAAAGGGGAGAGATGTAGCAC 1559

Oy 1560 ACGGCTGCTGTTGGAGAGAAACGCTTGCTCAACAGAGTGAAGCTTTGAGGGCGGACGCC 1619
 Db 1560 ACGGCTGCTGTTGGAGAGAAACGCTTGCTCAACAGAGTGAAGCTTTGAGGGCGGACGCC 1619
 Oy 1620 CATGCAAGTGGCTGCGCAGAGACGGGCAAGAGAAATATGTGTCGCACTCTGCTGCGGAGG 1679
 Db 1620 CATGCAAGTGGCTGCGCAGAGACGGGCAAGAGAAATATGTGTCGCACTCTGCTGCGGAGG 1679
 Oy 1680 CTGTGACGTGAGCTTGCAGAGGCAAGATGCTGTGCTGCTGCACTGCACTACCTGTGCGCA 1739
 Db 1680 CTGTGACGTGAGCTTGCAGAGGCAAGATGCTGTGCTGCTGCACTGCACTACCTGTGCGCA 1739
 Oy 1740 GGGGCACTGCGCCATGCTCAAGCTGTGCGGCAAGCAGCAGCGGGGGTGAAGTGAAGCCCA 1799
 Db 1740 GGGGCACTGCGCCATGCTCAAGCTGTGCGGCAAGCAGCAGCGGGGGTGAAGTGAAGCCCA 1799
 Oy 1800 GACGCTGATGAGAGAGAGCAGCAATTGCACTGTGCGGCAACAGCGCGGCACTAACCGGTGGC 1859
 Db 1800 GACGCTGATGAGAGAGAGCAGCAATTGCACTGTGCGGCAACAGCGCGGCACTAACCGGTGGC 1859
 Oy 1860 CCGCATCTCATGCACTGTGCTGCGAGCTGCAAGCTGTGCAAGCTGTGCGCAAGACACC 1919
 Db 1860 CCGCATCTCATGCACTGTGCTGCGAGCTGCAAGCTGTGCAAGCTGTGCGCAAGACACC 1919
 Oy 1920 CTTGCAAGTGGCGCGGAGACGGGGCAACAGAGCACTGCAAGCGCTGTGCTGCAATGCGGG 1979
 Db 1920 CTTGCAAGTGGCGCGGAGACGGGGCAACAGAGCACTGCAAGCGCTGTGCTGCAATGCGGG 1979
 Oy 1980 CGCTGCAAGAGAGCGCTGTGACCTTCAAGCGGCTAACCGCTTGTGCACTGTGCTGCGCAA 2039
 Db 1980 CGCTGCAAGAGAGCGCTGTGACCTTCAAGCGGCTAACCGCTTGTGCACTGTGCTGCGCAA 2039
 Oy 2040 CGGACACTGTGCGCACTGTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2099
 Db 2040 CGGACACTGTGCGCACTGTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2099
 Oy 2100 ACCCTGAAACAGAGAGGGGCTGTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2159
 Db 2100 ACCCTGAAACAGAGAGGGGCTGTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2159
 Oy 2160 GGAATGCTGAGCGCCGATGATCATTTGACCTGTTGCAAGAGCAAGGAGGCTCAAGCGGCTGCA 2219
 Db 2160 GGAATGCTGAGCGCCGATGATCATTTGACCTGTTGCAAGAGCAAGGAGGCTCAAGCGGCTGCA 2219
 Oy 2220 CTTGCGCGCCAGGCGCGGCAAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2279
 Db 2220 CTTGCGCGCCAGGCGCGGCAAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2279
 Oy 2280 CATCAACTGTGAGAGCTTCAAGGTTTCAAGGCGGCTCATGAGGCTGCTGCTGCTGCTGCTG 2339
 Db 2280 CATCAACTGTGAGAGCTTCAAGGTTTCAAGGCGGCTCATGAGGCTGCTGCTGCTGCTGCTG 2339
 Oy 2340 GCGAAGCAAGACTAG 2355
 Db 2340 GCGAAGCAAGACTAG 2355

RESULT 9
 AAD64341
 ID AAD64341 standard; DNA; 2355 BP.
 XX AAD64341;
 AC 12-FEB-2004 (first entry)
 DT
 XX
 DE Human protein kinase C-associated kinase (PKC) variant DNA #3.
 XX Human; cellular signalling; protein kinase C-associated kinase; PKC; DK;
 KW RICK3; Nr-kapab activation; hyperglycaemia; gene therapy; ds.
 OS Homo sapiens.
 XX

US2003199462-A1.
23-OCT-2003.
23-APR-2002; 2002US-00128174.
23-APR-2002; 2002US-00128174.
(NINEZ/) NINEZ G.
(INOH/) INOHARA N.
(MUTO/) MUTO A.
Munez G, Inohara N, Muto A;
WPI; 2003-852808/79.
New nucleic acid encoding RICK3, useful in preparing a composition for inhibiting PKK induced NF-KB activation for treating hyperglycemia.
Disclosure: SEQ ID NO 16; Opp; English.

The invention relates to methods and compositions for modulating cellular signalling. In particular the present invention relates to protein kinase C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids encoding such proteins. The invention further relates to the use of PKK and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid molecules of the invention are useful in preparing a composition for inhibiting PKK induced NF-kappaB activation for treating hyperglycemia. The invention is also used in gene therapy. The present sequence is human PKK variant DNA

Sequence 2355 BP; 462 A; 739 C; 762 G; 392 T; 0 U; 0 Other;

Query Match 98.8%; Score 2327.2; DB 10; Length 2355;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

1 ATGAGGGGGAACGGCGGAGACCCCATGGGCGCTGGCGCTGCGCACTTGAGCGGGG 60
1 ATGAGGGGGAACGGCGGAGACCCCATGGGCGCTGGCGCTGCGCACTTGAGCGGGG 60
61 GAGTTCACGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAGTGGC 120
61 GAGTTCACGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTCGGGCAAGTGTACAAGTGGC 120
121 CATGTCCATGAGAGACTGGCTGGCCATCAAGTGTCTGCCAGCTTGCAAGTGCAGC 180
121 CATGTCCATGAGAGACTGGCTGGCCATCAAGTGTCTGCCAGCTTGCAAGTGCAGC 180
181 AGGAGGCCATGAGAGCTTTTGGAGAGACCAAGAGATGAGATGGCCAAAGTTTCGTAC 240
181 AGGAGGCCATGAGAGCTTTTGGAGAGACCAAGAGATGAGATGGCCAAAGTTTCGTAC 240
241 ATCTGCTGTGTATGATCTGCGCGCAACTGTGGCTGTGTATGATGAGATGAGAG 300
241 ATCTGCTGTGTATGATCTGCGCGCAACTGTGGCTGTGTATGATGAGATGAGAG 300
301 ACGGCTCTCTGGAAGAAAGCTGTGGCTTCGAGACCATGCAATGGAGATCTCGGTTCCGA 360
301 ACGGCTCTCTGGAAGAAAGCTGTGGCTTCGAGACCATGCAATGGAGATCTCGGTTCCGA 360
361 ATCATCCAGAGACGGCGGTGGGCAATGCACTTCGCACTGGATGGCCCGCACTCTCG 420
361 ATCATCCAGAGACGGCGGTGGGCAATGCACTTCGCACTGGATGGCCCGCACTCTCG 420
421 CACCTGGAATCAAGCCCGGCAACATCTGTGTGATGGCCACTACAGTCAAGATTCT 480
421 CACCTGGAATCAAGCCCGGCAACATCTGTGTGATGGCCACTACAGTCAAGATTCT 480
481 GATTTTGGTCTGGCAAGTGCACGGGCTGTCCACTGCAATGACCTTACAGATGATGCC 540
481 GATTTTGGTCTGGCAAGTGCACGGGCTGTCCACTGCAATGACCTTACAGATGATGCC 540

QY 541 CTGTTGGCAACATCGCTTACTCTCTCCAGACGATCAGGAGAGAGCCGCTCTTC 600
Db 541 CTGTTGGCAACATCGCTTACTCTCTCCAGACGATCAGGAGAGAGCCGCTCTTC 600
QY 601 GACACCAAGCAGATGTATACAGCTTTGCGATGTCACTGGGGCGTGTCAACAGAG 660
Db 601 GACACCAAGCAGATGTATACAGCTTTGCGATGTCACTGGGGCGTGTCAACAGAG 660
QY 661 AAGCCGTTTGCATATGAGAGAAATCCTCTGCAATCATGTGTGAAGGTGGAAGGGCAC 720
Db 661 AAGCCGTTTGCATATGAGAGAAATCCTCTGCAATCATGTGTGAAGGTGGAAGGGCAC 720
QY 721 CGCCCCGAGCTGCGCCGCTGTGCAAGAGCCCGGCGGCGCTGCAAGCCACTGTATAGC 780
Db 721 CGCCCCGAGCTGCGCCGCTGTGCAAGAGCCCGGCGGCGCTGCAAGCCACTGTATAGC 780
QY 781 CTCATGCAAGGCTGTGCGAGGGGATCCGCGAGTTAGCCCACTTCCAAAGAAATTACT 840
Db 781 CTCATGCAAGGCTGTGCGAGGGGATCCGCGAGTTAGCCCACTTCCAAAGAAATTACT 840
QY 841 TCTGAAACCGAGACCTGTGTGAAAAGCCGTGATGACGAATGAAAAGAACTGCTCATGAT 900
Db 841 TCTGAAACCGAGACCTGTGTGAAAAGCCGTGATGACGAATGAAAAGAACTGCTCATGAT 900
QY 901 CTGGAAGTGAAGAAAGCCCGGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
Db 901 CTGGAAGTGAAGAAAGCCCGGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
QY 961 GCCTTGGCCCACTTTGATTAAGACTACAGCTCTCCAGCTTCTTCAACAGCTGAGC 1020
Db 961 GCCTTGGCCCACTTTGATTAAGACTACAGCTCTCCAGCTTCTTCAACAGCTGAGC 1020
QY 1021 TCTGGAATTTTCCAGAGGTGTGAGGGGCGCGAGAGTCAAGCGCACTCTGAGTTC 1080
Db 1021 TCTGGAATTTTCCAGAGGTGTGAGGGGCGCGAGAGTCAAGCGCACTCTGAGTTC 1080
QY 1081 AAGCTGCATCTGTCCGAGTGGAGAGAGCTCTCGGGGATGTCTTCTGTGAGACTCCGC 1140
Db 1081 AAGCTGCATCTGTCCGAGTGGAGAGAGCTCTCGGGGATGTCTTCTGTGAGACTCCGC 1140
QY 1141 TTCTCTTCCAGAGATCATCTGTGTCTCTTTGAGCGGGAACCTTCAACAGCATCTG 1200
Db 1141 TTCTCTTCCAGAGATCATCTGTGTCTCTTTGAGCGGGAACCTTCAACAGCATCTG 1200
QY 1201 GGTACCAAGAGGTCCAGAGAGAAAGCTTTGGATGGCATGTGTCC-GGGACACAG 1259
Db 1201 GGTACCAAGAGGTCCAGAGAGAAAGCTTTGGATGGCATGTGTCCGGGAGACACAG 1259
QY 1260 CAAACTGATGAAGATCTGCAAGCGCGAGAGCTTGCACTGGCAAGCGGTGCAG 1319
Db 1260 CAAACTGATGAAGATCTGCAAGCGCGAGAGCTTGCACTGGCAAGCGGTGCAG 1319
QY 1320 CTTGCTCACCTGGCGGTGAGAGCGCGGCAAGAGAGTGGCCAGTGGCTGTCTCAA 1379
Db 1320 CTTGCTCACCTGGCGGTGAGAGCGCGGCAAGAGAGTGGCCAGTGGCTGTCTCAA 1379
QY 1380 CAAATGCCAACCCCAACTGAGCAACCGTAGGGGCTCCACCCTGTGCAATGGCCGAG 1439
Db 1380 CAAATGCCAACCCCAACTGAGCAACCGTAGGGGCTCCACCCTGTGCAATGGCCGAG 1439
QY 1440 GAGAGGGGTGCGGGGTGTGCTGAGAGCTCTGTGCGCGGGAATCATGATCAACGCGCAA 1499
Db 1440 GAGAGGGGTGCGGGGTGTGCTGAGAGCTCTGTGCGCGGGAATCATGATCAACGCGCAA 1499
QY 1500 GGATGAGAACCATGTAACAGCTTTCAGCGCCAGAACGGGAGTGAATGTATAGAC 1559
Db 1500 GGATGAGAACCATGTAACAGCTTTCAGCGCCAGAACGGGAGTGAATGTATAGAC 1559
QY 1560 ACGGCTCTGTGGAAGAAAGCGCTGGTCAACGAATGGAATTTGAGGGCGGAGAGCC 1619
Db 1560 ACGGCTCTGTGGAAGAAAGCGCTGGTCAACGAATGGAATTTGAGGGCGGAGAGCC 1619
QY 1620 CATGCAAGTGGCTGCGCAGGACGGGCGAGAGAAATATGTGCGCATCTGTGCGCGCAGG 1679

Db	1620	CATCAGCTGGCCCTCCGACAGCGGCGAGAGAAATATGTGGCATCTCTGCTGGCCGAGG	1679
Qy	1680	CGTGAAGCTGAGCCTGCGAGGGCAAGATATGCTGTGCGCATCTGACCTACGCTGCTGGCA	1739
Db	1680	CGTGAAGCTGAGCCTGCGAGGGCAAGATATGCTGTGCGCATCTGACCTACGCTGCTGGCA	1739
Qy	1740	GGGCAACCTGCGCATCTGTAAGCTGTCTGGCCAGACAGCCGGGGGTGATGTGAACGCCCA	1799
Db	1740	GGGCAACCTGCGCATCTGTAAGCTGTCTGGCCAGACAGCCGGGGGTGATGTGAACGCCCA	1799
Qy	1800	GACGCTGATGAGAGAGACGCCATATGACCTGTGGCCGACAGGGGGGGGCACTAACCGGCTGGC	1859
Db	1800	GACGCTGATGAGAGAGACGCCATATGACCTGTGGCCGACAGGGGGGGGCACTAACCGGCTGGC	1859
Qy	1860	CCGCAATCCTCATTCGACCTGTGCTCTCCGACGTCAACGCTCTGACGCTGTGCGACAGACACC	1919
Db	1860	CCGCAATCCTCATTCGACCTGTGCTCTCCGACGTCAACGCTCTGACGCTGTGCGACAGACACC	1919
Qy	1920	CCTGCAACGTGCGCGCGAGAGCGGGGACACGAGCATGTCCAGGCTGTCTCTGATCTGGGG	1979
Db	1920	CCTGCAACGTGCGCGCGAGAGCGGGGACACGAGCATGTCCAGGCTGTCTCTGATCTGGGG	1979
Qy	1980	CGCTGGCAAGAGGCGCGTGAACCTCAAGACGGCTACACCGCTGTGACCTGTGCGCCGCGAA	2039
Db	1980	CGCTGGCAAGAGGCGCGTGAACCTCAAGACGGCTACACCGCTGTGACCTGTGCGCCGCGAA	2039
Qy	2040	CGGACACCTGCGCACTGTCAAGCTGTCTGTGAGGAGAGAGGCGCATGTGCTGGCCCGGG	2099
Db	2040	CGGACACCTGCGCACTGTCAAGCTGTCTGTGAGGAGAGAGGCGCATGTGCTGGCCCGGG	2099
Qy	2100	ACCCCTGAACCAAGACGCGGCTGCACTTGGCTGGCCGCGCAAGGAGTGTGTGA	2159
Db	2100	ACCCCTGAACCAAGACGCGGCTGCACTTGGCTGGCCGCGCAAGGAGTGTGTGA	2159
Qy	2160	GGAAGTGGTCAAGCGCGCGATGTCACTGTTCACAGAGAGGGGCTCAACGCGGCTGCA	2219
Db	2160	GGAAGTGGTCAAGCGCGCGATGTCACTGTTCACAGAGAGGGGCTCAACGCGGCTGCA	2219
Qy	2220	CCTGGCGCGCCAGAGGGCGGGCAACGACAGCGGTGGAGACTCTGCTCAAGGCAATGGGGCCCA	2279
Db	2220	CCTGGCGCGCCAGAGGGCGGGCAACGACAGCGGTGGAGACTCTGCTCAAGGCAATGGGGCCCA	2279
Qy	2280	CATCAACTGCGAGAGCCTCAAGATTCCAGGGCGGCCATGACCCTCGGCGCAACTCTCTGG	2339
Db	2280	CATCAACTGCGAGAGCCTCAAGATTCCAGGGCGGCCATGACCCTCGGCGCAACTCTCTGG	2339
Qy	2340	GCGAAGCAAGACTTGG 2355	
Db	2340	GCGAAGCAAGACTTGG 2355	
RESULT 10			
AAD64344			
ID	AAD64344	standard; DNA; 2355 BP.	
XX	AAD64344;		
XX	12-FEB-2004 (first entry)		
XX	Human protein kinase C-associated kinase (PKK) variant DNA #6.		
XX	Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;		
XX	RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; da.		
XX	Homo sapiens.		
XX	US2003199462-A1.		
XX	23-OCT-2003.		
XX	23-APR-2002; 2002US-00128174.		
XX			

PR 23-APR-2002; 2002US-00128174.
XX (NINEZ G,
PA (INOH/) INOHARA N.
PA (MOTO/) MUTO A.
XX
PI Nunez G, Inohara N, Muto A;
XX WPI, 2003-852808/79.
XX
PT New nucleic acid encoding RICK3, useful in preparing a composition for
PT inhibiting PKK induced NF-KB activation for treating hyperglycemia.
XX
PS Disclosure; SEQ ID NO 19; 0bp; English.
XX
XX The invention relates to methods and compositions for modulating cellular
CC signalling. In particular the present invention relates to protein kinase
CC C-associated kinase (PKK/DIK) and RICK3 proteins and nucleic acids
CC associated such proteins. The invention further relates to the use of PKK
CC and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
CC molecules of the invention are useful in preparing a composition for
CC inhibiting PKK induced NF-kappaB activation for treating hyperglycaemia.
CC The invention is also used in gene therapy. The present sequence is human
CC PKK variant DNA
SQ Sequence 2355 BP; 462 A; 739 C; 762 G; 392 T; 0 U; 0 Other;

Query Match	98.8%	Score 2327.2;	DB 10;	Length 2355;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2351; Conservative	0;	Mismatches 3;	Indels 2;	Gaps 2

Oy	1	ATGAGAGGCGACGGCGGGACCCCAATGAGGCGCTCGCGCTCCTGCACTTTCACATCAGCGGCG	60
Db	1	ATGAGAGGCGACGGCGGGACCCCAATGAGGCGCTCGCGCTCCTGCACTTTCACAGCGGCG	60
Oy	61	GAGTTTCACGGGCTGGGAGAAAGTGGGCTTCGGGCGGCTTCGGGCAAGGTATACAAAGTGGCG	120
Db	61	GAGTTTCACGGGCTGGGAGAAAGTGGGCTTCGGGCGGCTTCGGGCAAGGTATACAAAGTGGCG	120
Oy	121	CATGTCACACTGGAAACCTGAGCTGGCCATCAAGTGTCTCGCCGACGCTGCACGTGCAGAC	180
Db	121	CATGTCACACTGGAAACCTGAGCTGGCCATCAAGTGTCTCGCCGACGCTGCACGTGCAGAC	180
Oy	181	AGGAGAGCCGATGAGAGCTTTTGGAGAAGGCCAAGAAATGGAAGATGGCCAAAGTTTCCTAC	240
Db	181	AGGAGAGCCGATGAGAGCTTTTGGAGAAGGCCAAGAAATGGAAGATGGCCAAAGTTTCCTAC	240
Oy	241	ATTCGAGCCGTGTATATGGCATCTGCGCGGAACCTGTGGGCTGGTCAATGAGATCATGAG	300
Db	241	ATTCGAGCCGTGTATATGGCATCTGCGCGGAACCTGTGGGCTGGTCAATGAGATCATGAG	300
Oy	301	ACGGGCTCCCTGGAAAAGCTGCGGCTGTGGAGCCATTGCGATGGATCTCCGGTTCCGA	360
Db	301	ACGGGCTCCCTGGAAAAGCTGCGGCTGTGGAGCCATTGCGATGGATCTCCGGTTCCGA	360
Oy	361	ATCATTCACAAGACGGCGGTGGGCAATGAATCTTCGACATGCATGAGCCCGCACCTCCTG	420
Db	361	ATCATTCACAAGACGGCGGTGGGCAATGAATCTTCGACATGCATGAGCCCGCACCTCCTG	420
Oy	421	CACCTGGAACCTCAAGCCCGCGAATCTCTGCTGAGATGCCCATTAACAAGTCAAGATTTCT	480
Db	421	CACCTGGAACCTCAAGCCCGCGAATCTCTGCTGAGATGCCCATTAACAAGTCAAGATTTCT	480
Oy	481	GATTTTGGTCTGGCCAAAGTGAACGGGCGTGCCTCCTGCATGAACCTCAAGCATGAGTGGC	540
Db	481	GATTTTGGTCTGGCCAAAGTGAACGGGCGTGCCTCCTGCATGAACCTCAAGCATGAGTGGC	540
Oy	541	CTGTTTGGCAATGCGCTTACCTCCTCCAGAGCGCATCAGGGAGAAAGCCGCTTTC	600
Db	541	CTGTTTGGCAATGCGCTTACCTCCTCCAGAGCGCATCAGGGAGAAAGCCGCTTTC	600
Oy	601	GACACCAAGCAGGTATACAGCTTTTGGATCTGATCMGGGCGGTCTCACACGAAG	660
Db	601	GACACCAAGCAGGTATACAGCTTTTGGATCTGATCMGGGCGGTCTCACACGAAG	660

Db 601 GACACCAAGCAGATGTATACAGCTTTGCATCGTCTG666GTGTCAACAAG 660
Qy 661 AAGCGTTTGCAGATGAGAAACAATCTTGCACATCATGTGAAAGTGTGAAGGCCAC 720
Db 661 AAGCGTTTGCAGATGAGAAACAATCTTGCACATCATGTGAAAGTGTGAAGGCCAC 720
Qy 721 GGGCCGAGCTGCGCGCGGTGTGCAGAGCCGCGCGCGCGCTGACGCACTGATACG 780
Db 721 GGGCCGAGCTGCGCGCGGTGTGCAGAGCCGCGCGCGCGCTGACGCACTGATACG 780
Qy 781 CTATGCAAGCGGTGTGCAGAGGGAGATCCGAGATTAGGCCCACTTCCAAAGAAATTACT 840
Db 781 CTATGCAAGCGGTGTGCAGAGGGAGATCCGAGATTAGGCCCACTTCCAAAGAAATTACT 840
Qy 841 TCTGAACCGAGAGACTGTGTGAAAAGCTTGATGACGAAGTGAAGAAAGAACTGTATAT 900
Db 841 TCTGAACCGAGAGACTGTGTGAAAAGCTTGATGACGAAGTGAAGAAAGAACTGTATAT 900
Qy 901 CTGGAAGTGAAGAGCCCGCGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
Db 901 CTGGAAGTGAAGAGCCCGCGAGCCGAGAGCGAGGTGTGCTGCGAGGCTCAAGCGG 960
Qy 961 GCCTGTGCCCCACTTGCATTAACAAGCTTCTCGAGCTTCTCAACAAGTGAAC 1020
Db 961 GCCTGTGCCCCACTTGCATTAACAAGCTTCTCGAGCTGCTCTCAACAAGTGAAC 1020
Qy 1021 TCTGAAGTTTCCAGAGCTGTGTGAAGGCCCCGAGAGCTCAAGCCGAGCTCTTGAAGTCC 1080
Db 1021 TCTGAAGTTTCCAGAGCTGTGTGAAGGCCCCGAGAGCTCAAGCCGAGCTCTTGAAGTCC 1080
Qy 1081 AAGCTGCATGTCGCGGAGTGAAGAGAGCTCTCGGGAGTGTCTCGTGAAGCTCGGC 1140
Db 1081 AAGCTGCATGTCGCGGAGTGAAGAGAGCTCTCGGGAGTGTCTCGTGAAGCTCGGC 1140
Qy 1141 TTCTCTTCCAGAGATCACTGTGTGTCTTTGAGCGGAAACTTTCACACAGCATCTG 1200
Db 1141 TTCTCTTCCAGAGATCACTGTGTGTCTTTGAGCGGAAACTTTCACACAGCATCTG 1200
Qy 1201 GGTACCAAGAAGCTTCAAGAAAGAAAGTGTGATGCTATGTGTCC-GGAGACAG 1259
Db 1201 GGTACCAAGAAGCTTCAAGAAAGAAAGTGTGATGCTATGTGTCC-GGAGACAG 1259
Qy 1260 CAATCTGATGAAGATCTGTGAGCGCAGAGCATGTGAGCTTGGAGCTCGGAGTGA 1319
Db 1260 CAATCTGATGAAGATCTGTGAGCGCAGAGCATGTGAGCTTGGAGCTCGGAGTGA 1319
Qy 1320 CCTGTGCACTGTGCGGTGTGAAGCGGCAAGAGAGTGTGCGCAAGTGTCTCA 1379
Db 1320 CCTGTGCACTGTGCGGTGTGAAGCGGCAAGAGAGTGTGCGCAAGTGTCTCA 1379
Qy 1380 CAATGCCAACCCCAACTGAGCAACCTTAAGGGCTCCACCCGTTGCAATGTGCGTGA 1439
Db 1380 CAATGCCAACCCCAACTGAGCAACCTTAAGGGCTCCACCCGTTGCAATGTGCGTGA 1439
Qy 1440 GAGGAGGTGTGCGGTGTGTGTGAGCTCTGTGCGCAAGAAATCATGTCTCAAGCCAA 1499
Db 1440 GAGGAGGTGTGCGGTGTGTGTGAGCTCTGTGCGCGGAAATCATGTCTCAAGCCAA 1499
Qy 1500 GGATGAGGACCAAGTGAAGCCCTTCACTTTGCAAGCCAGAAAGGGAGTGAAGTCTAGCAC 1559
Db 1500 GGATGAGGACCAAGTGAAGCCCTTCACTTTGCAAGCCAGAAAGGGAGTGAAGTCTAGCAC 1559
Qy 1560 ACGGCTGTGTGTGAGAAAGAGCTTGTCAACAGAGTGAAGCTTTGAGGGCCGAGCC 1619
Db 1560 ACGGCTGTGTGTGAGAAAGAGCTTGTGTCAACAGAGTGAAGCTTTGAGGGCCGAGCC 1619
Qy 1620 CATGCAAGTGCCTGCGCAAGCGGCAAGAAATATCTGAGCATCTGCTGCGCGAGG 1679
Db 1620 CATGCAAGTGCCTGCGCAAGCGGCAAGAAATATCTGAGCATCTGCTGCGCGAGG 1679
Qy 1680 CGTGAAGTGAAGCTTGAAGGAGCAAGATGCTGTGCGCACTGAAGTGTGCGTCTGCA 1739
Db 1680 CGTGAAGTGAAGCTTGAAGGAGCAAGATGCTGTGCGCACTGAAGTGTGCGTCTGCA 1739

Qy 1740 GGGGCACTGCGCCATGCTGCAAGCTGTGCGCAAGAGAGCCGCGGGGTGAGTGAAGGCCA 1799
Db 1740 GGGGCACTGCGCCATGCTGCAAGCTGTGCGCAAGAGAGCCGCGGGGTGAGTGAAGGCCA 1799
Qy 1800 GAGCGTGAATGAGAGAGAGCCCAATTGCACTGTGCGCAAGAGCGGCACTAACGCGTGC 1859
Db 1800 GAGCGTGAATGAGAGAGAGCCCAATTGCACTGTGCGCAAGAGCGGCACTAACGCGTGC 1859
Qy 1860 CCGCATCTTATGAGCTGTGTCTTCCAGTGAAGTGTGCAAGCTGTGCGCAAGACACC 1919
Db 1860 CCGCATCTTATGAGCTGTGTCTTCCAGTGAAGTGTGCAAGCTGTGCGCAAGACACC 1919
Qy 1920 CTGCAAGTGTGCGCGGAGAGCGGGGCAAGAGCACTGCAAGGCTGTGCTGCAAGCGGG 1979
Db 1920 CTGCAAGTGTGCGCGGAGAGCGGGGCAAGAGCACTGCAAGGCTGTGCTGCAAGCGGG 1979
Qy 1980 CGCTGCAAGAGAGCGCGTGAAGCTTGAAGCGCTACACCGCTCTGCAAGCTGTGCGCAA 2039
Db 1980 CGCTGCAAGAGAGCGCGTGAAGCTTGAAGCGCTACACCGCTCTGCAAGCTGTGCGCAA 2039
Qy 2040 CGGACACTGCGCACTGTCAAGCTGTGTGTGAGAGAGCGGCAATGTGCTGCGCGGG 2099
Db 2040 CGGACACTGCGCACTGTCAAGCTGTGTGTGAGAGAGCGGCAATGTGCTGCGCGGG 2099
Qy 2100 ACCGCTGAACGAGCGCGCTGCAAGCTGTGCGCGCCAGCGGCACTCGAGGTGTGGA 2159
Db 2100 ACCGCTGAACGAGCGCGCTGCAAGCTGTGCGCGCCAGCGGCACTCGAGGTGTGGA 2159
Qy 2160 GAGATTGTGAGCGCGCATGTCAATTGACCTGTGCAAGAGCAAGAGGCTCAAGCGCTGCA 2219
Db 2160 GAGATTGTGAGCGCGCATGTCAATTGACCTGTGCAAGAGCAAGAGGCTCAAGCGCTGCA 2219
Qy 2220 CTTGCGCGCCAGAGGCGCGGCAAGCAAGAGGTGAAGCTGTGCTCAAGGCAATGGGCTCA 2279
Db 2220 CTTGCGCGCCAGAGGCGCGGCAAGCAAGAGGTGAAGCTGTGCTCAAGGCAATGGGCTCA 2279
Qy 2280 CATCAACTGAGAGGCTCAAGTTTCCAGGGGCGCAATGAGCCGCGGCAACTCTGCG 2339
Db 2280 CATCAACTGAGAGGCTCAAGTTTCCAGGGGCGCAATGAGCCGCGGCAACTCTGCG 2339
Qy 2340 GCGAAGCAAGACTAG 2355
Db 2340 GCGAAGCAAGACTAG 2355

RESULT 11
AAH15762
ID AAH15762 standard; cDNA; 3876 BP.
XX
AC AAH15762;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14188.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.

XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI: 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
XX cDNAs.

PS Claim 8; SEQ ID NO 14188; 2537bp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialized methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX Sequence 3876 BP; 798 A; 1080 C; 1186 G; 812 T; 0 U; 0 Other;

XX
SQ
Query Match 98.8%; Score 2327.2; DB 4; Length 3876;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 ATGGAAGGCGAGCGCGGAGACCCCATGAGGCGCTGCGCTGCGGACCTTCACCGCGGCG 60
DB ATGGAAGGCGAGCGCGGAGACCCCATGAGGCGCTGCGCTGCGGACCTTCACCGCGGCG 125
QY 66 ATGGAAGGCGAGCGCGGAGACCCCATGAGGCGCTGCGCTGCGGACCTTCACCGCGGCG 125
DB 66 ATGGAAGGCGAGCGCGGAGACCCCATGAGGCGCTGCGCTGCGGACCTTCACCGCGGCG 125
QY 61 GAGTTACCGGCGTGGGAGAGGCGGCTGCGGCGGCTTGGCGGAGGTATACAAGGTGCGC 120
DB GAGTTACCGGCGTGGGAGAGGCGGCTGCGGCGGCTTGGCGGAGGTATACAAGGTGCGC 185
QY 126 GAGTTACCGGCGTGGGAGAGGCGGCTGCGGCGGCTTGGCGGAGGTATACAAGGTGCGC 185
DB 126 GAGTTACCGGCGTGGGAGAGGCGGCTGCGGCGGCTTGGCGGAGGTATACAAGGTGCGC 185
QY 121 CATGTCCACTGAGAGACTGTGCTGCGCATCAAGTGTGCGCCAGCTTGACGTCAGAGAC 180
DB CATGTCCACTGAGAGACTGTGCTGCGCATCAAGTGTGCGCCAGCTTGACGTCAGAGAC 245
QY 186 CATGTCCACTGAGAGACTGTGCTGCGCATCAAGTGTGCGCCAGCTTGACGTCAGAGAC 245
DB 186 CATGTCCACTGAGAGACTGTGCTGCGCATCAAGTGTGCGCCAGCTTGACGTCAGAGAC 245
QY 181 AGGAGACGCGATGAGAGCTTTTGGAGAGAGCCAGAGAGATGAGATGCGCAAGTTTCCCTAC 240
DB AGGAGACGCGATGAGAGCTTTTGGAGAGAGCCAGAGAGATGAGATGCGCAAGTTTCCCTAC 305
QY 246 AGGAGACGCGATGAGAGCTTTTGGAGAGAGCCAGAGAGATGAGATGCGCAAGTTTCCCTAC 305
DB 246 AGGAGACGCGATGAGAGCTTTTGGAGAGAGCCAGAGAGATGAGATGCGCAAGTTTCCCTAC 305
QY 241 ATCTGCGCTGTGTATGAGCATCTGCGCGGAGACCTGTGCGCTGTGTCATGAGATCATGAG 300
DB ATCTGCGCTGTGTATGAGCATCTGCGCGGAGACCTGTGCGCTGTGTCATGAGATCATGAG 365
QY 306 ATCTGCGCTGTGTATGAGCATCTGCGCGGAGACCTGTGCGCTGTGTCATGAGATCATGAG 365
DB 306 ATCTGCGCTGTGTATGAGCATCTGCGCGGAGACCTGTGCGCTGTGTCATGAGATCATGAG 365
QY 301 ACGGAGCTCCCTGAGAAAAGCTGTGCTTGGAGACCATTTGCGATGAGATCTCCGGTTCCGA 360
DB ACGGAGCTCCCTGAGAAAAGCTGTGCTTGGAGACCATTTGCGATGAGATCTCCGGTTCCGA 425
QY 366 ACGGAGCTCCCTGAGAAAAGCTGTGCTTGGAGACCATTTGCGATGAGATCTCCGGTTCCGA 425
DB 366 ACGGAGCTCCCTGAGAAAAGCTGTGCTTGGAGACCATTTGCGATGAGATCTCCGGTTCCGA 425
QY 361 ATCATTCACGAGAGCGGCGGTGGGATGAACTTCTGCACTGATGAGCCCGCCACTCTCG 420
DB ATCATTCACGAGAGCGGCGGTGGGATGAACTTCTGCACTGATGAGCCCGCCACTCTCG 485
QY 426 ATCATTCACGAGAGCGGCGGTGGGATGAACTTCTGCACTGATGAGCCCGCCACTCTCG 485
DB 426 ATCATTCACGAGAGCGGCGGTGGGATGAACTTCTGCACTGATGAGCCCGCCACTCTCG 485
QY 421 CACCTGGAAGCTCAAGCCCGGAGACATCTGCTGATGAGCCCACTACCAAGTCAGATTTTCT 480
DB CACCTGGAAGCTCAAGCCCGGAGACATCTGCTGATGAGCCCACTACCAAGTCAGATTTTCT 545

QY 481 GATTTGGTCTGAGCAAGTGCAGAGGCTGTGCCACTGCGATGACCTCAGCATGATGAGC 540
DB GATTTGGTCTGAGCAAGTGCAGAGGCTGTGCCACTGCGATGACCTCAGCATGATGAGC 605
QY 541 CTGTTTGGCACAATCGCTTACCTTCTCCAGAGGCGATCAGAGAGAAAGCGGCTCTTC 600
DB CTGTTTGGCACAATCGCTTACCTTCTCCAGAGGCGATCAGAGAGAAAGCGGCTCTTC 665
QY 606 CTGTTTGGCACAATCGCTTACCTTCTCCAGAGGCGATCAGAGAGAAAGCGGCTCTTC 665
DB 606 CTGTTTGGCACAATCGCTTACCTTCTCCAGAGGCGATCAGAGAGAAAGCGGCTCTTC 665
QY 601 GACACCAAGCAGATGATACAGCTTTTGGCATCTGATCTGAGGCGGTCTCACACAGAG 660
DB GACACCAAGCAGATGATACAGCTTTTGGCATCTGATCTGAGGCGGTCTCACACAGAG 725
QY 661 AAGCGTTTGGAGATGAGAGAAACATCTGCACTCATGAGTGAAGTGAAGGCGCAC 720
DB AAGCGTTTGGAGATGAGAGAAACATCTGCACTCATGAGTGAAGTGAAGGCGCAC 785
QY 726 AAGCGTTTGGAGATGAGAGAAACATCTGCACTCATGAGTGAAGTGAAGGCGCAC 785
DB 726 AAGCGTTTGGAGATGAGAGAAACATCTGCACTCATGAGTGAAGTGAAGGCGCAC 785
QY 721 CGCCCGAGCTGCGCGCGCTGTGAGAGCCCGCGCGCGCTGCAAGCCACTGATACG 780
DB CGCCCGAGCTGCGCGCGCTGTGAGAGCCCGCGCGCGCTGCAAGCCACTGATACG 845
QY 781 CTGATGAGCGGTGCTGAGAGGAGATCCGCAATGAGCTTCAAGTGAAGTGAAGTGAAGT 840
DB CTGATGAGCGGTGCTGAGAGGAGATCCGCAATGAGCTTCAAGTGAAGTGAAGTGAAGT 905
QY 841 TCTGAAACCGAGAGACCTGTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 900
DB TCTGAAACCGAGAGACCTGTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 965
QY 906 TCTGAAACCGAGAGACCTGTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 965
DB 906 TCTGAAACCGAGAGACCTGTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 965
QY 901 CTGAGCGTGAAGAACCCCGCGAGCCAGAGAGAGTGTGCTGCGAGGCTCAAGCGG 960
DB CTGAGCGTGAAGAACCCCGCGAGCCAGAGAGAGTGTGCTGCGAGGCTCAAGCGG 1025
QY 966 CTGAGCGTGAAGAACCCCGCGAGCCAGAGAGAGTGTGCTGCGAGGCTCAAGCGG 1025
DB 966 CTGAGCGTGAAGAACCCCGCGAGCCAGAGAGAGTGTGCTGCGAGGCTCAAGCGG 1025
QY 961 GCTTGTGCGCCGACCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB GCTTGTGCGCCGACCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
QY 1026 GCTTGTGCGCCGACCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
DB 1026 GCTTGTGCGCCGACCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
QY 1021 TCTGAGATTTTCCAGAGCTGTGAGAGAGCCCGAGAGACTCAGCGCATCTCTGATGTC 1080
DB TCTGAGATTTTCCAGAGCTGTGAGAGAGCCCGAGAGACTCAGCGCATCTCTGATGTC 1145
QY 1086 TCTGAGATTTTCCAGAGCTGTGAGAGAGCCCGAGAGACTCAGCGCATCTCTGATGTC 1145
DB 1086 TCTGAGATTTTCCAGAGCTGTGAGAGAGCCCGAGAGACTCAGCGCATCTCTGATGTC 1145
QY 1081 AAGCTGCGATGTCGCGAGAGTGGAGAGAGCTTCTGCGGAGTGTCTGCTGAGACTCGGCG 1140
DB AAGCTGCGATGTCGCGAGAGTGGAGAGAGCTTCTGCGGAGTGTCTGCTGAGACTCGGCG 1205
QY 1146 AAGCTGCGATGTCGCGAGAGTGGAGAGAGCTTCTGCGGAGTGTCTGCTGAGACTCGGCG 1205
DB 1146 AAGCTGCGATGTCGCGAGAGTGGAGAGAGCTTCTGCGGAGTGTCTGCTGAGACTCGGCG 1205
QY 1141 TTCTCTTCCAGAGATCACTGTGCTGCTTTTGAAGCGGAACTTCAACAGCATCTG 1200
DB TTCTCTTCCAGAGATCACTGTGCTGCTTTTGAAGCGGAACTTCAACAGCATCTG 1265
QY 1206 TTCTCTTCCAGAGATCACTGTGCTGCTTTTGAAGCGGAACTTCAACAGCATCTG 1265
DB 1206 TTCTCTTCCAGAGATCACTGTGCTGCTTTTGAAGCGGAACTTCAACAGCATCTG 1265
QY 1201 GGTATCCAAAGACCTGCGAGAGAGAGAGCTTGTGATGAGTGCATGCTGCTGCG -GGAGACGAG 1259
DB GGTATCCAAAGACCTGCGAGAGAGAGAGCTTGTGATGAGTGCATGCTGCTGCG -GGAGACGAG 1324
QY 1266 GGTATCCAAAGACCTGCGAGAGAGAGAGCTTGTGATGAGTGCATGCTGCTGCG -GGAGACGAG 1324
DB 1266 GGTATCCAAAGACCTGCGAGAGAGAGAGCTTGTGATGAGTGCATGCTGCTGCG -GGAGACGAG 1324
QY 1260 CAAACTGATGAAGATCTGCAAGCGCAGAGAGTGGACCTGCACTGCAAGCGGTGCGAG 1319
DB CAAACTGATGAAGATCTGCAAGCGCAGAGAGTGGACCTGCACTGCAAGCGGTGCGAG 1384
QY 1325 CAAACTGATGAAGATCTGCAAGCGCAGAGAGTGGACCTGCACTGCAAGCGGTGCGAG 1384
DB 1325 CAAACTGATGAAGATCTGCAAGCGCAGAGAGTGGACCTGCACTGCAAGCGGTGCGAG 1384
QY 1320 CCTGCTGACACTGCGGAGTGAAGGCGGCGCAAGAGAGTGCAGGATGAGCTGCTCAA 1379
DB CCTGCTGACACTGCGGAGTGAAGGCGGCGCAAGAGAGTGCAGGATGAGCTGCTCAA 1444
QY 1385 CCTGCTGACACTGCGGAGTGAAGGCGGCGCAAGAGAGTGCAGGATGAGCTGCTCAA 1444
DB 1385 CCTGCTGACACTGCGGAGTGAAGGCGGCGCAAGAGAGTGCAGGATGAGCTGCTCAA 1444
QY 1380 CAATGCGAACCCCAACTGAGAGAACCTGATGAGGCGCTCCACCCGTTGCAATGAGCGGTGA 1439
DB CAATGCGAACCCCAACTGAGAGAACCTGATGAGGCGCTCCACCCGTTGCAATGAGCGGTGA 1504
QY 1445 CAATGCGAACCCCAACTGAGAGAACCTGATGAGGCGCTCCACCCGTTGCAATGAGCGGTGA 1504
DB 1445 CAATGCGAACCCCAACTGAGAGAACCTGATGAGGCGCTCCACCCGTTGCAATGAGCGGTGA 1504
QY 1440 GAGGAGGAGTGGGAGTGTGAGAGCTCTGCTGCAAGGAGATCAAGTGTCAAGCCAA 1499
DB GAGGAGGAGTGGGAGTGTGAGAGCTCTGCTGCAAGGAGATCAAGTGTCAAGCCAA 1564
QY 1505 GAGGAGGAGTGGGAGTGTGAGAGCTCTGCTGCAAGGAGATCAAGTGTCAAGCCAA 1564
DB 1505 GAGGAGGAGTGGGAGTGTGAGAGCTCTGCTGCAAGGAGATCAAGTGTCAAGCCAA 1564
QY 1500 GAGTGAAGACAGTGAAGAGCCCTTCACTTTGCAAGCCCAAGCGGAGTGAATCTAGCAC 1559
DB GAGTGAAGACAGTGAAGAGCCCTTCACTTTGCAAGCCCAAGCGGAGTGAATCTAGCAC 1624
QY 1565 GAGTGAAGACAGTGAAGAGCCCTTCACTTTGCAAGCCCAAGCGGAGTGAATCTAGCAC 1624
DB 1565 GAGTGAAGACAGTGAAGAGCCCTTCACTTTGCAAGCCCAAGCGGAGTGAATCTAGCAC 1624

QY 1560 ACGGCTGCTGTTGAGAGAAAGCGCTGGTCAACAGAGGTGAGCTTTGAGGGCCGGAAGCC 1619
DB 1625 ACGGCTGCTGTTGAGAGAAAGCGCTGGTCAACAGAGGTGAGCTTTGAGGGCCGGAAGCC 1684
QY 1620 CATGCACTGGGCTGCTGCGACAGCGGCAAGAGATATCTGTCGACCTCTGCGCCGAGG 1679
DB 1685 CATGCACTGGGCTGCTGCGACAGCGGCAAGAGATATCTGTCGACCTCTGCGCCGAGG 1744
QY 1680 CGTGAAGCTGAGACCTGCAAGGGAGAGATGCTGGCTGCGACCTGCACTACGCTGCTGGCA 1739
DB 1745 CGTGAAGCTGAGACCTGCAAGGGAGAGATGCTGGCTGCGACCTGCACTACGCTGCTGGCA 1804
QY 1740 GGGGCACTGGCCCATGATCAAGCTGCTGAGCCCAAGCAAGCGGGGGGAGTGTGAACGGCCA 1799
DB 1805 GGGGCACTGGCCCATGATCAAGCTGCTGAGCCCAAGCAAGCGGGGGGAGTGTGAACGGCCA 1864
QY 1800 GACGCTGATGGAGAGAGCGCCATTGCACTGGCCGCAAGCGCGGGCACTAACCGGTGGC 1859
DB 1865 GACGCTGATGGAGAGAGCGCCATTGCACTGGCCGCAAGCGCGGGCACTAACCGGTGGC 1924
QY 1860 CCGCATCTCTCATCGACCTGTGCTCCGACGTCAAAGCTGCAAGCTGCTGGGCAAGACACC 1919
DB 1925 CCGCATCTCTCATCGACCTGTGCTCCGACGTCAAAGCTGCAAGCTGCTGGGCAAGACACC 1984
QY 1920 CCTGCAAGTGGCGCGAGAGCGGGGCAAGCAAGCACTGCGACGCTGCTGCACTGCACTGGG 1979
DB 1985 CCTGCAAGTGGCGCGAGAGCGGGGCAAGCAAGCACTGCGACGCTGCTGCTGCACTGCGG 2044
QY 1980 CGCTGGCAAGAGAGCGCTGACCTGACAGAGCGCTTACACCGCTCTGCACTGGCTGCGGCA 2039
DB 2045 CGCTGGCAAGAGAGCGCTGACCTGACAGAGCGCTTACACCGCTCTGCACTGGCTGCGGCA 2104
QY 2040 CGGAACTGTGGCTCACTGTCAAGCTGCTGTGAGAGAGAGAGCGGCTGCTGCTGCGGCGG 2099
DB 2105 CGGAACTGTGGCTCACTGTCAAGCTGCTGTGAGAGAGAGAGCGGCTGCTGCTGCGGCGG 2164
QY 2100 ACCCTGAAACAGAGCGGCTGCACTGAGCTGCGCCCAAGCGGCACTGAGAGTGTGA 2159
DB 2165 ACCCTGAAACAGAGCGGCTGCACTGAGCTGCGCCCAAGCGGCACTGAGAGTGTGA 2224
QY 2160 GAGAGTGTGTCAGCGCGCATGTCATTGACCTGTTGAGAGAGAGCGGCTTCAAGCGGCTGCA 2219
DB 2225 GAGAGTGTGTCAGCGCGCATGTCATTGACCTGTTGAGAGAGAGCGGCTTCAAGCGGCTGCA 2284
QY 2220 CTTGCGCGCGCGCGCGCGCGAGCAAGAGCTGCTGCTCAAGGCAATGGGGCCCA 2279
DB 2285 CTTGCGCGCGCGCGCGCGCGAGCAAGAGCTGCTGCTCAAGGCAATGGGGCCCA 2344
QY 2280 CATCAACCTGAGAGCTCAAGTTTCAGGGCGGCGCATGGCGCGCGCAACTCTGCG 2339
DB 2345 CATCAACCTGAGAGCTCAAGTTTCAGGGCGGCGCATGGCGCGCGCAACTCTGCG 2404
QY 2340 GCGAAGCAAGACTAG 2355
DB 2405 GCGAAGCAAGACTAG 2420

RESULT 12
AAD64329
ID AAD64329 standard; DNA; 2355 BP.
XX
XX AAD64329;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Human protein kinase C-associated kinase (PKC) DNA.
DE
XX
XX Human; cellular signalling; protein kinase C-associated kinase; PKC; DIK;
KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; gene; de.
OS Homo sapiens.
XX
XX
XX
FH Key Location/Qualifiers

PT CDS 1..2355
FT /tag= a
FT /product= "Human PKC protein"
XX
XX US2003199462-A1.
XX
XX 23-OCT-2003.
XX
XX 23-APR-2002; 2002US-00128174.
XX
XX 23-APR-2002; 2002US-00128174.
XX
XX 23-APR-2002; 2002US-00128174.
XX
XX (NONE/) NUNEZ G.
XX (INOH/) INOHARA N.
XX (MUTO/) MUTO A.
XX
XX Nunez G, Inohara N, Muto A;
XX
XX WPI; 2003-852808/79.
XX
XX P-PSDB; ABM02412.
XX
XX
XX New nucleic acid encoding RICK3, useful in preparing a composition for
XX inhibiting PKC induced NF-KB activation for treating hyperglycemia.
XX
XX Disclosure; SEQ ID NO 1; 0bp; English.
XX
XX The invention relates to methods and compositions for modulating cellular
XX signalling. In particular the present invention relates to protein kinase
XX C-associated kinase (PKC/DIK) and RICK3 proteins and nucleic acids
XX encoding such proteins. The invention further relates to the use of PKC
XX and RICK3 proteins in modulating NF-kappaB signalling. Nucleic acid
XX molecules of the invention are useful in preparing a composition for
XX inhibiting PKC induced NF-kappaB activation for treating hyperglycemia.
XX The invention is also used in gene therapy. The present sequence is human
XX PKC DNA
XX
SQ Sequence 2355 BP; 462 A; 740 C; 762 G; 391 T; 0 U; 0 Other;
Query Match 98.8%; Score 2325.6; DB 10; Length 2355;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2350; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 1 ATGAGAGGCGACAGCGCGGAGCCCATGAGGCGCTGCGTGCACCTTGCAGCGCGGC 60
DB 1 ATGAGAGGCGACAGCGCGGAGCCCATGAGGCGCTGCGTGCACCTTGCAGCGCGGC 60
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DB 361 ATCATCCAGAGAGCGGCTGGGATGAATCTCTGCACTGCAATGGCCCGGCACTCTCG 420
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 RESULT 13
 AAD64348
 ID AAD64348 standard; DNA; 2355 BP.
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 AC AAD64348;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human protein kinase C-associated kinase (PKK) variant DNA #10.
 XX
 KW Human; cellular signalling; protein kinase C-associated kinase; PKK; DIK;
 KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
 OS Homo sapiens.
 XX
 PN US2003199462-A1.

XX 23-OCT-2003.
PD 23-APR-2002; 2002US-00128174.
XX 23-APR-2002; 2002US-00128174.
XX 23-APR-2002; 2002US-00128174.
PR 23-APR-2002; 2002US-00128174.
XX (NINEZ/) NINEZ G.
PA (INOH/) INOHARA N.
PA (MUTO/) MUTO A.
XX Nunez G, Inohara N, Muto A;
XX WPI; 2003-852808/79.
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PT inhibiting PKK induced NF-kB activation for treating hyperglycemia.
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CC signaling. In particular the present invention relates to protein kinase
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CC and RICK3 proteins in modulating NF-kappaB signaling. Nucleic acid
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CC PKK variant DNA
SQ Sequence 2355 BP; 461 A; 740 C; 763 G; 391 T; 0 U; 0 Other;
Query Match 98.7%; Score 2324; DB 10; Length 2355;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2349; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
QY 1 ATGGAGGCGCAGACGGGCGGAGCCCATGGGCGCTGTGCGGACCTTGAGCGCGGCG 60
DB 1 ATGGAGGCGCAGACGGGCGGAGCCCATGGGCGCTGTGCGGACCTTGAGCGCGGCG 60
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 RESULT 14
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 ID AAD64342 standard; DNA; 2355 BP.
 AC AAD64342;
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 DT 12-FEB-2004 (first entry)
 XX
 DE Human protein kinase C-associated kinase (PKC) variant DNA #4.
 XX
 KW Human; cellular signalling; protein kinase C-associated kinase; PKC; DIK;
 KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PN US2003199462-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 23-APR-2002; 2002US-00128174.
 XX
 PR 23-APR-2002; 2002US-00128174.

XX (NUNEZ G.
 PA (INOHARA N.
 PA (INOHARA N.
 XX (MUTO A.
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 PI Nunez G, Inohara N, Muto A;
 DR WPI: 2003-852808/79.
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RESULT 15
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ID AAD64345 standard; DNA; 2355 BP.
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XX
DT 12-FEB-2004 (first entry)
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DE Human protein kinase C-associated kinase (PKC) variant DNA #7.
XX
KW Human; cellular signalling; protein kinase C-associated kinase; PKC; DIK;
KW RICK3; NF-kappaB activation; hyperglycaemia; gene therapy; ds.
OS Homo sapiens.
XX
PN US2003199462-A1.
XX
PD 23-OCT-2003.
XX
PF 23-APR-2002; 2002US-00128174.
XX
PR 23-APR-2002; 2002US-00128174.
XX
PA (NINEZ/) NUNEZ G.
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PA (MUTO/) MUTO A.
XX
PI Nunez G, Inohara N, Muto A;

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC
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Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2355	100.0	2355	6 AR406004	AR406004 Sequence
2	2355	100.0	3860	6 AR406003	AR406003 Sequence
3	2330.4	99.0	3879	9 HSA278016	AJ278016 Homo sapi
4	2327.2	98.8	3876	6 BD157754	BD157754 Primer fo
5	2327.2	98.8	3876	6 AX879283	AX879283 Sequence
6	2327.2	98.8	3876	9 AK027424	AK027424 Homo sapi
7	2327.2	98.8	3882	9 AB047783	AB047783 Homo sapi
8	2322.4	98.6	3867	9 BC035755	BC035755 Homo sapi
9	2173.2	92.3	2499	6 CO731804	CO731804 Sequence
10	2173.2	92.3	2499	6 AX166548	AX166548 Sequence
11	1748	74.2	3559	10 AF302127	AF302127 Mus muscu
12	1746.4	74.1	3558	10 BC057871	BC057871 Mus muscu
13	1745.4	74.1	2370	6 BD251844	BD251844 Death abs
14	1745.4	74.1	2370	6 AR258256	AR258256 Sequence
15	1745.4	74.1	3516	6 BD209707	BD209707 Compositi
16	1745.4	74.1	3516	6 AR341513	AR341513 Sequence
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ALIGNMENTS

RESULT 1
AR406004 Sequence 3 from patent US 6630335.
LOCUS AR406004
DEFINITION AR406004.1 GI:40155104
ACCESSION AR406004.1
VERSION AR406004.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2355)
AUTHORS Kapeller-Libermann, R.
TITLE 14171 protein kinase, a novel human protein kinase and uses thereof
JOURNAL Patent: US 6630335-A 3 07-OCT-2003;
FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
AR406003
LOCUS AR406003 3860 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 1 from patent US 6630335.
ACCESSION AR406003
VERSION AR406003.1 GI:40155103
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3860)
AUTHORS Kapeller-Lieberman, R.
TITLE 14171 protein kinase, a novel human protein kinase and uses thereof
JOURNAL Patent: US 6630335-A 1 07-OCT-2003;
FEATURES
source location/Qualifiers
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Matches 2355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1201 GGTACCAACAGACGTCCAGAAAGAAAGCTTGTGATGCCATGCTGTCCGAGACACAGC 1260
DB 1217 GGTACCAACAGACGTCCAGAAAGAAAGCTTGTGATGCCATGCTGTCCGAGACACAGC 1276
QY 1261 AAACGTATGAAGATCTGACAGCCGCAAGAGAGCTGAGACCTGAGACAGGCGTGCAGC 1320
DB 1277 AAACGTATGAAGATCTGACAGCCGCAAGAGAGCTGAGACCTGAGACAGGCGTGCAGC 1336
QY 1321 CTGCTGCACTGAGCGGTGAGAGCGGCGCAAGAGATGTCGCAAGTGGCTGTCTAAC 1380
DB 1337 CTGCTGCACTGAGCGGTGAGAGCGGCGCAAGAGATGTCGCAAGTGGCTGTCTAAC 1396
QY 1381 AATGCCAACCCCAACTGAGCAACGTAGGGGCTTCACCCCGTTGACATGCGCTGAG 1440
DB 1397 AATGCCAACCCCAACTGAGCAACGTAGGGGCTTCACCCCGTTGACATGCGCTGAG 1456
QY 1441 AGAGGGTGGCGGGTGTGTGAGACTCTGTGTGCAACGGAAGATCAAGTGAACGCGAAG 1500
DB 1457 AGAGGGTGGCGGGTGTGTGAGACTCTGTGTGCAACGGAAGATCAAGTGAACGCGAAG 1516
QY 1501 GATGAGACCAAGTGAACAGCCCTTCACTTTGCAAGCCAGAAAGGGAGATGATCTAGACA 1560
DB 1517 GATGAGACCAAGTGAACAGCCCTTCACTTTGCAAGCCAGAAAGGGAGATGATCTAGACA 1576
QY 1561 CGGCTGTGTGAGAGAAAGCCTCGGTCAACGAGGTGAATTTGAGGGCCGAGCGCC 1620
DB 1577 CGGCTGTGTGAGAGAAAGCCTCGGTCAACGAGGTGAATTTGAGGGCCGAGCGCC 1636
QY 1621 ATGCACTGTGGCTGCAACAGAGGCGGAGAGAAATATGTCGCCCATCTGCGCGGAGG 1680
DB 1637 ATGCACTGTGGCTGCAACAGAGGCGGAGAGAAATATGTCGCCCATCTGCGCGGAGG 1696
QY 1681 GTGAGCGAGAGCGTGCAGGGAGAGATGCTGTGCTGCACTGACATGACGCTGCGAG 1740
DB 1697 GTGAGCGAGAGCGTGCAGGGAGAGATGCTGTGCTGCACTGACATGACGCTGCGAG 1756
QY 1741 GGCACCTGCCCATCTGTCAAGCTGTGCGCAAGCAGCGGGGGTGAATGTGAACCCAG 1800
DB 1757 GGCACCTGCCCATCTGTCAAGCTGTGCGCAAGCAGCGGGGGTGAATGTGAACCCAG 1816
QY 1801 ACGCTGATGTGAGAGAGCGCATTTGCACTGTGCGCGGACAGCGCGGCGCATACCGGTGGC 1860
DB 1817 ACGCTGATGTGAGAGAGCGCATTTGCACTGTGCGCGGACAGCGCGGCGCATACCGGTGGC 1876
QY 1861 CGCATCTCATGACCTGTGCTCGAGCTCAAGCTCAAGCTTGTGCGACAGACCC 1920

Db	1877	CGCATTCCTCATCGACCTGTGCTCCGACGTTCAACGTTCTGACGCTCTGTGGCAACACACCC	1936
QY	1921	CTGCACCTGGCCGGGAGACCGGGGCAACGAGCACTGGCAGGCTTGCTCTGCATCGGGG	1980
Db	1997	CTGCACGTTGGCCGGAGACCGGGGCAACGAGCACTGGCAGGCTTGCTCTGCATCGGGG	1996
QY	1981	GCTGGCAAGAGAGGCGGTGACCTCAGACGGCTTACAACCGTCTTGACACTGGCTGGCCGAC	2040
Db	1997	GCTGGCAAGAGAGGCGGTGACCTCAGACGGCTTACAACCGTCTTGACACTGGCTGGCCGAC	2056
QY	2041	GGACACCTGGGCACTGTCAAGCTGTTGTGAGAGAGAGGCGAGTGTCTGACCCGGGGA	2100
Db	2057	GGACACCTGGGCACTGTCAAGCTGTTGTGAGAGAGAGGCGAGTGTCTGACCCGGGGA	2116
QY	2101	CCCGTGAACCAACGGCGCTGCACTGGCTGGCCGCCACGGGCACTCGAGGTGTGTAG	2160
Db	2117	CCCGTGAACCAACGGCGCTGCACTGGCTGGCCGCCACGGGCACTCGAGGTGTGTAG	2176
QY	2161	GAGTTGTGTACAGCGCGGATGTCAATTGACCTGTTTCAACGAGCAGGGGCTCAGCGGCTGAC	2220
Db	2177	GAGTTGTGTACAGCGCGGATGTCAATTGACCTGTTTCAACGAGCAGGGGCTCAGCGGCTGAC	2238
QY	2221	CTGGCGGCGCCAGGGCGGGGCAACGACGAGCGGAGAGCTTGCTCAGGCAATGGGCGCAC	2280
Db	2237	CTGGCGGCGCCAGGGCGGGGCAACGACGAGCGGAGAGCTTGCTCAGGCAATGGGCGCAC	2296
QY	2281	ATCAACCTGCAAGGCTCAAGTTCCAGGGCGGGCAATGGCCCCGCGGCAACTCTCTGGG	2340
Db	2297	ATCAACCTGCAAGGCTCAAGTTCCAGGGCGGGCAATGGCCCCGCGGCAACTCTCTGGG	2356
QY	2341	CGAAGCAAGACTTAG 2355	
Db	2357	CGAAGCAAGACTTAG 2371	

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RESULT 3
HSA278016                                3879 bp      mRNA      linear      PRI 19-NOV-2000

LOCUS      HSA278016
DEFINITION Homo sapiens mRNA for protein kinase (dik gene).
ACCESSION  AJ278016
VERSION     AJ278016.1 GI:9886710
KEYWORDS   dik gene; protein kinase.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  1
AUTHORS    Bhr, C., Rohwer, A., Stempka, L., Rincke, G., Marks, F. and Gschwendt, M.
TITLE      Dik, a novel protein kinase that interacts with protein kinase
             Cdelta. Cloning, characterization, and gene analysis
             J. Biol. Chem. 275 (46), 36350-36357 (2000)

JOURNAL    20549657
MEDLINE    10948194
REFERENCE  2 (bases 1 to 3879)
AUTHORS    Gschwendt, M.
TITLE      Direct Submission
             Submitted (18-MAY-2000) Gschwendt M., Blochemistry of
             Tissue-specific Regulation, German Cancer Research Center, Im
             Neuenheimer Feld 280, D-69151 Heidelberg, GERMANY

FEATURES   Location/Qualifiers
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone_lib="Hacat"
            1..3879
                /gene="dik"
            49..2403
                /gene="dik"
                /function="protein phosphorylation"
                /codon_start=1
                /evidence=experimental

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Query Match	Best Local Similarity	99.9%	Score	2330.4	DB	9	Length	3879	
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Db	49	ATGAGAGGCGACGCGGGGACCCCATGAGGCGCTCGCGCTGCTGCGCACCTTCGACGCGGCG	108						
QY	61	GAGTTCAAGCGGCTGGGAGAAAGTGGGCTCGCGCGGCTTCGCGCAGGTGTAACAAGTGGGCG	120						
Db	109	GAGTTCAAGCGGCTGGGAGAAAGTGGGCTCGCGCGGCTTCGCGCAGGTGTAACAAGTGGGCG	168						
QY	121	CATGTCACCTGAAAGACTGGCTGGCCATCAAGTCTCGGCCAGGCTGCACCTGCACGAC	180						
Db	169	CATGTCACCTGAAAGACTGGCTGGCCATCAAGTCTCGGCCAGGCTGCACGCTGCACGAC	228						
QY	181	AGGAGCGCATGAGCTTTGGAGAGAGCCCAAGAGATGAGATGGCCAGTTCGCTAC	240						
Db	229	AGGAGCGCATGAGCTTTGGAGAGAGCCCAAGAGATGAGATGGCCAGTTCGCTAC	288						
QY	241	ATCTGCTGCTGTATGATGATCTGCGCGGCACTGTGCGGCTGCTGATGAGATGATGAG	300						
Db	289	ATCTGCTGCTGTATGATGATCTGCGCGGCACTGTGCGGCTGCTGATGAGATGATGAG	348						
QY	301	ACGGGCTCCCTGGAGAAAGCTGCGCTTCGAGAGCATGGGATCTCCGGTTCCGA	360						
Db	349	ACGGGCTCCCTGGAGAAAGCTGCGCTTCGAGAGCATGGGATCTCCGGTTCCGA	408						
QY	361	ATCATCCACGAGACGCGCGGTGGGATGAACTTCTCGCATGTCATGAGCGCCCGCACTCTG	420						
Db	409	ATCATCCACGAGACGCGCGGTGGGATGAACTTCTCGCATGTCATGAGCGCCCGCACTCTG	468						
QY	421	CACCTGCACTCAAGCCCGCGCAATCTCTGCTGATGTCCTTACCAAGTCAAGATTTCT	480						
Db	469	CACCTGCACTCAAGCCCGCGCAATCTCTGCTGATGTCCTTACCAAGTCAAGATTTCT	528						
QY	491	GATTTTGGTGGGCAAGTGGCAAGGGGCTGTCCCATCTGCATGACCTTCAGATGATGAGC	540						
Db	529	GATTTTGGTGGGCAAGTGGCAAGGGGCTGTCCCATCTGCATGACCTTCAGATGATGAGC	588						
QY	541	CTGTTTGGACACATGCGCTTACCTCCCTCCAGAGCGCATTCAGGAGAAAGCGGCTCTTC	600						
Db	589	CTGTTTGGACACATGCGCTTACCTCCCTCCAGAGCGCATTCAGGAGAAAGCGGCTCTTC	648						
QY	601	GACACCAAGACGATGATATACGCTTTGGATGTCATCTGGGGGCTGCTCAACAAG	660						
Db	649	GACACCAAGACGATGATATACGCTTTGGATGTCATCTGGGGGCTGCTCAACAAG	708						
QY	661	AAGCGTTTGACATGAGAGAAACATCTGACATCATGATGTAAGTGGTGAAGGCGCAC	720						

Query Match	Similarity	99.0%	Score	230.4	DB	9	Length	3879
Best Local	Similarity	99.9%	Pred.	No.	0			
Match	2553	Conservative	0	Mismatches	1	Indels	2	Gaps
QY	1	ATGAGAGGCGACGGGGGAGCCCATATGGGCTCTGGCTGTCTGCGCACCTTGACGCGGCG	60					
Db	49	ATGAGAGGCGACGGGGGAGCCCATATGGGCTCTGGGCGCTGTCTGCGCACCTTGACGCGGCG	108					
QY	61	GAGTTCAAGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTCGCGCAGATGTACAAGAGTGGCG	120					
Db	109	GAGTTCAAGGGCTGGGAGAAAGTGGGCTCGGGCGGCTTCGCGCAGATGTACAAGATGGCG	168					
QY	121	CATGTCCACTGAAAGACCTGGCTGGCCATCAAGTGTCTGCGCAGCTGCACGTGACGAC	180					
Db	169	CATGTCCACTGAAAGACCTGGCTGGCCATCAAGTGTCTGCGCAGCTGCACGTGACGAC	228					
QY	181	AGGAGGCGCATGAGAGCTTTTGGAGAAACCAGAAAGATGGAGATGGCCAAAGTTTGGCTAC	240					
Db	229	AGGAGGCGCATGAGAGCTTTTGGAGAAACCAGAAAGATGGAGATGGCCAAAGTTTGGCTAC	288					
QY	241	ATCCGACCTGTGTATGGCATCTGC CGCGAAACCTGT CGGCTGTGATGAGATACATGAG	300					
Db	289	ATCCGACCTGTGTATGGCATCTGC CGCGAAACCTGT CGGCTGTGATGAGATACATGAG	348					
QY	301	ACGGGCTCCCTGGAAAAGCTGTGGCTTCGAGACCATTTGCCATGGGATCTCCGGTTCCGA	360					
Db	349	ACGGGCTCCCTGGAAAAGCTGTGGCTTCGAGACCATTTGCCATGGGATCTCCGGTTCCGA	408					
QY	361	ATCATATCCAGAGACGGCGGTGGGATGTAACTTCCTCGCATGTGATGGCCCCGCGACCTCG	420					
Db	409	ATCATATCCAGAGACGGCGGTGGGATGTAACTTCCTCGCATGTGATGGCCCCGCGACCTCG	468					
QY	421	CACCTGAGACTTCAGACCGCGCAGACATCTCTGTGATGTGCCACTACACGTCACAAATTTCT	480					
Db	469	CACCTGAGACTTCAGACCGCGCAGACATCTCTGTGATGTGCCACTACACGTCACAAATTTCT	528					
QY	481	GATTTTGGTCTGGGCCAAGTGCACGGGCTGTCTCCACTGGCATGACTCAGCATTGAATGGC	540					
Db	529	GATTTTGGTCTGGGCCAAGTGCACGGGCTGTCTCCACTGGCATGACTCAGCATTGAATGGC	588					
QY	541	CTGTTTGGACAATCGCTACTCTCCCTCCAGAGGCATTCAGGGAGAAAGACGGGCTCTTC	600					
Db	589	CTGTTTGGACAATCGCTACTCTCCCTCCAGAGGCATTCAGGGAGAAAGACGGGCTCTTC	648					
QY	601	GACACCAAGACGATGTATACAGCTTTGGATGTCTATCTGGGGCGTGTCTCACACGAAG	660					
Db	649	GACACCAAGACGATGTATACAGCTTTGGATGTCTATCTGGGGCGTGTCTCACACGAAG	708					
QY	661	AAGCGTTTGCAGATGAGAAAGACATCTCGGCATCATGTGTAAAGGTGTGAAAGGCGCAC	720					

Db 709 AAGCCGTTTGAGATGAGAAAGATCTCTGCAATCATGTGAAAGTGTGAGAGGCGAC 768
 Qy 721 GCGCCGAGCTGCGCCCGGTGTGAGAGAGCCCGCGCGCGCTGTGAGCACTTGATAGC 780
 Db 769 GCGCCGAGCTGCGCCCGGTGTGAGAGAGCCCGCGCGCGCTGTGAGCACTTGATAGC 828
 Qy 781 CTGATGAGCGGTGTGAG 840
 Db 829 CTGATGAGCGGTGTGAG 888
 Qy 841 TCTGAAACGAGAGAGCTGTGTGAAAGAGCTGATGAGAGAGAGAGAGAGAGAGAGAG 900
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 Qy 901 CTGAG 960
 Db 949 CTGAG 1008
 Qy 961 GCGTGTGCGCCGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
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 Qy 1021 TCTGAGAGTTTCCAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 Db 1069 TCTGAGAGTTTCCAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
 Qy 1081 AAGCTGAG 1140
 Db 1129 AAGCTGAG 1188
 Qy 1141 TCTGAGAGTTTCCAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 Db 1189 TCTGAGAGTTTCCAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1248
 Qy 1201 GGTACCAAG 1259
 Db 1249 GGTACCAAG 1307
 Qy 1260 CAAG 1319
 Db 1308 CAAG 1367
 Qy 1320 CCGTGTGAG 1379
 Db 1368 CCGTGTGAG 1427
 Qy 1380 CAATGAG 1439
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 Qy 1440 GAG 1499
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 Qy 1500 GATGAG 1559
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 Qy 1560 AGGAG 1619
 Db 1608 AGGAG 1667
 Qy 1620 CATGAG 1679
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 Db 1728 CGTGAAG 1787
 Qy 1740 GGGAG 1799
 Db 1788 GGGAG 1847

Qy 1800 GAGCGTGAATGAG 1859
 Db 1848 GAGCGTGAATGAG 1907
 Qy 1860 CCGCATCTCATGAG 1919
 Db 1908 CCGCATCTCATGAG 1967
 Qy 1920 CTGAG 1979
 Db 1968 CTGAG 2027
 Qy 1980 GCGTGAAG 2039
 Db 2028 GCGTGAAG 2087
 Qy 2040 GCGAG 2099
 Db 2088 GCGAG 2147
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 Qy 2160 GGAAGTGTGAG 2219
 Db 2208 GGAAGTGTGAG 2267
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 Db 2268 CCGTGAAG 2327
 Qy 2280 CATGAG 2339
 Db 2328 CATGAG 2387
 Qy 2340 GCGAG 2355
 Db 2388 GCGAG 2403

RESULT 4
 BD157754
 LOCUS 3876 bp DNA linear PAT 17-JAN-2003
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION BD157754.1 GI:27863512
 VERSION BD157754.1 GI:27863512
 KEYWORDS JP 2002191363-A/12597.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3876)
 AUTHORS Ota,T., Isegai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE Primer for synthesizing full-length cDNA and use thereof
 JOURNAL Patent: JP 2002191363-A 12597 09-JUN-2002;
 HELIX RESEARCH INSTITUTE
 OS Homo sapiens (human)
 PN JP 2002191363-A/12597
 PD 09-JUN-2002
 PP 28-JUN-2000 JP 2000280990
 PI TOSHIO OTA,TAKAO ISEGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
 PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
 PI KEIICHI NAGAI,TETSUJI OTSUKI
 PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/00
 10. PC C12P21/02,C12Q1/68//C12P21/08,G06F1/30,C12N15/00,C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key
 Location/Qualifiers

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ORIGIN			
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Matches 2351; Conservative		0;	Mismatches 3; Indels 2; Gaps 2;
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Db	66	ATGAGGGCGAGAGGGGGAGCCCATGGGCGCTGGCGCATCTTGACGCGGGC	125
Qy	61	GAGTTCAGGGGCTGGGAGAGAGGTGGGCTTCGGGCGGCTTCGGGCAAGTGAAGTGGC	120
Db	126	GAGTTCAGGGGCTGGGAGAGAGGTGGGCTTCGGGCGGCTTCGGGCAAGTGAAGTGGC	185
Qy	121	CATGTCCAATGGAGAACTGGCTGGCCATCAAGTCTCTGCCCAAGCTTCAGACGAC	180
Db	186	CATGTCCAATGGAGAACTGGCTGGCCATCAAGTCTCTGCCCAAGCTTCAGACGAC	245
Qy	181	AGGAGCGCATGAGACTTTTGGAGAGAGCCAAAGATGAGATGAGCCAAAGTTTCCTAC	240
Db	246	AGGAGCGCATGAGACTTTTGGAGAGAGCCAAAGATGAGATGAGCCAAAGTTTCCTAC	305
Qy	241	ATCTGCGCTGTGTATGGCATCTGCCCGGAACCTGTGGGCTGTGATGAGATACATGAG	300
Db	306	ATCTGCGCTGTGTATGGCATCTGCCCGGAACCTGTGGGCTGTGATGAGATACATGAG	365
Qy	301	ACGGGCTCCCTGGAGAAAGCTGTGGCTTCGAGACCATGGGCAATGGGATCTCGGTTCCGA	360
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Qy	361	ATCATCCAGAGACGGCGGTGGGATGAATCTTCTGCACCTGATGAGCCCGCCTCTCTG	420
Db	426	ATCATCCAGAGACGGCGGTGGGATGAATCTTCTGCACCTGATGAGCCCGCCTCTCTG	485
Qy	421	CACCTGAGACTCAAGCCCGGGAACATCTGTGTGATGCCCACTACCAAGTATTTCT	480
Db	486	CACCTGAGACTCAAGCCCGGGAACATCTGTGTGATGCCCACTACCAAGTATTTCT	545
Qy	481	GATTTTGTGTCTGGCCAAATGTCACCGGGTGTCCCACTGGCATGACCTCAAGATGATGGC	540
Db	546	GATTTTGTGTCTGGCCAAATGTCACCGGGTGTCCCACTGGCATGACCTCAAGATGATGGC	605
Qy	541	CTGTTTGGCAAAATGCTTCTCTCCAGAGCGCATCAAGAGAGAGCGGCTTTC	600
Db	606	CTGTTTGGCAAAATGCTTCTCTCCAGAGCGCATCAAGAGAGAGCGGCTTTC	665
Qy	601	GACACCAAGCAGATGTATACAGCTTTTGCATCTGAGTCTGGGCGTGTCAACAGAG	660
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Db	786	CGCCCCGAGCTGCGCGGTGTGAGAGCCCGGCGCGGCTGTGACGCACTGATACGC	845
Qy	781	CTCATGACAGCGGTGTGTCAGAGGGGATCCGCGAGTTAGGCCCACTTTCAGAAATTAATCT	840
Db	846	CTCATGACAGCGGTGTGTCAGAGGGGATCCGCGAGTTAGGCCCACTTTCAGAAATTAATCT	905
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Db		1146	AAGCTGCATCTGTCCGAGCTGGAGAGAGGCTCTCGGAGGTGTCTTCGATGACCTCGGC	1205	
Qy		1141	TTCCTTCCAGAGATATCTGTGCTCTCTTTGAAGGGGAACTTCAACCAAGATCTG	1200	
Db		1206	TTCCTTCCAGAGATATCTGTGCTCTCTTTGAAGGGGAACTTCAACCAAGATCTG	1265	
Qy		1201	GGTACCAAGAGCGTCCAGAGAGAGCTTGTGATGGCATGTGTC-GGGACACAG	1259	
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Qy		1260	CAAACTGATGAAGATCTCTGAGCCGACAGACGTGACCTGACACGCGTGCAG	1319	
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Qy		1320	CTGTCTGCACTTGGCGGTGAGAGCGCGGCAAGAGAGTGGCCCAATGGCTGCTCAA	1379	
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Qy		1380	CAATGCCAACCCCAACCTGAGCAACGCTAGAGGGCTCCACCCTGTGACATGGCCGCGGA	1439	
Db		1445	CAATGCCAACCCCAACCTGAGCAACGCTAGAGGGCTCCACCCTGTGACATGGCCGCGGA	1504	
Qy		1440	GAGAGGGGTGCGGGGTGTCTGTGAGCTCTGTGCACTGGAGATCATGATCAAACGCAA	1499	
Db		1505	GAGAGGGGTGCGGGGTGTCTGTGAGCTCTGTGCACTGGAGATCATGATCAAACGCAA	1564	
Qy		1500	GGATGAGAGCAATGTCACAGCCCTTCCACTTTGACAGCCCAAGAGGAGTGAAGTTCAGAC	1559	
Db		1565	GGATGAGAGCAATGTCACAGCCCTTCCACTTTGACAGCCCAAGAGGAGTGAAGTTCAGAC	1624	
Qy		1560	ACGGCTGTGTGAGAGAAACGCTGTGATCAAGAGTGAAGCTTTGAGGGCGGAGCGC	1619	
Db		1625	ACGGCTGTGTGAGAGAAACGCTGTGATCAAGAGTGAAGCTTTGAGGGCGGAGCGC	1684	
Qy		1620	CATGCACTGAGCTGCCAGACCGGCGAGAGAAATATGTGCGCATCTGTGCGCCGAGG	1679	
Db		1685	CATGCACTGAGCTGCCAGACCGGCGAGAGAAATATGTGCGCATCTGTGCGCCGAGG	1744	
Qy		1680	CTGTGAGAGTGAAGCTTGCAGAGGCAAGATGCTGTGCTGCACTGACCTACCTGCTGGCA	1739	
Db		1745	CTGTGAGAGTGAAGCTTGCAGAGGCAAGATGCTGTGCTGCACTGACCTACCTGCTGGCA	1804	
Qy		1740	GGGCACTGCGCAATGTCAGAGCTGTGCAAGCAGCAGCGGGGTGAGTGTGAACGCGCA	1799	
Db		1805	GGGCACTGCGCAATGTCAGAGCTGTGCAAGCAGCAGCGGGGTGAGTGTGAACGCGCA	1864	
Qy		1800	GAGCCTGATGAGAGAGCGCATTTGCACTGTGCGCAACAGCGGCGCATCAACGCGTGGC	1859	
Db		1865	GAGCCTGATGAGAGAGCGCATTTGCACTGTGCGCAACAGCGGCGCATCAACGCGTGGC	1924	
Qy		1860	CCGATCTCATGACCTGTGTCTCCAGCTGCAAGTGTGACGCTGTGCGACAGACACC	1919	
Db		1925	CCGATCTCATGACCTGTGTCTCCAGCTGCAAGTGTGACGCTGTGCGACAGACACC	1984	
Qy		1920	CTGCAAGTGGCGCGGAGAGCGGGGCAAGAGCATGGCAAGGCTGTCTGAGATGGGG	1979	
Db		1985	CTGCAAGTGGCGCGGAGAGCGGGGCAAGAGCATGGCAAGGCTGTCTGAGATGGGG	2044	
Qy		1980	CGTGGCAAGAGGCTGTGACCTTCAAGCGCTACACCGCTCTGACCTGTGCGCGCAA	2039	

Db	2045	CGCTGGCAGGAGGCGCTGACCTCAGACGGGCTACACGGCTCTGCACCTGCTGCCCGCA	2104
Qy	2040	CGGACACCTGGCCCACTGTCAAGCTGCTTGTGCAAGAGAGAGCCGATGTGCTGGCCGGG	2099
Db	2105	CGGACACCTGGCCCACTGTCAAGCTGCTTGTGCAAGAGAGAGCCGATGTGCTGGCCGGG	2164
Qy	2100	ACCCCTGAACCAAGACGGCGCTGACACTTGGCTGCGCCCACTGCGACCTCGAGGTGTGGA	2159
Db	2165	ACCCCTGAACCAAGACGGCGCTGACACTTGGCTGCGCCCACTGCGACCTCGAGGTGTGGA	2224
Qy	2160	GGAGTGGATCGACGCCCGGATGTCACTTGAACCTGTGACAGAGAGGGGCTCAGCGGCTGCA	2219
Db	2225	GGAGTGGATCGACGCCCGGATGTCACTTGAACCTGTGACAGAGAGGGGCTCAGCGGCTGCA	2284
Qy	2220	CCTGGCCGCCCAAGGGCCGGCAAGCAGACGGTGGAGACTGTCTCAGGCAATGGGGCCCA	2279
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Qy	2280	CATCAACCTGCAAGACCTCTCAAGTTCAGAGGCGGGCCATATGGCCCCCGCCCAACTTCCTGG	2339
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REFERENCE	1	Ota,T., Iwoga,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Iishi,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsubu,T.	
AUTHORS		Primers for synthesising full-length cDNA and their use	
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 ORGANISM
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 REFERENCE
 AUTHORS
 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, M., Nishi, T., Shibahara, T., Tanaka, H., Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, H., Iehi, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikawa, E., Omura, Y., Abe, K., Kamihara, K., Katsura, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimura, M., Matsumura, M., Hiraoaka, S., Chiba, Y., Iehida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoshida, M., Hoshino, T., Kusan, J., Kaneshiro, K., Takahashi, Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togaya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Mutsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohara, N., Sano, S., Moriya, S., Momiya, H., Sato, H., Mizoguchi, H., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Omori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsunaga, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Sato, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuo, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isegaki, T. and Sugano, S.
 Complete sequencing and characterization of 21,243 full-length human cDNAs
 Nat. Genet. 36 (1), 40-45 (2004)
 JOURNAL
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 REFERENCE
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 Isegaki, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Iehida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Iehi, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuo, Y., Ninomiya, K. and Iwayanagi, T.
 NEO human cDNA sequencing project
 Unpublished
 3 (bases 1 to 3876)

AUTHORS Isogai, T. and Otsuki, T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@helix.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

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Location/Qualifiers

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CDS**ORIGIN**

Query Match 98.8%; Score 2337.2; DB 9; Length 3876;
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RESULT 7
AB047783 3882 bp mRNA linear PRI 30-MAY-2001
LOCUS Homo sapiens ANKRD3 mRNA for dual-specificity Ser/Thr/Tyr kinase,
DEFINITION complete cds.
ACCESSION AB047783
VERSION AB047783.1 GI:14245728
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Shimizu,N., Kudoh,J. and Shibuya,K.
TITLE Homo sapiens mRNA for ANKRD3, complete cds
JOURNAL Published Only in Database (2001)
REFERENCE
AUTHORS Shimizu,N., Kudoh,J. and Shibuya,K.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-2000) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8582, Japan (E-mail: nshimizu@med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)

FEATURES
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ORIGIN
Query Match 98.8%; Score 2327.2; DB 9; Length 3882;
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Matches 2351; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
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DEFINITION IMAGE:5760485), partial cds.
ACCESSION BC035755
VERSION BC035755.1 GI:23242902
KEYWORDS
SOURCE Homo sapiens (human)

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1 (bases 1 to 3867)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Yoshiyuki, S., Abramson, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Cay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Heltin, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Kizylinski, M.I., Skalska, U., Smolins, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A. full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
1247932
JOURNAL 2 (bases 1 to 3867)
PUBMED Strausberg, R.
REFERENCE Direct Submission
AUTHORS Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
TITLE NIH-MGC Project URL: <http://mgc.nci.nih.gov>
CONTACT: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNU)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@bglr.nih.gov
Ahter, N., Ayale, K., Beckert, S., Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Grant, S., Guan, X., Gupta, P., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Manduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McQuell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W., Tsurgen, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, J., H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNU, at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10190675.
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Df	2282	CATCAACTGTGAGAGCCCTCAAGTTCCAGGGGGGCGCATAGGCCCGGCGCAACTCTGCG	2341
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Df	2342	GCGAAGCAAGACTTAG 2357	
RESULT 9			
LOCUS	COJ31804	2499 bp DNA	linear PAT 03-FEB-2004
DEFINITION	Sequence 17738 from Patent WO02068579.		
ACCESSION	COJ31804		
VERSION	COJ31804.1 GI:42309361		
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1	Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W. Kites, such as nucleic acid arrays, comprising a majority of humanecons or transcripts, for detecting expression and other uses thereof	
AUTHORS			
TITLE			
JOURNAL	Patent: WO 02068579-A, 17738 06-SEP-2002;		
FEATURES	Location/Qualifiers		
source	1..2499 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		
ORIGIN			
Query Match	92.3%; Score 2173.2; DB 6; Length 2499;		
Best Local Similarity	94.0%; Pred.No. 0;		
Matches 2351; Conservative	0; Mismatches 3; Indels 146; Gaps 3,		
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Df	1	ATGAGAGGCGCACGCGCGGAGCCCATCTGGGCGCTGGCGCTGCGCGCACCTTTGAGACGGCGC	60
OY	61	GAGTTCA CGGGCTGGGAGAAAGGTGGGCTCGGGCGGCTTT CGGGCAAGTGTACAAGGTGGC	120
Df	61	GAGTTCA CGGGCTGGGAGAAAGGTGGGCTCGGGCGGCTTT CGGGCAAGTGTACAAGGTGGC	120
OY	121	CATGTCCA CTGAGAAAGCTTGGCTGGCCATCAAGTCTTGCC CAGCTTGACGTGACGAC	180
Df	121	CATGTCCA CTGAGAAAGCTTGGCTGGCCATCAAGTCTTGCC CAGCTTGACGTGACGAC	180
OY	181	AGGAGAGCGCATGAGACTTTTGGAGAGAACCAAGAGAGATGGAGATGGCCAAAGTTTCGTAC	240
Df	181	AGGAGAGCGCATGAGACTTTTGGAGAGAACCAAGAGAGATGGAGATGGCCAAAGTTTCGTAC	240
OY	241	ATCCGCGCTGTGTATGATGCGATCTGGCGCGGACCTGTGCGGCTCATGAGATGATGAG	300
Df	241	ATCCGCGCTGTGTATGATGCGATCTGGCGCGGACCTGTGCGGCTCATGAGATGATGAG	300
OY	301	ACGGGCTCCCTGAAAAGCTGCTTGAGAGCCATTGGCAATGGATCTTCGGTTCGA	360
Df	301	ACGGGCTCCCTGAAAAGCTGCTTGAGAGCCATTGGCAATGGATCTTCGGTTCGA	360
OY	361	ATCATTCACAGACGGCGGTGGCATGAATTCTTCGCA CTCAGATGGCCCGGCACTCGTG	420
Df	361	ATCATTCACAGACGGCGGTGGCATGAATTCTTCGCA CTCAGATGGCCCGGCACTCTG	420

QY 421 CACCTGACCTCAAGCCCGGAGACATCTGTGATGCGCCATCAAGCTCAAGATTCT 480
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DB 1236 CTTGCACTGACAG 1355
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DB 1440 CTTGCACTGACAG 1499
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RESULT 10
AX16548
LOCUS AX16548 2499 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 39 from Patent WO0138503.
ACCESSION AX16548

VERSION AX166548.1 GI:14546893
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R., Planagan, P., and Clary, D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNML Patent: WO 0138503-A 39 31-MAY-2001;
Sugen, Inc. (US)
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 92.3%; Score 2173.2; DB 6; Length 2499;
Best Local Similarity 94.0%; Pred. No. 0;
Matches 2251; Conservative 0; Mismatches 3; Indels 146; Gaps 3;
QY 1 ATGAGGGCGACGGGGGACCCCATGGGCGCTGGCGCTGGCGACCTTGACGGGGG 60
Db 1 ATGAGGGCGACGGGGGACCCCATGGGCGCTGGCGCTGGCGACCTTGACGGGGG 60
QY 61 GAGTTCA CGGCGCTGGGAGAGAGTGGGCTCGGCGGCTTCGGGCAAGGTGCGC 120
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AF302127 3559 bp mRNA linear ROD 08-JAN-2002
LOCUS AF302127
DEFINITION Mus musculus PKC-regulated kinase PKK mRNA, complete cds.
ACCESSION AF302127.3 GI:18087895
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3559)
Chen, L., Haider, K., Ponda, M., Cariappa, A., Rowitch, D. and Pillai, S.
Protein kinase C-associated kinase (PKK), a novel
membrane-associated, ankyrin repeat-containing protein kinase
J. Biol. Chem. 276 (24), 21737-21744 (2001)
JOURNAL
MEDLINE
PUBMED
11278362
2 (bases 1 to 3559)
Chen, L., Haider, K., Cariappa, A. and Pillai, S.
Direct Submission
JOURNAL
Submitted (01-SEP-2000) Cancer Center, Massachusetts General
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
3 (bases 1 to 3559)
Chen, L., Haider, K., Cariappa, A. and Pillai, S.
Direct Submission
JOURNAL
Submitted (07-JAN-2002) Cancer Center, Massachusetts General

REMARK
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE
CDS
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
Sequence update by submitter
4 (bases 1 to 3559)
Chen, L., Haider, K., Cariappa, A. and Pillai, S.
Direct Submission
Submitted (08-JAN-2002) Cancer Center, Massachusetts General
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
Nucleotide sequence update by submitter
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ORIGIN
Query Match 74.2%; Score 1748; DB 10; Length 3559;
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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MUS MUSCULUS (house mouse)
REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT
OS Mus musculus (mouse)
PN JP 2002526038-A/1
PD 20-AUG-2002
PF 04-AUG-1998 JP 2000563800
PR 04-AUG-1998 US 60/095269, 11-SEP-1998 US 60/099973 PR
09-FEB-1999 US 60/119353
PI TIMOTHY A BIRD, DUKE G VIRCA
PC C12N15/09, A61K45/00, A61P29/00, A61P37/02, A61P43/00, A61P43/00,
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PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/12, C12Q1/48, G06F17/
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DEFINITION Sequence 1 from patent US 6489130.
ACCESSION AR258256
VERSION AR258256.1 GI:27308494
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 2370)
AUTHORS Bird,T.A. and Virca,G.D.
TITLE Death associated kinase containing ankyrin repeats (DAKAR)
JOURNAL Patent: US 6489130-A 1 03-DEC-2002;
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Query Match 74.1%; Score 1745.4; DB 6; Length 2370;
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Db 131 ATGTGACATGGAAGACGTGGCTGCGCAATCAAGTGTCTGCGCCAGGCTGCACTGACGACA 190
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Db	1930	ACAACCTCTGCACATGTTGCTGCAGAGACTGTGAACAACATAGTACTGCCAGGCTACTCTTGAT	1989
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ACCESSION	BD209707	Compositions isolated from skin cells and methods for their use.			
VERSION	BD209707.1	GI:33019477			
KEYWORDS	JP 2002512798-A/179.				
SOURCE	Mus sp.				
ORGANISM	Mus sp.				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Scleromorphi; Muridae; Murinae; Mus.				

REFERENCE	TITLE	JOURNAL	COMMENT
1 (bases 1 to 3516) Strachan, I., Sleeman, M., Watson, J.D., Onrust, R., Kumble, A. and Muirson, J.G.	Compositions isolated from skin cells and methods for their use	Patent: JP 2002512798-A 179 08-MAY-2002;	
	GENESIS RESEARCH AND DEVELOPMENT CORP LTD	Mus sp. (mouse)	

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PN JP 2002512798-A/179
PD 08-MAY-2002
PF 29-APR-1999 JP 2000546009
PR 29-APR-1998 US 09/065726, 09-NOV-1998 US 09/188930
LOENA STRACHMAN, MATTHEW SLEEMAN, JAMES DOUGLAS WATSON, RENNE PI
ONRUST.
PC ANAND KIMBLE, JAMES GREG MURRISON
PI C12N15/09, A6IK38/00, A6I29/00, A6I17/00, A6I29/00, A6I31/18, PC
A6I35/00,
PC C07K14/47, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12N15/
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CC Compositions isolated from skin cells and methods for their
CC use.
FH key Location/Qualifiers
FH source 1..3516
FH 1..3516 /organism='Mus sp. (mouse)'.
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source Location/Qualifiers
1..3516

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ORIGIN

Query Match	74.18; Score 1745.4; DB 6; Length 3516;
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14	3616	88.7	786	14	US-10-128-174-33	Sequence 33, Appl
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17	1967	48.2	439	14	US-10-128-174-28	Sequence 28, Appl
18	1804	44.2	335	16	US-10-664-421-140	Sequence 140, Appl
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21	1457	35.7	286	14	US-10-128-174-27	Sequence 27, Appl
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27	1207.5	29.6	765	14	US-10-128-174-42	Sequence 39, Appl
28	1207.5	29.6	765	14	US-10-128-174-39	Sequence 42, Appl
29	1205.5	29.6	765	14	US-10-128-174-35	Sequence 35, Appl
30	1205.5	29.6	765	14	US-10-128-174-36	Sequence 36, Appl
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33	1200.5	29.4	765	14	US-10-128-174-34	Sequence 34, Appl
34	1198.5	29.4	765	14	US-10-128-174-41	Sequence 41, Appl
35	1196.5	29.3	752	14	US-10-146-473-59	Sequence 59, Appl
36	838	20.5	720	15	US-10-433-794-20	Sequence 20, Appl
37	663	16.3	132	15	US-10-276-774-1509	Sequence 1509, Appl
38	541.5	13.3	540	9	US-09-748-537-1	Sequence 1, Appl1
39	541.5	13.3	540	9	US-09-728-721-2	Sequence 2, Appl1
40	541.5	13.3	540	9	US-09-771-161A-184	Sequence 184, Appl
41	541.5	13.3	540	9	US-09-862-027-78	Sequence 28, Appl1
42	541.5	13.3	540	10	US-09-981-397A-14	Sequence 14, Appl1
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45	541.5	13.3	540	13	US-10-118-984-2	Sequence 2, Appl1

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US-10-658-904-2
Sequence 2, Application US/10658904
Publication No. US20040048305A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 14171 Protein Kinase, A No. US20040048305A1 Human
TITLE OF INVENTION: Protein Kinase and Uses Thereof
FILE REFERENCE: MP100-010P1RC1M
CURRENT APPLICATION NUMBER: US/10/658,904
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 09/781,882
PRIOR FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/182,096
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 784
TYPE: PRT
ORGANISM: H. sapiens
US-10-658-904-2

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[illegible]

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Db 61 RERMELEBEAKKMEMAKFRYILPVYGI CREBPVGLVMEYMETGSELEKLLASPLPMDLFR 120
Qy 121 IIHETAVGMNPLHCAAPPLHLDLKRPANILLDAHRYKISDFGLAKCNGLSHSHDLSMDG 180
Db 121 IIHETAVGMNPLHCAAPPLHLDLKRPANILLDAHRYKISDFGLAKCNGLSHSHDLSMDG 180
Qy 181 LFGTIAYLPERRIREKSRLEPDKHDVYSFAIYIWGVLTOKKPFADEKNILHIMVKVYKGH 240
Db 181 LFGTIAYLPERRIREKSRLEPDKHDVYSFAIYIWGVLTOKKPFADEKNILHIMVKVYKGH 240
Qy 241 RPELPVCRARPRACSHLIRLMORCMQGDPRVRPTFOBITSETBDLCEKPDDEVKETAHD 300
Db 241 RPELPVCRARPRACSHLIRLMORCMQGDPRVRPTFOBITSETBDLCEKPDDEVKETAHD 300
Qy 301 LDVSPPEPRSEVPARLKASAPTFDNDYSLSELSQLDSGVSAQVAGPEBELSRSSSES 360
Db 301 LDVSPPEPRSEVPARLKASAPTFDNDYSLSELSQLDSGVSAQVAGPEBELSRSSSES 360
Qy 361 KLPSGSGKRLSGVSVDSAFSSRSGSLSPFEREPSTDLGTTTRPEEBAQCHRVADTS 420
Db 361 KLPSGSGKRLSGVSVDSAFSSRSGSLSPFEREPSTDLGTTTRPEEBAQCHRVADTS 420
Qy 421 KLMTKLQPOVDYDALDSGASILHLAVEAGQECCKMILLNNANPNLSNRGSTPLHMAVE 480
Db 421 KLMTKLQPOVDYDALDSGASILHLAVEAGQECCKMILLNNANPNLSNRGSTPLHMAVE 480
Qy 481 RRVGVVELLARKISVNAKDQDWTALHPAQNQDDESSTRLLEKNASVNEVDPEGRTP 540
Db 481 RRVGVVELLARKISVNAKDQDWTALHPAQNQDDESSTRLLEKNASVNEVDPEGRTP 540
Qy 541 MHVACQHOENIVRILLRGDVSLQGDQAWMLPLHYAAMOGHLPIVKLLAKOPGVSVNAQ 600
Db 541 MHVACQHOENIVRILLRGDVSLQGDQAWMLPLHYAAMOGHLPIVKLLAKOPGVSVNAQ 600
Qy 601 TLDEGTPLHLAAQRGHYVARILLIDCSDVNVCISLAQTPPLHVAETGHTSTARILLRG 660
Db 601 TLDEGTPLHLAAQRGHYVARILLIDCSDVNVCISLAQTPPLHVAETGHTSTARILLRG 660
Qy 661 AGKEAVTSDGYTALHLAARNGHILAVKLYVEKQDVNARGPLNOYALHLAAHGSVEVE 720
Db 661 AGKEAVTSDGYTALHLAARNGHILAVKLYVEKQDVNARGPLNOYALHLAAHGSVEVE 720
Qy 721 ELVSAVDYDLFDEQGLSALHLAAQGRHAQVETTLRHGAHINLOSLKFGQGHGPAATLLR 780
Db 721 ELVSAVDYDLFDEQGLSALHLAAQGRHAQVETTLRHGAHINLOSLKFGQGHGPAATLLR 780
Qy 781 RSKT 784
Db 781 RSKT 784

RESULT 2
US-10-354-358-38
; Sequence 38, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Leeson, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4463,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MP102-020P1RMONMIM
```

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; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-358-38

Query Match 97.6%; Score 3980; DB 14; Length 784;
Best Local Similarity 98.2%; Pred. No. 2.7e-273;
Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MEGDGTPLMALALRTEDAGEFTGMEKVGSGFGQYKVRHVHKTWLAIKCSPSLHVD 60
Db 1 MEGDGTPLMALALRTEDAGEFTGMEKVGSGFGQYKVRHVHKTWLAIKCSPSLHVD 60
Qy 61 RERMELEBEAKKMEMAKFRYILPVYGI CREBPVGLVMEYMETGSELEKLLASPLPMDLFR 120
Db 61 RERMELEBEAKKMEMAKFRYILPVYGI CREBPVGLVMEYMETGSELEKLLASPLPMDLFR 120
Qy 121 IIHETAVGMNPLHCAAPPLHLDLKRPANILLDAHRYKISDFGLAKCNGLSHSHDLSMDG 180
Db 121 IIHETAVGMNPLHCAAPPLHLDLKRPANILLDAHRYKISDFGLAKCNGLSHSHDLSMDG 180
Qy 181 LFGTIAYLPERRIREKSRLEPDKHDVYSFAIYIWGVLTOKKPFADEKNILHIMVKVYKGH 240
Db 181 LFGTIAYLPERRIREKSRLEPDKHDVYSFAIYIWGVLTOKKPFADEKNILHIMVKVYKGH 240
Qy 241 RPELPVCRARPRACSHLIRLMORCMQGDPRVRPTFOBITSETBDLCEKPDDEVKETAHD 300
Db 241 RPELPVCRARPRACSHLIRLMORCMQGDPRVRPTFOBITSETBDLCEKPDDEVKETAHD 300
Qy 301 LDVSPPEPRSEVPARLKASAPTFDNDYSLSELSQLDSGVSAQVAGPEBELSRSSSES 360
Db 301 LDVSPPEPRSEVPARLKASAPTFDNDYSLSELSQLDSGVSAQVAGPEBELSRSSSES 360
Qy 361 KLPSGSGKRLSGVSVDSAFSSRSGSLSPFEREPSTDLGTTTRPEEBAQCHRVADTS 420
Db 361 KLPSGSGKRLSGVSVDSAFSSRSGSLSPFEREPSTDLGTTTRPEEBAQCHRVADTS 420
Qy 421 KLMTKLQPOVDYDALDSGASILHLAVEAGQECCKMILLNNANPNLSNRGSTPLHMAVE 480
Db 421 KLMTKLQPOVDYDALDSGASILHLAVEAGQECCKMILLNNANPNLSNRGSTPLHMAVE 480
Qy 481 RRVGVVELLARKISVNAKDQDWTALHPAQNQDDESSTRLLEKNASVNEVDPEGRTP 540
Db 481 RRVGVVELLARKISVNAKDQDWTALHPAQNQDDESSTRLLEKNASVNEVDPEGRTP 540
Qy 541 MHVACQHOENIVRILLRGDVSLQGDQAWMLPLHYAAMOGHLPIVKLLAKOPGVSVNAQ 600
Db 541 MHVACQHOENIVRILLRGDVSLQGDQAWMLPLHYAAMOGHLPIVKLLAKOPGVSVNAQ 600
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Db      541  MVAACOHGQENIVRIILRRGVDSLOGKDAMIPLHYAAMQGHLPVYKLAKOPGVSVNAQ 600
Qy      601  TLDRTPHLHAAQRGHYRVARILIDLCSDVNVCSLLAQTPHLVAEFGHTSTARLLHRG 660
Db      601  TLDRTPHLHAAQRGHYRVARILIDLCSDVNVCSLLAQTPHLVAEFGHTSTARLLHRG 660
Qy      661  AKGKAVTSNGYTAHLHAARNGHATYKLVVEEKADYLANGPILNORLHMAAHGSEVVE 720
Db      661  AKGKAVTSNGYTAHLHAARNGHATYKLVVEEKADYLANGPILNORLHMAAHGSEVVE 720
Qy      721  ELVSADVIDLPEQGLSALHLAAQGRHAQTVETLLRHGAHINLOSLKFGGHPAATLLR 780
Db      721  ELVSADVIDLPEQGLSALHLAAQGRHAQTVETLLRHGAHINLOSLKFGGHPAATLLR 780
Qy      781  RSKT 784
Db      781  RSKT 784

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RESULT 3
US-10-128-174-12
; Sequence 12, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohito
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; PRIORITY FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-174-12

```

```

Query Match      97.6%; Score 3980; DB 14; Length 784;
Best Local Similarity 98.2%; Pred. No. 2.7e-273;
Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy      1  MEGDGTFWALALRTFDAGFTGMEKVGSGFGQYKVRVHMKWTMLAIKCSPLHYDD 60
Db      1  MEGDGTFWALALRTFDAGFTGMEKVGSGFGQYKVRVHMKWTMLAIKCSPLHYDD 60
Qy      61  RERMELEBAKKEAKKEMAKFRYILPVYIGICREPVGLVMEYMETGSLKLLASBPPLMDLRF 120
Db      61  RERMELEBAKKEAKKEMAKFRYILPVYIGICREPVGLVMEYMETGSLKLLASBPPLMDLRF 120
Qy      121  IIHETAVGNMFLHCMAPELHLDLKPANILLDAHVHKISDFGLAKCNGLSHSHDLSMDG 180
Db      121  IIHETAVGNMFLHCMAPELHLDLKPANILLDAHVHKISDFGLAKCNGLSHSHDLSMDG 180
Qy      181  LFGTIAIYLPERRIRBKSLPFTKHDVYSFAIVIGVLTOKKPPADBNKIILHIMVKVVG 240
Db      181  LFGTIAIYLPERRIRBKSLPFTKHDVYSFAIVIGVLTOKKPPADBNKIILHIMVKVVG 240
Qy      241  RPELPVPCARAPRACSHLIRLMQRCWQODPRVPRPTFOEITSETEDLCEKPDDEVKETAHD 300
Db      241  RPELPVPCARAPRACSHLIRLMQRCWQODPRVPRPTFOEITSETEDLCEKPDDEVKETAHD 300
Qy      301  LDVKSPPRSESEVVPARLKRASAPTFDNDYSLSELLISQLDGVSQAVEGPEELSRSSSS 360
Db      301  LDVKSPPRSESEVVPARLKRASAPTFDNDYSLSELLISQLDGVSQAVEGPEELSRSSSS 360
Qy      361  KLPSSSSGKRLSEVSVSDAFSGRGLSLSFEREPESTDLGTRRREBEACGHRARDTS 420
Db      361  KLPSSSSGKRLSEVSVSDAFSGRGLSLSFEREPESTDLGTRRREBEACGHRARDTS 420
Qy      421  KLMKTIQPODVDAIALSGASILHLIAVEAGQEECAKMLLNANPNLSNRGSGTPLLMAVE 480
Db      421  KLMKTIQPODVDAIALSGASILHLIAVEAGQEECAKMLLNANPNLSNRGSGTPLLMAVE 480

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Qy      481  RRVGVVBEILLARKISYNANDEDDWTALHRAQNGDESSRLLLEKNASVNEVDFEGRT 540
Db      481  RRVGVVBEILLARKISYNANDEDDWTALHRAQNGDESSRLLLEKNASVNEVDFEGRT 540
Qy      541  MVAACOHGQENIVRIILRRGVDSLOGKDAMIPLHYAAMQGHLPVYKLAKOPGVSVNAQ 600
Db      541  MVAACOHGQENIVRIILRRGVDSLOGKDAMIPLHYAAMQGHLPVYKLAKOPGVSVNAQ 600
Qy      601  TLDRTPHLHAAQRGHYRVARILIDLCSDVNVCSLLAQTPHLVAEFGHTSTARLLHRG 660
Db      601  TLDRTPHLHAAQRGHYRVARILIDLCSDVNVCSLLAQTPHLVAEFGHTSTARLLHRG 660
Qy      661  AKGKAVTSNGYTAHLHAARNGHATYKLVVEEKADYLANGPILNORLHMAAHGSEVVE 720
Db      661  AKGKAVTSNGYTAHLHAARNGHATYKLVVEEKADYLANGPILNORLHMAAHGSEVVE 720
Qy      721  ELVSADVIDLPEQGLSALHLAAQGRHAQTVETLLRHGAHINLOSLKFGGHPAATLLR 780
Db      721  ELVSADVIDLPEQGLSALHLAAQGRHAQTVETLLRHGAHINLOSLKFGGHPAATLLR 780
Qy      781  RSKT 784
Db      781  RSKT 784

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RESULT 4
US-10-164-080-7
; Sequence 7, Application US/10164080
; Publication No. US20030087411A1
; GENERAL INFORMATION:
; APPLICANT: BIRD, Timothy, A.
; APPLICANT: HOLLAND, Pamela, M.
; APPLICANT: PESCHON, Jacques, J.
; APPLICANT: VIRCA, George, D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR) AND ME
; FILE REFERENCE: 3280-B
; CURRENT APPLICATION NUMBER: US/10/164,080
; PRIORITY FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/295,959
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/334,362
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-080-7

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```

Query Match      97.5%; Score 3977; DB 14; Length 784;
Best Local Similarity 98.1%; Pred. No. 4.4e-273;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy      1  MEGDGTFWALALRTFDAGFTGMEKVGSGFGQYKVRVHMKWTMLAIKCSPLHYDD 60
Db      1  MEGDGTFWALALRTFDAGFTGMEKVGSGFGQYKVRVHMKWTMLAIKCSPLHYDD 60
Qy      61  RERMELEBAKKEAKKEMAKFRYILPVYIGICREPVGLVMEYMETGSLKLLASBPPLMDLRF 120
Db      61  RERMELEBAKKEAKKEMAKFRYILPVYIGICREPVGLVMEYMETGSLKLLASBPPLMDLRF 120
Qy      121  IIHETAVGNMFLHCMAPELHLDLKPANILLDAHVHKISDFGLAKCNGLSHSHDLSMDG 180
Db      121  IIHETAVGNMFLHCMAPELHLDLKPANILLDAHVHKISDFGLAKCNGLSHSHDLSMDG 180
Qy      181  LFGTIAIYLPERRIRBKSLPFTKHDVYSFAIVIGVLTOKKPPADBNKIILHIMVKVVG 240
Db      181  LFGTIAIYLPERRIRBKSLPFTKHDVYSFAIVIGVLTOKKPPADBNKIILHIMVKVVG 240
Qy      241  RPELPVPCARAPRACSHLIRLMQRCWQODPRVPRPTFOEITSETEDLCEKPDDEVKETAHD 300

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Db 241 RPELPVCRARPRACSHLIRLMORCMQCDPRVRPTFOGTTSETBDCRKPDEYKETHND 300
Qy 301 LDVSPPEPSEVVPARLKASAPTFDNDYSLSELSQLDSGVSAQVGPBELSRSSSES 360
Db 301 LDVSPPEPSEVVPARLKASAPTFDNDYSLSELSQLDSGVSAQVGPBELSRSSSES 360
Qy 361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSPERBSTSDIGTTRPEEACGCHRVRTS 420
Db 361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSPERBSTSDIGTTRPEEACGCHRVRTS 420
Qy 421 KLMTKLOPOVDYLDLDSGASLHLAVEAGOEBCAKMLLNNANPNLSNRGSTPLHMAVE 480
Db 421 KLMTKLOPOVDYLDLDSGASLHLAVEAGOEBCAKMLLNNANPNLSNRGSTPLHMAVE 480
Qy 481 RRVGAVVELLARKISVNAKDEQWTAHFPAQNGDESTRLLLEKNASVNEVDFEGRT 540
Db 481 RRVGAVVELLARKISVNAKDEQWTAHFPAQNGDESTRLLLEKNASVNEVDFEGRT 540
Qy 541 MHVACQHGQENIVRLIRGVDVSLQGDAMLPLHYAMOGHLPVTKLAKOPGVSVNAQ 600
Db 541 MHVACQHGQENIVRLIRGVDVSLQGDAMLPLHYAMOGHLPVTKLAKOPGVSVNAQ 600
Qy 601 TLDSRTPLHLAAQRGHYVARILIDCSDVNVCSLLAQTPHVAETGHTSTARLLHRG 660
Db 601 TLDSRTPLHLAAQRGHYVARILIDCSDVNVCSLLAQTPHVAETGHTSTARLLHRG 660
Qy 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEEKADVLRGPINQTAHLAAAHGSEVVE 720
Db 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEEKADVLRGPINQTAHLAAAHGSEVVE 720
Qy 721 ELVSADVLDLFDQGLSALHLAAQGRHAQVETTLRRGHAINLQSLKFQGGHGAATLLR 780
Db 721 ELVSADVLDLFDQGLSALHLAAQGRHAQVETTLRRGHAINLQSLKFQGGHGAATLLR 780
Qy 781 RSKT 784
Db 781 RSKT 784
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RESULT 5

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US-10-258-951-70
; Sequence 70, Application US/10258951
; Publication No. US20040033504A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kahnlick, Karen
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Xie, Qing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50025
; CURRENT APPLICATION NUMBER: US/10/258,951
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/13360
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/199,963
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/203,336
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/207,087
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,546
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-258-951-70

Query Match 97.5%; Score 3977; DB 15; Length 784;
Beet Local Similarity 96.1%; Pred. No. 4,4e-273;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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Qy 1 MEGDGTTPMALALRTFDAGEFTGMEKVGSGFGQVYKVRHVWKTALAKCSPSLHVD 60
Db 1 MEGDGTTPMALALRTFDAGEFTGMEKVGSGFGQVYKVRHVWKTALAKCSPSLHVD 60
Qy 61 RERMELLEBAKMKEMAFRYILPYGICREBPVGLVMEYMETGSLLEKLAEEPLPMDLRF 120
Db 61 RERMELLEBAKMKEMAFRYILPYGICREBPVGLVMEYMETGSLLEKLAEEPLPMDLRF 120
Qy 121 ITHETAQNPLOHMAEPLHLDLKPNITLLDAHYHKISDFGLAKNGLSHSHDLSMDG 180
Db 121 ITHETAQNPLOHMAEPLHLDLKPNITLLDAHYHKISDFGLAKNGLSHSHDLSMDG 180
Qy 181 LFGTIAVLPERRIREKSLPDTKADVSPFAIVIWGLTQKKPFADEKNILHIMVKVYKG 240
Db 181 LFGTIAVLPERRIREKSLPDTKADVSPFAIVIWGLTQKKPFADEKNILHIMVKVYKG 240
Qy 241 RPELPVCRARPRACSHLIRLMORCMQCDPRVRPTFOGTTSETBDCRKPDEYKETHND 300
Db 241 RPELPVCRARPRACSHLIRLMORCMQCDPRVRPTFOGTTSETBDCRKPDEYKETHND 300
Qy 301 LDVSPPEPSEVVPARLKASAPTFDNDYSLSELSQLDSGVSAQVGPBELSRSSSES 360
Db 301 LDVSPPEPSEVVPARLKASAPTFDNDYSLSELSQLDSGVSAQVGPBELSRSSSES 360
Qy 361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSPERBSTSDIGTTRPEEACGCHRVRTS 420
Db 361 KLPSGSGKRLSGVSVDSAFSSRGSLSLSPERBSTSDIGTTRPEEACGCHRVRTS 420
Qy 421 KLMTKLOPOVDYLDLDSGASLHLAVEAGOEBCAKMLLNNANPNLSNRGSTPLHMAVE 480
Db 421 KLMTKLOPOVDYLDLDSGASLHLAVEAGOEBCAKMLLNNANPNLSNRGSTPLHMAVE 480
Qy 481 RRVGAVVELLARKISVNAKDEQWTAHFPAQNGDESTRLLLEKNASVNEVDFEGRT 540
Db 481 RRVGAVVELLARKISVNAKDEQWTAHFPAQNGDESTRLLLEKNASVNEVDFEGRT 540
Qy 541 MHVACQHGQENIVRLIRGVDVSLQGDAMLPLHYAMOGHLPVTKLAKOPGVSVNAQ 600
Db 541 MHVACQHGQENIVRLIRGVDVSLQGDAMLPLHYAMOGHLPVTKLAKOPGVSVNAQ 600
Qy 601 TLDSRTPLHLAAQRGHYVARILIDCSDVNVCSLLAQTPHVAETGHTSTARLLHRG 660
Db 601 TLDSRTPLHLAAQRGHYVARILIDCSDVNVCSLLAQTPHVAETGHTSTARLLHRG 660
Qy 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEEKADVLRGPINQTAHLAAAHGSEVVE 720
Db 661 AGKEAVTSDGYTALHLAARNGHLATVKLVEEKADVLRGPINQTAHLAAAHGSEVVE 720
Qy 721 ELVSADVLDLFDQGLSALHLAAQGRHAQVETTLRRGHAINLQSLKFQGGHGAATLLR 780
Db 721 ELVSADVLDLFDQGLSALHLAAQGRHAQVETTLRRGHAINLQSLKFQGGHGAATLLR 780
Qy 781 RSKT 784
Db 781 RSKT 784
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RESULT 6

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US-10-923-035-56
; Sequence 56, Application US/10923035
; Publication No. US20050130189A1
; GENERAL INFORMATION:
; APPLICANT: Paricha, Pankaj
; APPLICANT: Shenoy, Mohan
; APPLICANT: Winston, John
; TITLE OF INVENTION: Compositions and Methods for Treating and Diagnosing
; Iritable Bowel Syndrome
```

```

; FILE REFERENCE: 9511-136-27
; CURRENT APPLICATION NUMBER: US/10/923,035
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US 60/496,716
; PRIOR FILING DATE: 2003-08-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 56
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-035-56

Query Match          97.5%; Score 3977; DB 18; Length 784;
Best Local Similarity 98.1%; Pred. No. 4,4e-273;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEGDGTFWALALRTFDAGFTGMEKVGSGFGQVYKRVHVKMTWLAICSPSLHYDD 60
DB 1 MEGDGTFWALALRTFDAGFTGMEKVGSGFGQVYKRVHVKMTWLAICSPSLHYDD 60
QY 61 RRMELLEBAKMKEMAKRYIIPVYIGICREPVGLVMEYMETGSLKLLASBPDLRFR 120
DB 61 RRMELLEBAKMKEMAKRYIIPVYIGICREPVGLVMEYMETGSLKLLASBPDLRFR 120
QY 121 IIHETAVGNFLHCAAPPLHLDLKPAIILDAHYHVKISDFGLAKCNGLSHSHDLSMDG 180
DB 121 IIHETAVGNFLHCAAPPLHLDLKPAIILDAHYHVKISDFGLAKCNGLSHSHDLSMDG 180
QY 181 LFGTIAVLPERRIREKSLFPTKHDVYSPAIVYIGVLTOKKPPADEKNIILIMKVYVGH 240
DB 181 LFGTIAVLPERRIREKSLFPTKHDVYSPAIVYIGVLTOKKPPADEKNIILIMKVYVGH 240
QY 241 RPELPVPCARAPRACSHLIRLMQRCQGPVRPFOETSTEDLCEKPDDEVKETAHD 300
DB 241 RPELPVPCARAPRACSHLIRLMQRCQGPVRPFOETSTEDLCEKPDDEVKETAHD 300
QY 301 LDVKSPPRPSSEVPARLKRASAPTFDNDYSLSELLSQLDSGVSQAVGPEELSRSSSES 360
DB 301 LDVKSPPRPSSEVPARLKRASAPTFDNDYSLSELLSQLDSGVSQAVGPEELSRSSSES 360
QY 361 KLPSSSGSKRLSGVSSVDASFSRGLSLSFEREPESTDLGTTDVQKKLVDAIVSGDTS 420
DB 361 KLPSSSGSKRLSGVSSVDASFSRGLSLSLFEREPESTDLGTTDVQKKLVDAIVSGDTS 420
QY 421 KLMKTILOPDVDLALDSGASLHLAVEAGQEBKAKMLNNANPNLSNRGSTPLHMAVE 480
DB 421 KLMKTILOPDVDLALDSGASLHLAVEAGQEBKAKMLNNANPNLSNRGSTPLHMAVE 480
QY 481 RRVGVEVLELLARKISVNAKEDDQWTALHFAAQNGDESTRLLLEKNASVNEVDPEGRTP 540
DB 481 RRVGVEVLELLARKISVNAKEDDQWTALHFAAQNGDESTRLLLEKNASVNEVDPEGRTP 540
QY 541 MHVACQHGQENIVRILIRRGVDVSLQKQDAMLPLHYAAWQGHLPYKLLAQPGVSVNAQ 600
DB 541 MHVACQHGQENIVRILIRRGVDVSLQKQDAMLPLHYAAWQGHLPYKLLAQPGVSVNAQ 600
QY 601 TLIDGRTPHLAAQRGHYVARILIDLCSDVNVCSLAQTPLVHAAETGHTSTARLLHKG 660
DB 601 TLIDGRTPHLAAQRGHYVARILIDLCSDVNVCSLAQTPLVHAAETGHTSTARLLHKG 660
QY 661 AGKEAVTSDGYTALHAAARNGHATVKKLVESKADVLAGPLNQTLHAAAHGSEVVE 720
DB 661 AGKEAVTSDGYTALHAAARNGHATVKKLVESKADVLAGPLNQTLHAAAHGSEVVE 720
QY 721 ELVSAVYIDLFDQGSALHLAAQGHQVETLHGHANINQSLKFGGHPATTLR 780
DB 721 ELVSAVYIDLFDQGSALHLAAQGHQVETLHGHANINQSLKFGGHPATTLR 780
QY 781 RSKT 784
DB 781 RSKT 784

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RESULT 7
US-10-648-593-153
; Sequence 153; Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 153
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-153

Query Match          97.5%; Score 3976; DB 16; Length 784;
Best Local Similarity 98.1%; Pred. No. 5.2e-273;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEGDGTFWALALRTFDAGFTGMEKVGSGFGQVYKRVHVKMTWLAICSPSLHYDD 60
DB 1 MEGDGTFWALALRTFDAGFTGMEKVGSGFGQVYKRVHVKMTWLAICSPSLHYDD 60
QY 61 RRMELLEBAKMKEMAKRYIIPVYIGICREPVGLVMEYMETGSLKLLASBPDLRFR 120
DB 61 RRMELLEBAKMKEMAKRYIIPVYIGICREPVGLVMEYMETGSLKLLASBPDLRFR 120
QY 121 IIHETAVGNFLHCAAPPLHLDLKPAIILDAHYHVKISDFGLAKCNGLSHSHDLSMDG 180
DB 121 IIHETAVGNFLHCAAPPLHLDLKPAIILDAHYHVKISDFGLAKCNGLSHSHDLSMDG 180
QY 181 LFGTIAVLPERRIREKSLFPTKHDVYSPAIVYIGVLTOKKPPADEKNIILIMKVYVGH 240
DB 181 LFGTIAVLPERRIREKSLFPTKHDVYSPAIVYIGVLTOKKPPADEKNIILIMKVYVGH 240
QY 241 RPELPVPCARAPRACSHLIRLMQRCQGPVRPFOETSTEDLCEKPDDEVKETAHD 300
DB 241 RPELPVPCARAPRACSHLIRLMQRCQGPVRPFOETSTEDLCEKPDDEVKETAHD 300
QY 301 LDVKSPPRPSSEVPARLKRASAPTFDNDYSLSELLSQLDSGVSQAVGPEELSRSSSES 360
DB 301 LDVKSPPRPSSEVPARLKRASAPTFDNDYSLSELLSQLDSGVSQAVGPEELSRSSSES 360
QY 361 KLPSSSGSKRLSGVSSVDASFSRGLSLSFEREPESTDLGTTDVQKKLVDAIVSGDTS 420
DB 361 KLPSSSGSKRLSGVSSVDASFSRGLSLSLFEREPESTDLGTTDVQKKLVDAIVSGDTS 420
QY 421 KLMKTILOPDVDLALDSGASLHLAVEAGQEBKAKMLNNANPNLSNRGSTPLHMAVE 480
DB 421 KLMKTILOPDVDLALDSGASLHLAVEAGQEBKAKMLNNANPNLSNRGSTPLHMAVE 480
QY 481 RRVGVEVLELLARKISVNAKEDDQWTALHFAAQNGDESTRLLLEKNASVNEVDPEGRTP 540
DB 481 RRVGVEVLELLARKISVNAKEDDQWTALHFAAQNGDESTRLLLEKNASVNEVDPEGRTP 540
QY 541 MHVACQHGQENIVRILIRRGVDVSLQKQDAMLPLHYAAWQGHLPYKLLAQPGVSVNAQ 600
DB 541 MHVACQHGQENIVRILIRRGVDVSLQKQDAMLPLHYAAWQGHLPYKLLAQPGVSVNAQ 600
QY 601 TLIDGRTPHLAAQRGHYVARILIDLCSDVNVCSLAQTPLVHAAETGHTSTARLLHKG 660
DB 601 TLIDGRTPHLAAQRGHYVARILIDLCSDVNVCSLAQTPLVHAAETGHTSTARLLHKG 660
QY 661 AGKEAVTSDGYTALHAAARNGHATVKKLVESKADVLAGPLNQTLHAAAHGSEVVE 720
DB 661 AGKEAVTSDGYTALHAAARNGHATVKKLVESKADVLAGPLNQTLHAAAHGSEVVE 720

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Db 661 AGKAVTSDGYTALHLAARNGHLATVKLLVEBKADVLRARGLNQTALHLAAHGHSEVVE 720
Qy 721 ELVSVADVIDLDFDEQGLSALHLAAQGRHAQTYETLLRHGAHINLQSLKQGCGHPATLLR 780
Db 721 ELVSVADVIDLDFDEQGLSALHLAAQGRHAQTYETLLRHGAHINLQSLKQGCGHPATLLR 780
Qy 781 RSKT 784
Db 781 RSKT 784

RESULT 8

US-10-164-080-2
; Sequence 2, Application US/10164080
; Publication No. US20030087411A1
; GENERAL INFORMATION:
; APPLICANT: BIRD, Timothy, A.
; APPLICANT: HOLLAND, Pamela, M.
; APPLICANT: PESCHON, Jacques, J.
; APPLICANT: VIRCA, George, D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKRYIN REPEATS (DAKAR) AND ME
; TITLE OF INVENTION: USE
; FILE REFERENCE: 3280-B
; CURRENT APPLICATION NUMBER: US/10/164,080
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/295,959
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/334,362
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-164-080-2

Query Match 89.0%; Score 3628; DB 14; Length 786;

Best Local Similarity 88.9%; Pred. No. 2.5e-248;

Matches 699; Conservative 34; Mismatches 51; Indels 2; Gaps 1;

Qy 1 MEGDGTWALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHKTWLAIKCPSLHAYDD 60
Db 1 MEGDGRGHWALGLRTFDAGEFTGMEKVGSGGFGQVYKVRHVHKTWLAIKCPSLHAYDD 60
Qy 61 RRRMELLEBAKKMMAKFRYIIPYVGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
Db 61 RRRMELLEBAKKMMAKFRYIIPYVGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
Qy 121 ITHETAVGNMFLHGMAPPILLHLDKPANILLDAHVHKISDFGLAKCNGSHSHSLMDG 180
Db 121 ITHETAVGNMFLHGMAPPILLHLDKPANILLDAHVHKISDFGLAKCNGSHSHSLMDG 180
Qy 181 LFGTIALVLPERRIREKSRLLFTKHDVYSPFAIVMGVLTQKKPFADEKNILHIMKVYKGH 240
Db 181 LFGTIALVLPERRIREKSRLLFTKHDVYSPFAIVMGVLTQKKPFADEKNILHIMKVYKGH 240
Qy 241 RPELPVPCARPRACSHLIRLMORCMQGDPRVRPTFOETSTEDLCEKPDDEVKETAHD 300
Db 241 RPELPVPCARPRACSHLIRLMORCMQGDPRVRPTFOETSTEDLCEKPDDEVKETAHD 300
Qy 241 RPELPVPCARPRACSHLIRLMORCMQGDPRVRPTFOETSTEDLCEKPDDEVKETAHD 300
Db 241 RPELPVPCARPRACSHLIRLMORCMQGDPRVRPTFOETSTEDLCEKPDDEVKETAHD 300
Qy 301 LDVKSPPPEPRSEVVP--ARLKASAPTFDNDYSLSELLSQLDSGVSOAVEGPEELSRSS 358
Db 301 LDVKSPPPEPRSEVVP--ARLKASAPTFDNDYSLSELLSQLDSGVSOAVEGPEELSRSS 358
Qy 361 RRRMELLEBAKKMMAKFRYIIPYVGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
Db 361 RRRMELLEBAKKMMAKFRYIIPYVGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
Qy 419 TSRLMKTILOPOVDIVLDSASLHLHVAAGQEBECVAKMLLNANPNLNRGSTRPLMA 478
Db 419 TSRLMKTILOPOVDIVLDSASLHLHVAAGQEBECVAKMLLNANPNLNRGSTRPLMA 478
Qy 421 TSRLMKTILOPOVDIVLDSASLHLHVAAGQEBECVAKMLLNANPNLNRGSTRPLMA 480
Db 421 TSRLMKTILOPOVDIVLDSASLHLHVAAGQEBECVAKMLLNANPNLNRGSTRPLMA 480

Qy 479 VERRRVEVELLARKISVNAKDEQWTALHFAAQNDESSSTLLLEKNASVNEVDEGR 538
Db 481 VERKRGITVELLARKISVNAKDEQWTALHFAAQNDESSSTLLLEKNASVNEVDEGR 540
Qy 539 TPEHVAQCHQENIVRILLRGVDVSLQGDAMLPHTYAAWQGLPIVLLAAQPGVSVN 598
Db 541 TPEHVAQCHQENIVRILLRGVDVSLQGDAMLPHTYAAWQGLPIVLLAAQPGVSVN 600
Qy 599 AQTLDGRTPLHLAARNGHVARILLIDGSDVNCSLAQTPLHVAETGHTSTARLLH 658
Db 601 AQTLDGRTPLHLAARNGHVARILLIDGSDVNCSLAQTPLHVAETGHTSTARLLH 660
Qy 659 RGAKKAVTSDGYTALHLAARNGHLATVKLLVEBKADVLRARGLNQTALHLAAHGHSEV 718
Db 661 RGAKKAVTSDGYTALHLAARNGHLATVKLLVEBKADVLRARGLNQTALHLAAHGHSEV 720
Qy 719 VEEIVSADVIDLDFDEQGLSALHLAAQGRHAQTYETLLRHGAHINLQSLKQGCGHPATL 778
Db 721 VEEIVSADVIDLDFDEQGLSALHLAAQGRHAQTYETLLRHGAHINLQSLKQGCGSSAATL 780
Qy 779 LRRSKT 784
Db 781 LRRSKT 786

RESULT 9

US-10-299-327-2
; Sequence 2, Application US/10299327
; Publication No. US20030104482A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corp.
; APPLICANT: Bird, Timothy
; APPLICANT: Virca, G.D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKRYIN REPEATS
; TITLE OF INVENTION: (DAKAR)
; FILE REFERENCE: 2889-US
; CURRENT APPLICATION NUMBER: US/10/299,327
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/09/509,802
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-299-327-2

Query Match 89.0%; Score 3628; DB 14; Length 786;

Best Local Similarity 88.9%; Pred. No. 2.5e-248;

Matches 699; Conservative 34; Mismatches 51; Indels 2; Gaps 1;

Qy 1 MEGDGTWALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHKTWLAIKCPSLHAYDD 60
Db 1 MEGDGRGHWALGLRTFDAGEFTGMEKVGSGGFGQVYKVRHVHKTWLAIKCPSLHAYDD 60
Qy 61 RRRMELLEBAKKMMAKFRYIIPYVGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
Db 61 RRRMELLEBAKKMMAKFRYIIPYVGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
Qy 121 ITHETAVGNMFLHGMAPPILLHLDKPANILLDAHVHKISDFGLAKCNGSHSHSLMDG 180
Db 121 ITHETAVGNMFLHGMAPPILLHLDKPANILLDAHVHKISDFGLAKCNGSHSHSLMDG 180
Qy 181 LFGTIALVLPERRIREKSRLLFTKHDVYSPFAIVMGVLTQKKPFADEKNILHIMKVYKGH 240
Db 181 LFGTIALVLPERRIREKSRLLFTKHDVYSPFAIVMGVLTQKKPFADEKNILHIMKVYKGH 240
Qy 241 RPELPVPCARPRACSHLIRLMORCMQGDPRVRPTFOETSTEDLCEKPDDEVKETAHD 300
Db 241 RPELPVPCARPRACSHLIRLMORCMQGDPRVRPTFOETSTEDLCEKPDDEVKETAHD 300
Qy 301 LDVKSPPPEPRSEVVP--ARLKASAPTFDNDYSLSELLSQLDSGVSOAVEGPEELSRSS 358
Db 301 LDVKSPPPEPRSEVVP--ARLKASAPTFDNDYSLSELLSQLDSGVSOAVEGPEELSRSS 358


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Db 301 PGRSSLSKSBARPESSRLKRAAPFDNDGSLSELLSOLDGSLQTLGPEBELSRSS 360
Qy 359 ESKLPSSGSGKRLSGVSSVDSAFSSRGSLSLSPFEREPSTDLGTRPEBEACGCHVRD 418
Db 361 ECKLPSSSGKRLSGVSSVDSAFSSRGSLSLSPFEREASTDGLPTDIOKKLVDAIISGD 420
Qy 419 TSKLMKTIQPOVDVLADSGASLSLHLAVEAGOECAKWLNNANPNLSNRGSTPLHMA 478
Db 421 TSKLMKTIQPOVDVLADSGASLSLHLAVEAGOECAKWLNNANPNLSNRGSTPLHMA 480
Qy 479 VERBVRGVVELLARKTSVNAKEDQWTLHFAAQNDEBSTRLLBKNSVNEVDEGR 538
Db 481 VERBVRGVVELLARKTSVNAKEDQWTLHFAAQNDEBSTRLLBKNSVNEVDEGR 540
Qy 539 TPMHVAQCHGQENIVRTLRRGVDSLOQKDALPLHYAAWQGHLPYKLLAKOPGVSVN 598
Db 541 TPMHVAQCHGQENIVRTLRRGVDSLOQKDALPLHYAAWQGHLPYKLLAKOPGVSVN 600
Qy 599 AQTLDGRTPLHAAQRGHYVARILIDCSVNVCSLLAQTPLHYAAWQGHLPYKLLAKOPGVSVN 658
Db 601 AQTLDGRTPLHAAQRGHYVARILIDCSVNVCSLLAQTPLHYAAWQGHLPYKLLAKOPGVSVN 660
Qy 659 RGAGKEAVTSDGYTALHAAQRGHYVARILIDCSVNVCSLLAQTPLHYAAWQGHLPYKLLAKOPGVSVN 718
Db 661 RGAGKEAVTSDGYTALHAAQRGHYVARILIDCSVNVCSLLAQTPLHYAAWQGHLPYKLLAKOPGVSVN 720
Qy 719 VEBLSADVIDLFDGEGSALHAAQGRHQAQVETLLRHGAHINLSQIKFGGSGHPAATL 778
Db 721 VEBLSADVIDLFDGEGSALHAAQGRHQAQVETLLRHGAHINLSQIKFGGSGHPAATL 780
Qy 779 LRRSKT 784
Db 781 LRRSKT 786

RESULT 10
US-10-128-174-13
; Sequence 13, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohito
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-13

Query Match 89.0%; Score 3628; DB 14; Length 786;
Best Local Similarity 88.9%; Pred. No. 2.5e-248;
Matches 699; Conservative 34; Mismatches 51; Indels 2; Gaps 1;

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Db 181 LFGTIAYLPEPERIREKSLFDTKGDVYSPFAIVMGVLTQKKPADEKNILHMKVKGH 240
Qy 241 RPELPICRARPAACSHLIRLMORCMQGDPRVPTFOETSETEDLCEKPEDEKETAHD 300
Db 241 RPELPICRARPAACSHLIRLMORCMQGDPRVPTFOETSETEDLCEKPEDEKETAHD 300
Qy 301 LDVSGPPEPSRSEVVP--ARLKRAAPFDNDGSLSELLSOLDGSGVSAVEGPEBELSRSS 358
Db 301 PGRSSLSKSBARPESSRLKRAAPFDNDGSLSELLSOLDGSLQTLGPEBELSRSS 360
Qy 359 ESKLPSSGSGKRLSGVSSVDSAFSSRGSLSLSPFEREPSTDLGTRPEBEACGCHVRD 418
Db 361 ECKLPSSSGKRLSGVSSVDSAFSSRGSLSLSPFEREASTDGLPTDIOKKLVDAIISGD 420
Qy 419 TSKLMKTIQPOVDVLADSGASLSLHLAVEAGOECAKWLNNANPNLSNRGSTPLHMA 478
Db 421 TSKLMKTIQPOVDVLADSGASLSLHLAVEAGOECAKWLNNANPNLSNRGSTPLHMA 480
Qy 479 VERBVRGVVELLARKTSVNAKEDQWTLHFAAQNDEBSTRLLBKNSVNEVDEGR 538
Db 481 VERBVRGVVELLARKTSVNAKEDQWTLHFAAQNDEBSTRLLBKNSVNEVDEGR 540
Qy 539 TPMHVAQCHGQENIVRTLRRGVDSLOQKDALPLHYAAWQGHLPYKLLAKOPGVSVN 598
Db 541 TPMHVAQCHGQENIVRTLRRGVDSLOQKDALPLHYAAWQGHLPYKLLAKOPGVSVN 600
Qy 599 AQTLDGRTPLHAAQRGHYVARILIDCSVNVCSLLAQTPLHYAAWQGHLPYKLLAKOPGVSVN 658
Db 601 AQTLDGRTPLHAAQRGHYVARILIDCSVNVCSLLAQTPLHYAAWQGHLPYKLLAKOPGVSVN 660
Qy 659 RGAGKEAVTSDGYTALHAAQRGHYVARILIDCSVNVCSLLAQTPLHYAAWQGHLPYKLLAKOPGVSVN 718
Db 661 RGAGKEAVTSDGYTALHAAQRGHYVARILIDCSVNVCSLLAQTPLHYAAWQGHLPYKLLAKOPGVSVN 720
Qy 719 VEBLSADVIDLFDGEGSALHAAQGRHQAQVETLLRHGAHINLSQIKFGGSGHPAATL 778
Db 721 VEBLSADVIDLFDGEGSALHAAQGRHQAQVETLLRHGAHINLSQIKFGGSGHPAATL 780
Qy 779 LRRSKT 784
Db 781 LRRSKT 786

RESULT 11
US-09-866-050A-334
; Sequence 334, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Muriison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c4v
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Mouse
US-09-866-050A-334

Query Match 88.9%; Score 3624; DB 10; Length 787;
Best Local Similarity 88.8%; Pred. No. 4.7e-248;
Matches 698; Conservative 35; Mismatches 51; Indels 2; Gaps 1;

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Db 2 VEGEGRGWALGLRTFDAGEPAGMEKVGSGFGQVYKVRHVHMKMTLAIKCSPSLHVD 61
QY 61 RERWELLBEAKKMEMAKFRYILPYVGICREPVGLVMEYMTGSLSEKLLASEPLPMDLFR 120
Db 62 RERWELLBEAKKMEMAKFRYILPYVGICREPVGLVMEYMTGSLSEKLLASEPLPMDLFR 121
QY 121 I I H E T A V G N F L H C M A P P L H L D L K P A N I L D A H Y H K I S D F G L A K C N G S H S H D L S M D G 180
Db 122 I V H E T A V G N F L H C M A P P L H L D L K P A N I L D A H Y H K I S D F G L A K C N G S H S H D L S M D G 181
QY 181 L F G T I A V L P P E R I R E K S R L F D T K H D V S F A I V I W G V L T Q K K P A D E K N I I H I M K V Y K G H 240
Db 182 L F G T I A V L P P E R I R E K S R L F D T K H D V S F A I V I W G V L T Q K K P A D E K N I I H I M K V Y K G H 241
QY 241 R P E L P V C R A P R A C S H L I R L M O R C W G D P R A P T F Q E I T S E T E D L C E K P D E E K D L A H E 300
Db 242 R P E L P I C R P R A C A S L I G L M O R C M H A D P O V R P T F Q E I T S E T E D L C E K P D E E K D L A H E 301
QY 301 L D V K S P P E R S E V P - - A R L K R A S A P T F D N D Y S L S E L L S O L D S G V S Q A V E G P E E L S R S S 358
Db 302 P G E K S L S E S K S E A R P E S S R L K R A S A P P F D N D C S L S E L L S O L D S G I S Q T L E G P E E L S R S S 361
QY 359 E S K L P S S G S G K R L S G V S V D S A F S S R G S L S F E R E P S T S D L G T T R P E E E A C G C H R V D 418
Db 362 E C K L P S S S S G K R L S G V S V D S A F S S R G S L S F E R E A S T G D L G P T D I O K K L V D A I I S G D 421
QY 419 T S K L M K I I Q P O D V D L A D S G A S L H L A V E A G O E C A K W L L N N A N P U L S N R G S T P L M A 478
Db 422 T S R L M K I I Q P O D V D L A D S S A S L H L A V E A G O E C V K W L L N N A N P U L T N R K G S T P L M A 481
QY 479 V E R R V R G V E L L A R K I S V N A K D E D O M T A L H P A A N G D E S T R L L E K N A S V N E V D P E G R 538
Db 482 V E R K R G I V E L L A R K T S V N A K D E D O M T A L H P A A N G D E A S T R L L E K N A S V N E V D P E G R 541
QY 539 T P M H V A C O H G E N I V R I L L R G V D V S L O G K A M L P L H Y A A M O G H L P I V K L L A K O P G V S V N 598
Db 542 T P M H V A C O H G E N I V R I L L R G V D V G L O G K A M L P L H Y A A M O G H L P I V K L L A K O P G V S V N 601
QY 599 A Q T L D G R T P L H L A A R G H Y V A R I I L D C S D V N V C S L L A O T P L H A A E T G H T S T A R L L H 658
Db 602 A Q T L D G R T P L H L A A R G H Y V A R I I L D C S D V N I C S L A Q T P L H A A E T G H T S T A R L L H 661
QY 659 R G A G E A V T S D G Y T A L H L A A R N G H L A T V K L I V E E K A D V L A R G P L N O T A L H L A A H G S E V 718
Db 662 R G A G E A L T S E G Y T A L H L A A O N G H L A T V K L I E E K A D V M A R G P L N O T A L H L A A H G S E V 721
QY 719 V E E L V S A D V I D L F D E Q G L S A L H L A A O G R H A Q V E T I L L R H G A H I N L O S L K F O G G S A A T L 778
Db 722 V E E L V S A D L I D L S D E Q G L S A L H L A A O G R H S Q V E T I L L K H G A H I N L O S L K F O G G S A A T L 781
QY 779 L R R S K T 784
Db 782 L R R S K T 787

RESULT 12
US-10-128-174-31
; Sequence 31, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-31

Query Match 88.8%; Score 3620; DB 14; Length 786;
Best Local Similarity 88.8%; Pred. No. 9,1e-248;
Matches 698; Conservative 34; Mismatches 52; Indels 2; Gaps 1;
QY 1 M E G D G T P M A L A L R T P D A G E P T G W E K V G S G F G Q V Y K V R H V H M K M T L A I K C S P S L H V D 60
Db 1 M E G D G R W M A L G L R T D A G E P A G M E K V G S G F G Q V Y K V R H V H M K M T L A I K C S P S L H V D 60
QY 61 R E R W E L L B E A K K M E M A K F R Y I L P Y V G I C R E P V G L V M E Y M T G S L S E K L L A S E P L P M D L F R 120
Db 61 R E R W E L L B E A K K M E M A K F R Y I L P Y V G I C R E P V G L V M E Y M T G S L S E K L L A S E P L P M D L F R 120
QY 121 I I H E T A V G N F L H C M A P P L H L D L K P A N I L D A H Y H K I S D F G L A K C N G S H S H D L S M D G 180
Db 121 I V H E T A V G N F L H C M A P P L H L D L K P A N I L D A H Y H K I S D F G L A K C N G S H S H D L S M D G 180
QY 181 L F G T I A V L P P E R I R E K S R L F D T K H D V S F A I V I W G V L T Q K K P A D E K N I I H I M K V Y K G H 240
Db 181 L F G T I A V L P P E R I R E K S R L F D T K H D V S F A I V I W G V L T Q K K P A D E K N I I H I M K V Y K G H 240
QY 241 R P E L P V C R A P R A C S H L I R L M O R C W G D P R A P T F Q E I T S E T E D L C E K P D E E K D L A H E 300
Db 241 R P E L P I C R P R A C A S L I G L M O R C M H A D P O V R P T F Q E I T S E T E D L C E K P D E E K D L A H E 300
QY 301 L D V K S P P E R S E V P - - A R L K R A S A P T F D N D Y S L S E L L S O L D S G V S Q A V E G P E E L S R S S 358
Db 301 P G E K S L S E S K S E A R P E S S R L K R A S A P P F D N D C S L S E L L S O L D S G I S Q T L E G P E E L S R S S 360
QY 359 E S K L P S S G S G K R L S G V S V D S A F S S R G S L S F E R E P S T S D L G T T R P E E E A C G C H R V D 418
Db 361 E C K L P S S S S G K R L S G V S V D S A F S S R G S L S F E R E A S T G D L G P T D I O K K L V D A I I S G D 420
QY 419 T S K L M K I I Q P O D V D L A D S G A S L H L A V E A G O E C A K W L L N N A N P U L S N R G S T P L M A 478
Db 421 T S R L M K I I Q P O D V D L A D S S A S L H L A V E A G O E C V K W L L N N A N P U L T N R K G S T P L M A 480
QY 479 V E R R V R G V E L L A R K I S V N A K D E D O M T A L H P A A N G D E S T R L L E K N A S V N E V D P E G R 538
Db 481 V E R K R G I V E L L A R K T S V N A K D E D O M T A L H P A A N G D E A S T R L L E K N A S V N E V D P E G R 540
QY 539 T P M H V A C O H G E N I V R I L L R G V D V S L O G K A M L P L H Y A A M O G H L P I V K L L A K O P G V S V N 598
Db 541 T P M H V A C O H G E N I V R I L L R G V D V G L O G K A M L P L H Y A A M O G H L P I V K L L A K O P G V S V N 600
QY 599 A Q T L D G R T P L H L A A R G H Y V A R I I L D C S D V N V C S L L A O T P L H A A E T G H T S T A R L L H 658
Db 601 A Q T L D G R T P L H L A A R G H Y V A R I I L D C S D V N I C S L A Q T P L H A A E T G H T S T A R L L H 660
QY 659 R G A G E A V T S D G Y T A L H L A A R N G H L A T V K L I V E E K A D V L A R G P L N O T A L H L A A H G S E V 718
Db 661 R G A G E A L T S E G Y T A L H L A A O N G H L A T V K L I E E K A D V M A R G P L N O T A L H L A A H G S E V 720
QY 719 V E E L V S A D V I D L F D E Q G L S A L H L A A O G R H A Q V E T I L L R H G A H I N L O S L K F O G G S A A T L 778
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QY 779 L R R S K T 784
Db 781 L R R S K T 786

RESULT 13
US-10-128-174-32
; Sequence 32, Application US/10128174
; Publication No. US20030199462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patent version 3.1
SEQ ID NO 32
LENGTH: 786
TYPE: prt
ORGANISM: Mus musculus
US-10-128-174-32

Query Match 88.7%; Score 3619; DB 14; Length 786;
Best Local Similarity 88.5%; Pred. No. 1.1e-247;
Matches 696; Conservative 37; Mismatches 51; Indels 2; Gaps 1;

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Db 1 MEGDGRGFWALGILRTFDAGFAGMEKVGSGGFGQYKVRHVHMTWLAIKCSPLAHVD 60
QY 61 RRMELLEBAKKMEAKFRYILPYVGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
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Db 61 RRMELLEBAKKMEAKFRYILPYVGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
QY 121 ITHETAVGNMFLHCAPPLHLDLKPANILLDAHNVKISDFGLAKCNGLSHSDLSMDG 180
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Db 121 ITHETAVGNMFLHCAPPLHLDLKPANILLDAHNVKISDFGLAKCNGMAHDLAMDG 180
QY 181 LFGTAYLPERIRKESLPTDKHDVYSFAIVIGVLTOKKPPADEKNILHIMKVVGKH 240
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Db 181 LFGTAYLPERIRKESLPTDKHDVYSFAIVIGVLTOKKPPADEKNILHIMKVVGKH 240
QY 241 REBELPVCRAPRACSHLRLMORCMQDPVRVPTFOEITSETEDLCEKPDDEVKETAHD 300
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Db 241 REBELPICRPRACASLIGLMORCMHADPOVAPTFQETITSETEDLCEKPDDEVKDLAHE 300
QY 301 LDVKSPPERSEVVP--ARLKASAPTFDNDYSLSELISQDSCVSAVEGPEELSRSS 358
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Db 301 PEKKSLEKSKBARPESSRLKASAPFPDNCISLSDLSQDLSQTLGEPBELSRSS 360
QY 359 ESKLPSSGSGRLSGVSVDSAFSSRGSLSPFERPSTSDGTRPREBEACGCHRYVD 418
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 ECKLPSSSGKRLSGVSVDSAFSSRGSLSPFERASTGDLGPTDIOKKLVDAIISGD 420
QY 419 TSKLMKILQPOVDLALDSGASLHLAVEAGQECCKWLLNNANPNLSNRGSTPLHMA 478
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Db 421 TSKLMKILQPOVDLALDSGASLHLAVEAGQECCKWLLNNANPNLTNRKGSTPLHMA 480
QY 479 VERRVGVVELLARKISVNAKDEDMTALHPAONGDESSSTRLLLEKNAVNEVDPEGR 538
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Db 481 VERKGGIYELLARKTSVNAKDEDMTALHPAONGDEASTRLLEKNAVNEVDPEGR 540
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Db 541 TPMHVAACHQGENIVRIILRRGVNLSQKDAWLPHYAAMOGHLPYVLLAKQGVSVN 600
QY 599 AQTLDRTPLHLAARGHYRVARILIDCSDVNVCSLAQTPLHYAAETGHTSTARLLH 658
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Db 601 AQTLDRTPLHLAARGHYRVARILIDCSDVNVCSLAQTPLHYAAETGHTSTARLLH 660
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Db 661 RGAGKEALTSBGYTALHAAANGHLATVKLLIEEKADVMARGLNQTALHAAAGHSEV 720
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Db 721 VEELVSADVIDLFDQGLSALHLAAGRNAQTVEITLRGAININLSLKFQGGSSAATL 780
QY 779 LRRSKT 784
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Db 781 LRRSKT 786
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RESULT 14
US-10-128-174-33
; Sequence 33, Application US/10128174
; Publication No. US20030199462A1

GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128,174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patent version 3.1
SEQ ID NO 33
LENGTH: 786
TYPE: prt
ORGANISM: Mus musculus
US-10-128-174-33

Query Match 88.7%; Score 3616; DB 14; Length 786;
Best Local Similarity 88.5%; Pred. No. 1.7e-247;
Matches 696; Conservative 34; Mismatches 54; Indels 2; Gaps 1;

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QY 61 RRMELLEBAKKMEAKFRYILPYVGICREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
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QY 121 ITHETAVGNMFLHCAPPLHLDLKPANILLDAHNVKISDFGLAKCNGLSHSDLSMDG 180
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QY 241 REBELPVCRAPRACSHLRLMORCMQDPVRVPTFOEITSETEDLCEKPDDEVKETAHD 300
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QY 301 LDVKSPPERSEVVP--ARLKASAPTFDNDYSLSELISQDSCVSAVEGPEELSRSS 358
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QY 479 VERRVGVVELLARKISVNAKDEDMTALHPAONGDESSSTRLLLEKNAVNEVDPEGR 538
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Db 481 VERKGGIYELLARKTSVNAKDEDMTALHPAONGDEASTRLLEKNAVNEVDPEGR 540
QY 539 TPMHVAACHQGENIVRIILRRGVNLSQKDAWLPHYAAMOGHLPYVLLAKQGVSVN 598
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QY 659 RGAGKEAVTSDGYTALHAAANGHLATVKLLVEEKADVLARGLNQTALHAAAGHSEV 718
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QY 719 VEELVSADVIDLFDQGLSALHLAAGRNAQTVEITLRGAININLSLKFQGGHGPAAATL 778
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QY 779 LRRSKT 784
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Db 781 LRRSKT 786

Job time : 4687.9 secs

RESULT 15

US-09-866-050A-409

; Sequence 409, Application US/09866050A

Publication No. US20030040471A1

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Onrust, Rene

APPLICANT: Murison, James G.

APPLICANT: Kumble, Krishanand D

TITLE OF INVENTION: Compositions Isolated From Skin Cells

1 TITLE OF INVENTION: and Methods for Their Use

FILE REFERENCE: 11000.1011c4U

CURRENT APPLICATION NUMBER: US/09/866,050A

CURRENT FILING DATE: 2001-05-24

NUMBER OF SEO ID NOS: 725

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SOFTWARE: FastSEO for Windows Version 4.0
NUMBER OF SEQ ID NOS: 123

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SOFTWARE: F8
: SEO ID NO 409

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; SEQ ID NO 403
; LENGTH: 590

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LENGTH: 390
TYPE: PRT

TYPE: PRI
ORGANISM: Mollusca

; ORGANISM: MOUS
ITS-09-866-050A-409

Query Match	Score	DB	Length
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Best Local Similarity 87.3%; Pred. No. 4.6e-182;

Matches 514; Conservative 27; Mismatches 46; Indels 2; Gaps 1;

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OY	61	REREELLE	EAKKEMAKFRYLIPVVGICRE	PGLYMEYMEVSGSEKTLASERLEPMDLFR	120
OY	62	REREELLE	EAKKEMAKFRYLIPVYICCE	PGLYMEYMEVSGSEKTLASERLEPMDLFR	121
OY	121	IYHETAVGN	PLHCOMAPPLIHLADL	KPANILLDAHYVAKISDFGLACKNGLSHSHDSLMDG	180
OY	122	IYHETAVGN	PLHCOMSPPLIHLADL	KPANILLDAHYVAKISDFGLACKNGLSHSHDSLMDG	181
OY	181	LFGLTAL	PEPERREKSRLEPOT	HDVYSFAIYMGVLOCKKPRADENKXILHIMKYVKGH	240
OY	182	LFGLTAL	PEPERREKSRLEPOT	HDVYSFAIYMGVLOCKKPRADENKXILHIMKYVKGH	241
OY	241	RPELPPY	CRAPRAPACSHLIRLMOR	CQSGPRVRPTFOBITSETBEDLCEKPDVEKETAHD	300
OY	242	RPELPPY	CRAPRAPACSHLIRLMOR	CQSGPRVRPTFOBITSETBEDLCEKPDVEKETAHD	301
OY	301	LDVKS	PEPEPRSEVPP-ARIK	RASAPTPPNNDYLSLSLSLSOLDGVSQAVGEPEELSSSS	358
OY	302	PGEKSS	LESSEKSEARPESSSR	LKRASAPFPNDSCSLSELSDSGISQTLPEPEBELSSSS	361
OY	359	ESKLP	SSSGGRLSGVSSVDS	AFSSRSGSLSPSEPEPSTSDGTRRPEBEACCGHYRD	418
OY	362	ECKLP	SSSGGRLSGVSSVDS	AFSSRSGSLSPSEPEPSTSDGTRRPEBEACCGHYRD	419
OY	419	TSKLM	KLILOP	ODVLDALDSGASLIHLAVEAGOECAKMLLNNANPNLSNRGSTPLHMA	478
OY	422	TSRLM	KLILOP	ODVLDALDSGASLIHLAVEAGOECEKMLLNNANPNLTNRKGSSTPLHMA	481
OY	479	VEREVR	GVVELLARKISVNAK	ODEMTALHPAONDESSSTRLLLEKONASVNEVDYBGR	538
OY	482	VERKGR	IVELLARKISVNAK	ODEMTALHPAONDESTRLLLEKONASVNEVDYBGR	541
OY	539	TPMHV	AOCHOGENTVRLIR	GVDSLOGDVDMPLPHYAAMGCHPLPYK	587
OY	542	TPMHV	AOCHOGENTVRLIR	GVDSLOGDVDMPLPHYAAMGCHPLPYK	590

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 17, 2005, 02:33:25 ; Search time 942.919 Seconds
(without alignments)
62.068 Million cell updates/sec

Title: US-10-658-904-2

Perfect score: 4078
Sequence: 1 MEGDGTGTPMALALRTFDAG.....SLKRGSGHGPATILIRSKT 784

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4078	100.0	784	US-09-781-882-2	Sequence 2, Appl 1
2	3980	97.6	787	US-09-949-016-11076	Sequence 11076, A
3	3976	97.5	784	US-09-949-016-6974	Sequence 6974, Ap
4	3628	89.0	786	US-09-509-802-2	Sequence 2, Appl 1
5	3624	88.9	787	US-09-188-930-334	Sequence 334, App
6	3624	88.9	787	US-09-312-283C-334	Sequence 334, App
7	2691	66.0	590	US-09-312-283C-409	Sequence 409, App
8	2269	55.6	536	US-09-188-930-185	Sequence 185, App
9	2269	55.6	536	US-09-312-283C-185	Sequence 185, App
10	545	13.4	530	US-09-069-023-3	Sequence 3, Appl 1
11	541.5	13.3	531	US-09-069-023-1	Sequence 1, Appl 1
12	541.5	13.3	540	US-09-019-942-1	Sequence 2, Appl 1
13	541.5	13.3	540	US-09-099-041A-2	Sequence 27, Appl 1
14	541.5	13.3	540	US-09-069-023-27	Sequence 2, Appl 1
15	541.5	13.3	540	US-09-245-281-2	Sequence 2, Appl 1
16	541.5	13.3	540	US-09-470-271-1	Sequence 2, Appl 1
17	541.5	13.3	540	US-09-207-359B-2	Sequence 2, Appl 1
18	541.5	13.3	540	US-09-340-620A-2	Sequence 28, Appl 1
19	541.5	13.3	540	US-09-345-473B-28	Sequence 2, Appl 1
20	541.5	13.3	540	US-09-865-364-2	Sequence 1, Appl 1
21	541.5	13.3	540	US-09-748-537-1	Sequence 4, Appl 1
22	532.5	13.1	300	US-09-099-041A-4	Sequence 4, Appl 1
23	532.5	13.1	300	US-09-245-281-4	Sequence 4, Appl 1
24	532.5	13.1	300	US-09-207-359B-4	Sequence 4, Appl 1
25	532.5	13.1	300	US-09-340-620A-4	Sequence 4, Appl 1
26	532.5	13.1	300	US-09-865-364-4	Sequence 4, Appl 1
27	512	12.6	264	US-09-069-023-7	Sequence 7, Appl 1

28	509.5	12.5	4377	4	US-09-949-016-6978	Sequence 6978, Ap
29	500	12.3	1719	4	US-09-949-016-6966	Sequence 6966, Ap
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31	500	12.3	1880	4	US-09-949-016-5876	Sequence 5876, Ap
32	500	12.3	1881	4	US-09-949-016-6965	Sequence 6965, Ap
33	500	12.3	1883	4	US-09-949-016-9010	Sequence 9010, Ap
34	500	12.3	1883	4	US-09-949-016-9011	Sequence 9011, Ap
35	500	12.3	1883	4	US-09-949-016-9012	Sequence 9012, Ap
36	500	12.3	1883	4	US-09-949-016-9013	Sequence 9013, Ap
37	500	12.3	1883	4	US-09-949-016-9014	Sequence 9014, Ap
38	500	12.3	1883	4	US-09-949-016-9015	Sequence 9015, Ap
39	500	12.3	1883	4	US-09-949-016-9016	Sequence 9016, Ap
40	500	12.3	1883	4	US-09-949-016-9017	Sequence 9017, Ap
41	498	12.2	1745	2	US-09-031-485-33	Sequence 33, Appl 1
42	498	12.2	1745	2	US-08-847-429A-33	Sequence 33, Appl 1
43	498	12.2	1745	2	US-09-065-474-33	Sequence 33, Appl 1
44	498	12.2	1745	2	US-09-557-034-33	Sequence 33, Appl 1
45	489	12.0	478	3	US-09-069-023-4	Sequence 4, Appl 1

ALIGNMENTS

RESULT 1									
US-09-781-882-2									
; Sequence 2, Application US/09781882									
; Patent No. 6630335									
; GENERAL INFORMATION:									
; APPLICANT: Kapeller-Libermann, Rosana									
; TITLE OF INVENTION: 14171 Protein Kinase, a No. 6630335el Human									
; FILE REFERENCE: 035800-209014(5800-6									
; CURRENT FILING DATE: 2001-02-12									
; PRIOR APPLICATION NUMBER: U.S. 60/182,096									
; PRIOR FILING DATE: 2000-02-11									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 784									
; TYPE: PRT									
; ORGANISM: H. sapiens									
US-09-781-882-2									
Query Match									
Best Local Similarity 100.0%; Score 4078; DB 4; Length 784;									
Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MEGDGTGTPMALALRTFDAGFTGKGVYKVRHVHWKTWLAIKSPSLAYDD	60						
DB	1	MEGDGTGTPMALALRTFDAGFTGKGVYKVRHVHWKTWLAIKSPSLAYDD	60						
QY	61	RRMELLEAKMKEMAKERYILPVYIGREPVGLMEYETGSLKELIASSEPLPMDLRR	120						
DB	61	RRMELLEAKMKEMAKERYILPVYIGREPVGLMEYETGSLKELIASSEPLPMDLRR	120						
QY	121	IIHETAVGNTLHCAPPLHLDLKPANILLDAHRYKISDPGLACKNGLSHSLSDMG	180						
DB	121	IIHETAVGNTLHCAPPLHLDLKPANILLDAHRYKISDPGLACKNGLSHSLSDMG	180						
QY	181	LFGTAVYLPERRIRKSLPFTKHDVYFAIVYGVLTQKKPFADEKNIILHIMVYVKGH	240						
DB	181	LFGTAVYLPERRIRKSLPFTKHDVYFAIVYGVLTQKKPFADEKNIILHIMVYVKGH	240						
QY	241	REPPLPVCARARACSHLIRLMQRCWQDPVPRPTFOBITSETEDLCCKPDDEVKETAHD	300						
DB	241	REPPLPVCARARACSHLIRLMQRCWQDPVPRPTFOBITSETEDLCCKPDDEVKETAHD	300						
QY	301	LDVKSPPPRSVVYVARKKASAPTFNDYLSLISGLDGSVQAVGPELSRSSSES	360						
DB	301	LDVKSPPPRSVVYVARKKASAPTFNDYLSLISGLDGSVQAVGPELSRSSSES	360						
QY	361	KLPSGSGKRLSGVSVSAFSSRGLSLSPFERPSTDLGTTTRAPREBACGHRVDRTS	420						

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Db 361 KLPSSGSKRLSGVSDSAFSSRGSLSLSPEREPTSDGTTTARRPEEACGCHRVDT 420
Qy 421 KLMKILOPQVDLALDSGASLHLAVAGOECAKMLLNANPNLSNRGSTPLHVAVE 480
Db 421 KLMKILOPQVDLALDSGASLHLAVAGOECAKMLLNANPNLSNRGSTPLHVAVE 480
Qy 481 RRVGVVELLARKISVNAKEDQMTALHFAQNGDESSSTRLLLEKASVNEVDFEGRT 540
Db 481 RRVGVVELLARKISVNAKEDQMTALHFAQNGDESSSTRLLLEKASVNEVDFEGRT 540
Qy 541 MHVACQHGQENIVILIRRGDVSLQGDAMLPHYAAMQGHPIVYLLAKQPGSVNAQ 600
Db 541 MHVACQHGQENIVILIRRGDVSLQGDAMLPHYAAMQGHPIVYLLAKQPGSVNAQ 600
Qy 601 TLDRTPHLAAQRGHYVARILIDLCSDVNVCSLLAQTPLVAAETGHTSTARLLHRG 660
Db 601 TLDRTPHLAAQRGHYVARILIDLCSDVNVCSLLAQTPLVAAETGHTSTARLLHRG 660
Qy 661 AGKAVTSDGYTALHAAQNGHATVYKLVBEKADVARGPLNQTALHAAHGHSEVE 720
Db 661 AGKAVTSDGYTALHAAQNGHATVYKLVBEKADVARGPLNQTALHAAHGHSEVE 720
Qy 721 ELVSADVIDLFDDEGLSALHLAAQGRHAQVETILLRGAHINLOSLKFGGHPAATLLR 780
Db 721 ELVSADVIDLFDDEGLSALHLAAQGRHAQVETILLRGAHINLOSLKFGGHPAATLLR 780
Qy 781 RSKT 784
Db 781 RSKT 784
```

```
RESULT 2
US-09-949-016-11076
; Sequence 11076, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11076
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11076

Query Match 97.6%; Score 3980; DB 4; Length 787;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 770; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
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Qy 1 MEGDGTWALALATPAGFTGMEKVGSGGFGVYVRHVMKMTWLAIKSPSLHYDD 60
Db 4 MEGDGTWALALATPAGFTGMEKVGSGGFGVYVRHVMKMTWLAIKSPSLHYDD 63
Qy 61 RERMLLEBAKMEKAKFRYILPVYIGREPVLMEVETSLSEKLLASBFLPMDLFR 120
Db 64 RERMLLEBAKMEKAKFRYILPVYIGREPVLMEVETSLSEKLLASBFLPMDLFR 123
Qy 121 IIEHTAVGNPLHCAAPPLHLIDLPANILDAHYHVKISDGLAKCNGLSHSDLSMDG 180
Db 124 IIEHTAVGNPLHCAAPPLHLIDLPANILDAHYHVKISDGLAKCNGLSHSDLSMDG 183
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Qy 181 LFGTIATLPPERIREKSRLEFDTHGDVYSFAIVIMGVLTQKKPPEADENKILHIMVKVKG 240
Db 184 LFGTIATLPPERIREKSRLEFDTHGDVYSFAIVIMGVLTQKKPPEADENKILHIMVKVKG 243
Qy 241 RPELIPVCRAPRACSHLILMORCWQGDPRVPRPTOEITSEYEDLCEKDDVEKETAHD 300
Db 244 RPELIPVCRAPRACSHLILMORCWQGDPRVPRPTOEITSEYEDLCEKDDVEKETAHD 303
Qy 301 LDVKSPEEPSVVPAPALKRASAPTPNDNYSLELLISQLDSGVSQAVGPEELSRSSSES 360
Db 304 LDVKSPEEPSVVPAPALKRASAPTFPNDNYSLELLISQLDSGVSQAVGPEELSRSSSES 363
Qy 361 KLPSSGSKRLSGVSDSAFSSRGSLSLSPEREPTSDGTTTARRPEEACGCHRVDT 420
Db 364 KLPSSGSKRLSGVSDSAFSSRGSLSLSPEREPTSDGTTTARRPEEACGCHRVDT 423
Qy 421 KLMKILOPQVDLALDSGASLHLAVAGOECAKMLLNANPNLSNRGSTPLHVAVE 480
Db 424 KLMKILOPQVDLALDSGASLHLAVAGOECAKMLLNANPNLSNRGSTPLHVAVE 483
Qy 481 RRVGVVELLARKISVNAKEDQMTALHFAQNGDESSSTRLLLEKASVNEVDFEGRT 540
Db 484 RRVGVVELLARKISVNAKEDQMTALHFAQNGDESSSTRLLLEKASVNEVDFEGRT 543
Qy 541 MHVACQHGQENIVILIRRGDVSLQGDAMLPHYAAMQGHPIVYLLAKQPGSVNAQ 600
Db 544 MHVACQHGQENIVILIRRGDVSLQGDAMLPHYAAMQGHPIVYLLAKQPGSVNAQ 603
Qy 601 TLDRTPHLAAQRGHYVARILIDLCSDVNVCSLLAQTPLVAAETGHTSTARLLHRG 660
Db 604 TLDRTPHLAAQRGHYVARILIDLCSDVNVCSLLAQTPLVAAETGHTSTARLLHRG 663
Qy 661 AGKAVTSDGYTALHAAQNGHATVYKLVBEKADVARGPLNQTALHAAHGHSEVE 720
Db 664 AGKAVTSDGYTALHAAQNGHATVYKLVBEKADVARGPLNQTALHAAHGHSEVE 723
Qy 721 ELVSADVIDLFDDEGLSALHLAAQGRHAQVETILLRGAHINLOSLKFGGHPAATLLR 780
Db 724 ELVSADVIDLFDDEGLSALHLAAQGRHAQVETILLRGAHINLOSLKFGGHPAATLLR 783
Qy 781 RSKT 784
Db 784 RSKT 787
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RESULT 3
US-09-949-016-6974
; Sequence 6974, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6974
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6974
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Query Match 97.5%; Score 3976; DB 4; Length 784;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 769; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
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QY      1 MEGDGTGFWALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHMKWTALAIKCSPLHVD 60
DB      1 MEGDGTGFWALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHMKWTALAIKCSPLHVD 60
QY      61 RERMELEBAKMKEMAKFRYYILPYVGICREBPVGLVMEYMGSELEKILASEPLPMDLRF 120
DB      61 RERMELEBAKMKEMAKFRYYILPYVGICREBPVGLVMEYMGSELEKILASEPLPMDLRF 120
QY      121 IIHETAVGMNFIHCAAPPLHLDLKPANILLDAHNVKISDPGLAKCNGLSHSHDLSMDG 180
DB      121 IIHETAVGMNFIHCAAPPLHLDLKPANILLDAHNVKISDPGLAKCNGLSHSHDLSMDG 180
QY      181 LFGTIAVLPPEIRIREKSRIFDTKHDVYSPAIVGWLTQKKPFADKNIILHMKVYKGH 240
DB      181 LFGTIAVLPPEIRIREKSRIFDTKHDVYSPAIVGWLTQKKPFADKNIILHMKVYKGH 240
QY      241 RPELPVPCRARPRACSHLIRLMORCMQGDPRVPTFOETSETBDLCEKPDDEVETAH 300
DB      241 RPELPVPCRARPRACSHLIRLMORCMQGDPRVPTFOETSETBDLCEKPDDEVETAH 300
QY      301 LDVKSPPPEPRSEVPCARLKRASAPTFDNDYSLSEILLSQDSGVSAVEGPEELSRSSSS 360
DB      301 LDVKSPPPEPRSEVPCARLKRASAPTFDNDYSLSEILLSQDSGVSAVEGPEELSRSSSS 360
QY      361 KLPSSGSGKRLSGVSSVDSAFSSRGSLSIFEREPESTDLGTTTRPPEBEACGCHRVDT 420
DB      361 KLPSSGSGKRLSGVSSVDSAFSSRGSLSIFEREPESTDLGTTTRPPEBEACGCHRVDT 420
QY      421 KLMKTIOPDODVLDLDSGASLHLAVAGQEECAWLLNNANPNLSNRGSTPLHMAVE 480
DB      421 KLMKTIOPDODVLDLDSGASLHLAVAGQEECAWLLNNANPNLSNRGSTPLHMAVE 480
QY      481 BRVRGVVELLARKISVNAKDEDMWTALHFAAONGDESTRLLLEKNAVNEVDFEGR 540
DB      481 BRVRGVVELLARKISVNAKDEDMWTALHFAAONGDESTRLLLEKNAVNEVDFEGR 540
QY      541 MHVACQHQGENIVRILRRGVDSLOGKAMLPPLHYAAWQGHPIYKLLAKOGVSVNAQ 600
DB      541 MHVACQHQGENIVRILRRGVDSLOGKAMLPPLHYAAWQGHPIYKLLAKOGVSVNAQ 600
QY      601 TLDDGRTPLHLAAQGRHYRVARILLIDCSVNVCSLLAQTPLHVAETGHTSTARLLHNG 660
DB      601 TLDDGRTPLHLAAQGRHYRVARILLIDCSVNVCSLLAQTPLHVAETGHTSTARLLHNG 660
QY      661 ACKEATSDGYTALHLAANGHLATVKLVEEKADVLAGPLNQTLHLHAAAGHSEV 720
DB      661 ACKEATSDGYTALHLAANGHLATVKLVEEKADVLAGPLNQTLHLHAAAGHSEV 720
QY      721 ELVSADVIDLFDGQGLSALHLAAQGRHAQTVEITLHGHAINLQSLKFGQGHGPAATLLR 780
DB      721 ELVSADVIDLFDGQGLSALHLAAQGRHAQTVEITLHGHAINLQSLKFGQGHGPAATLLR 780
QY      781 RSKT 784
DB      781 RSKT 784

```

RESULT 4
US-09-509-802-2
; Sequence 2, Application US/09509802
; Patent No. 6489130
; GENERAL INFORMATION:
; APPLICANT: Immunex Corp.
; APPLICANT: Bird, Timothy
; APPLICANT: Witca, G.D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKTRIN REPEATS (DATA)

FILE REFERENCE: 2889-US
; CURRENT APPLICATION NUMBER: US/09/509,802
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent version 3.0
; SEQ ID NO 2

LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-509-802-2

Query Match 89.0%; Score 3628; DB 4; Length 786;
Best Local Similarity 88.9%; Pred. No. 2.86-314;
Matches 699; Conservative 34; Mismatches 51; Indels 2; Gaps 1;

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QY      1 MEGDGTGFWALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHMKWTALAIKCSPLHVD 60
DB      1 MEGDGTGFWALALRTFDAGEFTGMEKVGSGGFGQVYKVRHVHMKWTALAIKCSPLHVD 60
QY      61 RERMELEBAKMKEMAKFRYYILPYVGICREBPVGLVMEYMGSELEKILASEPLPMDLRF 120
DB      61 RERMELEBAKMKEMAKFRYYILPYVGICREBPVGLVMEYMGSELEKILASEPLPMDLRF 120
QY      121 IIHETAVGMNFIHCAAPPLHLDLKPANILLDAHNVKISDPGLAKCNGLSHSHDLSMDG 180
DB      121 IIHETAVGMNFIHCAAPPLHLDLKPANILLDAHNVKISDPGLAKCNGLSHSHDLSMDG 180
QY      181 LFGTIAVLPPEIRIREKSRIFDTKHDVYSPAIVGWLTQKKPFADKNIILHMKVYKGH 240
DB      181 LFGTIAVLPPEIRIREKSRIFDTKHDVYSPAIVGWLTQKKPFADKNIILHMKVYKGH 240
QY      241 RPELPVPCRARPRACSHLIRLMORCMQGDPRVPTFOETSETBDLCEKPDDEVETAH 300
DB      241 RPELPVPCRARPRACSHLIRLMORCMQGDPRVPTFOETSETBDLCEKPDDEVETAH 300
QY      301 LDVKSPPPEPRSEVPCARLKRASAPTFDNDYSLSEILLSQDSGVSAVEGPEELSRSSSS 360
DB      301 LDVKSPPPEPRSEVPCARLKRASAPTFDNDYSLSEILLSQDSGVSAVEGPEELSRSSSS 360
QY      361 KLPSSGSGKRLSGVSSVDSAFSSRGSLSIFEREPESTDLGTTTRPPEBEACGCHRVDT 420
DB      361 KLPSSGSGKRLSGVSSVDSAFSSRGSLSIFEREPESTDLGTTTRPPEBEACGCHRVDT 420
QY      421 KLMKTIOPDODVLDLDSGASLHLAVAGQEECAWLLNNANPNLSNRGSTPLHMAVE 480
DB      421 KLMKTIOPDODVLDLDSGASLHLAVAGQEECAWLLNNANPNLSNRGSTPLHMAVE 480
QY      481 BRVRGVVELLARKISVNAKDEDMWTALHFAAONGDESTRLLLEKNAVNEVDFEGR 540
DB      481 BRVRGVVELLARKISVNAKDEDMWTALHFAAONGDESTRLLLEKNAVNEVDFEGR 540
QY      541 MHVACQHQGENIVRILRRGVDSLOGKAMLPPLHYAAWQGHPIYKLLAKOGVSVNAQ 600
DB      541 MHVACQHQGENIVRILRRGVDSLOGKAMLPPLHYAAWQGHPIYKLLAKOGVSVNAQ 600
QY      601 TLDDGRTPLHLAAQGRHYRVARILLIDCSVNVCSLLAQTPLHVAETGHTSTARLLHNG 660
DB      601 TLDDGRTPLHLAAQGRHYRVARILLIDCSVNVCSLLAQTPLHVAETGHTSTARLLHNG 660
QY      661 ACKEATSDGYTALHLAANGHLATVKLVEEKADVLAGPLNQTLHLHAAAGHSEV 720
DB      661 ACKEATSDGYTALHLAANGHLATVKLVEEKADVLAGPLNQTLHLHAAAGHSEV 720
QY      721 ELVSADVIDLFDGQGLSALHLAAQGRHAQTVEITLHGHAINLQSLKFGQGHGPAATLLR 780
DB      721 ELVSADVIDLFDGQGLSALHLAAQGRHAQTVEITLHGHAINLQSLKFGQGHGPAATLLR 780
QY      781 RSKT 784
DB      781 RSKT 784

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RESULT 5
US-09-188-930-334
; Sequence 334, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna

FILE REFERENCE: 2889-US
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent version 3.0
; SEQ ID NO 2

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? APPLICANT: Sleeman, Matthew
? APPLICANT: Onrust, Rene
? TITLE OF INVENTION: Compositions Isolated From Skin Cells
? TITLE OF INVENTION: and Methods For Their Use
? FILE REFERENCE: 11000.101c1
? CURRENT APPLICATION NUMBER: US/09/188,930A
? CURRENT FILING DATE: 1998-11-09
? NUMBER OF SEQ ID NOS: 348
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 334
? LENGTH: 787
? TYPE: PRT
? ORGANISM: Mouse
? US-09-188-930-334

```

Query Match	88.9%;	Score 3624;	DB 3;	Length 787;
Best Local Similarity	88.8%;	Pred. No. 6,4e-314;		
Matches 698;	Conservative 35;	Mismatches 51;	Indels 2;	Gaps 1;

QY	1	WBGDGTPLAALLRFPDAGEFLPMKVS	CGGGOYKVRHVMKTMIAIKCSPLHYVD	60
Db	2	VEGBGRGRLGLRLTFDAGEFPMKVS	GGGOYKVRHVMKTMIAIKCSPLHYVD	61
QY	61	RRMELLBEAKOMENAKFRYIILPVVGI	CERPVGLVMEWETGSLBKLLASEPLRMDLRF	120
Db	62	RRMELLBEAKOMENAKFRYIILPVVGI	CQEPVGLVMEWETGSLBKLLASEPLRMDLRF	121
QY	121	ITHEFVAGNPLHCAAPPLIHLDLK	ANILLDAHYVKSIDFGLACNGISLHSDISM	180
Db	122	IYHEFVAGNPLHCAAPPLIHLDLK	ANILLDAHYVKSIDFGLACNGISLHSDISM	181
QY	181	LEGTAFLPERIRREKSRPLDTHDIV	YSFAIVMGVLTOKKPEADEKNILIHVMKYVKG	240
Db	182	LEGTAFLPERIRREKSRPLDTHDIV	SPRIYMGVLTOKKPEADEKNILIHVMKYVKG	241
QY	241	RELEPVPCARPRACSHLIRLMORC	WCQDPVRAPTVOETISEEDLCERKDEVEKTAHD	300
Db	242	RELPLPICRRPRACASLIGLMORC	HADPOVAPPTQETISSEEDLCERKDEVEKTAHD	301
QY	301	LDVKSPPERSEVVP--ABUKRASAP	TFPNDVLSLSLSQDSCVSOAVGPEPLSRSS	358
Db	302	PGEKSLERKSERPESSRLKASAP	PFNDSCLSLSLSQDSCVSIQTEGPEPLSRSS	359
QY	359	ESGLPSSGSGKLSGVSYDSAFSS	SGSLSPEREPTSDLTGTRRPEBAQCGCHVRD	418
Db	362	ECKLPSSSGSGKLSGVSYDSAFSS	SGSLSPEREPTSDLTGTRRPEBAQCGCHVRD	421
QY	419	TSKLMKLILOPOVDVLD	SGASILHLAVEGQECVKNLLANNANPNLSNRSGSTPLHMA	478
Db	422	TSRLMKLILOPOVDVLD	SSASILHLAVEGQECVKNLLANNANPNLTVRKSGSTPLHMA	481
QY	479	VERRARGVELLARKISVNAQ	DEDDWTALHPAONGDEBSTILLERKASVNEVDPEGR	538
Db	482	VERKRGVIELLARKISVNAQ	DEDDWTALHPAONGDEBSTILLERKASVNEVDPEGR	541
QY	539	TMFHYAACQHGQENIVYILRR	GVDSLOQKDAWLPHYAAMQSHLPVTKLLAKOPGVSN	598
Db	542	TMFHYAACQHGQENIVYILRR	GVDSLOQKDAWLPHYAAMQSHLPVTKLLAKOPGVSN	601
QY	599	AQTLDGRTPLHLAORGHY	RVARILLDLCSDVNVCSILAQTPHLVAEAETGHTSTARILLH	658
Db	602	AQTLDGRTPLHLAORGHY	RVARILLDLCSDVNVCSILAQTPHLVAEAETGHTSTARILLH	661
QY	659	RGAGKEAVTSDGTALHLA	ANGHLATVKLLVEKADVTARGPLNOTALHLAAHGHSEV	718
Db	662	RGAGKEAVTSDGTALHLA	ANGHLATVKLLVEKADVTARGPLNOTALHLAAHGHSEV	721
QY	719	VEELVSADVTIDFDEG	LSALHLAAGRBAQVETILLBGAHNLINLOSIFKQGGHGAATL	778
Db	722	VEELVSADVTIDFDEG	LSALHLAAGRBSQVETILLBGAHNLINLOSIFKQGGQSSAATL	781
QY	779	LRRSKT	784	

Db 782 LRRSKT 787

```

RESULT 6
US-09-312-283C-334
Sequence 334, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orrant, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated
FROM THE INVENTION: and Methods for Their
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 334
LENGTH: 787
TYPE: FRT
ORGANISM: Mouse
US-09-312-283C-334

```

Query Match	88.9%	Score 3624;	DB 4;	Length 787;
Best Local Similarity	88.8%;	Pred. No. 6.4e-314;		
Matches 698;	Conservative 35;	Mismatches 51;	Indels 2;	Gaps 1

QY	1	MBGDGGT	PMAALLRTFDAGEFTGMEKVGSGGFGQVYKVRHVHKTWLAIKCSPSLHVD	60
		:	:	
Db	2	VEEGCGRMA	LIGLRTFDAGEFAGMEKVGSGGFGQVYKVRHVHKTWLAIKCSPSLHVD	61
QY	61	REEMELLEAK	KQEMAKKPYVILPYVGICREPGVIMBEMETGSLKLIKLAASPLPMDLRF	120
Db	62	REEMELLEAK	KQEMAKKPYVILPYVGICREPGVIMBEMETGSLKLIKLAASPLPMDLRF	121
QY	121	I IHTAVGN	FLHCNAPPLHLDLKPANILLDAHVYKISDPGLAKNGLSHSHDLSMDG	180
		:	:	
Db	122	IYHTAVGN	FLHCNAPPLHLDLKPANILLDAHVYKISDPGLAKNGLSHSHDLSMDG	181
QY	181	LRGTIAYL	PPERIRETSRLFDTRKHVVSFAVYVQVLTQKKPPEDEKNILLIMVKVYKH	240
Db	182	LFGTIAYL	PPERIRETSRLFDTRKHVVSFAVYVQVLTQKKPPEDEKNILLIMVKVYKH	241
QY	241	RPELPRVCAR	PPRACSHLIRLMQRCMQSDPRVRPFOEITSETEDLCEKPDDEKETAHD	300
Db	242	RPELPRVCAR	PPRACSHLIRLMQRCMQSDPRVRPFOEITSETEDLCEKPDDEKETAHD	301
QY	301	LDVKSPPPE	SEVVP--ARLKRAAPFTDNDYSLSSELLSOLDGVSQAVBGPBELSRSS	358
		:	:	
Db	302	PGEKSSLS	EKSSEARPESSRLKRAAPFPFNCCSLSELLSOLDGSGISOTLRGPBELSRSS	361
QY	359	ESLTPSSG	SXRLSGVSVDSAFSSRGSLSLSEFEBSPTSLGTTTRPREEBACGCHVRD	418
Db	362	ECTLPSSG	SXRLSGVSVDSAFSSRGSLSLSEFEBSPTSLGTTTRPREEBACGCHVRD	421
QY	419	TSKILM	ILPOPVDVLDSGASILHLAVBAGOECAKMLLNANNPNLSNRRGSTPLHMA	478
		:	:	
Db	422	TSKILM	ILPOPVDVLDSGASILHLAVBAGOECAKMLLNANNPNLSNRRGSTPLHMA	481
QY	479	VEBRVGV	VELLIARKISVNAQDEQMTALHFAQNGDESTRILLLEKNASVNEVDEGR	538
		:	:	
Db	482	VEBRVGV	VELLIARKISVNAQDEQMTALHFAQNGDESTRILLLEKNASVNEVDEGR	541
QY	539	TPMHWAC	QHQENIYVILIRGVVDSLOGKQAMPLRTHAAQOGLPYVYLAKLOPGSVN	598
Db	542	TPMHWAC	QHQENIYVILIRGVVDSLOGKQAMPLRTHAAQOGLPYVYLAKLOPGSVN	601
QY	599	AQRTDGR	TPHLAAQGRHVVARILLDCSDVNNCSLLAQTPHLVAETGHTSTARLLH	658

DB 602 AOTLGRTPHLAARGHRAVRIILIDCSOVNICSLOAQTPHLAAETGHTSTRLILH 661
QY 659 RGAGKAVTSDGYTALHLAARNGHLATVTLVEEKADVLARGLNQTALHLAAHGHSEV 718
DB 662 RGAGKAVTSDGYTALHLAARNGHLATVTLVEEKADVLARGLNQTALHLAAHGHSEV 721
QY 719 VEELVSADVIDLFDQGSALHLAAQGRHQAQVEFTLHNGAHINQSLKFGQSGHGPATL 778
DB 722 VEELVSADVIDLFDQGSALHLAAQGRHQAQVEFTLHNGAHINQSLKFGQSGHGPATL 781
QY 779 LRRSKT 784
DB 782 LRRSKT 787

RESULT 7

US-09-312-283C-409
Sequence 409, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Muirson, James G.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 409
LENGTH: 590
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-409

Query Match 66.0%; Score 2691; DB 4; Length 590;
Best Local Similarity 87.3%; Pred. No. 6e-231;
Matches 514; Conservative 27; Mismatches 46; Indels 2; Gaps 1;

QY 1 MEGDGGTPWALALRTFDAGBFTGMEKVGSGFGQVYKVRHVHMTWLAIKCSPSLHVD 60
DB 2 VEGEGRGWALGLRTFDAGBFTGMEKVGSGFGQVYKVRHVHMTWLAIKCSPSLHVD 61
QY 61 RERMEILBEAKKEMAKFRYILPVYGCIBPVGVLVMEYMETGSLKTLASBPLPMDLRR 120
DB 62 RERMEILBEAKKEMAKFRYILPVYGCIBPVGVLVMEYMETGSLKTLASBPLPMDLRR 121
QY 121 ITHETAVGNFPLHCMAPELLHDLKPANILLDAHYVKISDFGLAKCNGLSHSHDLSMD 180
DB 122 ITHETAVGNFPLHCMAPELLHDLKPANILLDAHYVKISDFGLAKCNGLSHSHDLSMD 181
QY 181 LFTGIAYLPPERIREKSRLEFDTKHDVYSFAIVMGVLTOKKPPADEKNILHIMKVVYK 240
DB 182 LFTGIAYLPPERIREKSRLEFDTKHDVYSFAIVMGVLTOKKPPADEKNILHIMKVVYK 241
QY 241 RPELPVPCRRAPRACSHLIRLMORCMQGDPRVPTPOBITSETEDCEKPDDEVKETA 300
DB 242 RPELPVPCRRAPRACSHLIRLMORCMQGDPRVPTPOBITSETEDCEKPDDEVKETA 301
QY 301 LDVKSPPPEPRSEVVP--ARLKRASAPTFDNDYSLSELSQLDSGVSAVGEPELSRSS 358
DB 302 PGKSSLSLEKSKERAPSSRLKRAAPFPDNDCSLSLSQDSGICITLEGPELSRSS 361
QY 359 BSRLPSSSGSKRLSGVSVDSAFSSRGSLSLSEFEREPSTSDLGTTTRPEBEACGCHRV 418
DB 362 BSRLPSSSGSKRLSGVSVDSAFSSRGSLSLSEFEREPSTSDLGTTTRPEBEACGCHRV 421
QY 419 TSKLMKTILOQDVLDLSDGASLHLAAVBAQGECAKMLLNANPNLNSRSGSTFLHMA 478

DB 422 TSKLMKTILOQDVLDLSDGASLHLAAVBAQGECAKMLLNANPNLNSRSGSTFLHMA 481
QY 479 VERKRGVVELLARKISVNAKDEQWTALHFAQNDDESTRLLKKNASVNVDFEGR 538
DB 482 VERKRGVVELLARKISVNAKDEQWTALHFAQNDDESTRLLKKNASVNVDFEGR 541
QY 539 TPMHVACQHQENTIVRILRRGVDSLOGKDAWPLTHYAAQGHLPYK 587
DB 542 TPMHVACQHQENTIVRILRRGVDSLOGKDAWPLTHYAAQGHLPYK 590

RESULT 8

US-09-188-930-185
Sequence 185, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Muirson, James Greg
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 185
LENGTH: 536
TYPE: PRT
ORGANISM: mouse
US-09-188-930-185

Query Match 55.6%; Score 2269; DB 3; Length 536;
Best Local Similarity 84.1%; Pred. No. 2.1e-193;
Matches 438; Conservative 29; Mismatches 50; Indels 4; Gaps 3;

QY 1 MEGDGGTPWALALRTFDAGBFTGMEKVGSGFGQVYKVRHVHMTWLAIKCSPSLHVD 60
DB 2 VEGEGRGWALGLRTFDAGBFTGMEKVGSGFGQVYKVRHVHMTWLAIKCSPSLHVD 61
QY 61 RERMEILBEAKKEMAKFRYILPVYGCIBPVGVLVMEYMETGSLKTLASBPLPMDLRR 120
DB 62 RERMEILBEAKKEMAKFRYILPVYGCIBPVGVLVMEYMETGSLKTLASBPLPMDLRR 121
QY 121 ITHETAVGNFPLHCMAPELLHDLKPANILLDAHYV-KISDFGLAKCNGLSHSHDLSMD 179
DB 122 ITHETAVGNFPLHCMAPELLHDLKPANILLDAHYV-KISDFGLAKCNGLSHSHDLSMD 181
QY 180 GLFTGIAYLPPERIREKSRLEFDTKHDVYSFAIVMGVLTOKKPPADEKNILHIMKVVYK 239
DB 182 GLFTGIAYLPPERIREKSRLEFDTKHDVYSFAIVMGVLTOKKPPADEKNILHIMKVVYK 241
QY 240 HRPPLPVCRRAPRACSHLIRLMORCMQGDPRVPTPOBITSETEDCEKPDDEVKETA 299
DB 242 HRPPLPVCRRAPRACSHLIRLMORCMQGDPRVPTPOBITSETEDCEKPDDEVKETA 301
QY 300 DLDVKSPPPEPRSEVVP--ARLKRASAPTFDNDYSLSELSQLDSGV-SQAVGEPELSRS 356
DB 302 EGRGSSLSLEKSKERAPSSRLKRAAPFPDNDCSLSLSQDSGICITLEGPELSRS 361
QY 357 SSESRLPSSSGSKRLSGVSVDSAFSSRGSLSLSEFEREPSTSDLGTTTRPEBEACGCHRV 416
DB 362 SSESRLPSSSGSKRLSGVSVDSAFSSRGSLSLSEFEREPSTSDLGTTTRPEBEACGCHRV 421
QY 417 RPSKLMKTILOQDVLDLSDGASLHLAAVBAQGECAKMLLNANPNLNSRSGSTFLHMA 476
DB 422 RPSKLMKTILOQDVLDLSDGASLHLAAVBAQGECAKMLLNANPNLNSRSGSTFLHMA 481
QY 477 MAYERVRGVVELLARKISVNAKDEQWTALHFAQNDDESTRLLKKNASVNVDFEGR 517

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Dp                               482  MAVERKGRIVELLARTKTSVNAKDEDMTALHPAQNQDE 522

RESULT 9
US-09-312-283C-185
; Sequence 185, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-185

```

Query Match	55.6%;	Score 2269;	DB 4;	Length 536;
Best Local Similarity	84.1%;	Pred. No. 2.1e-193;		
Matches 438;	Conservative 29;	Mismatches 50;	Indels 4;	Gaps 3;

```

QY      NEGDDGTAPALLALTRFDGDFGFMGEKVSGGGQYKVRHMYKMTWLAIKCPSLHYDD 60
:|:|:|
2  VEGBERGRNALGLTRTFDNGEFGAMEKVSGGGQYKVRHMYKMTWLAIKCPSLHYDD 61
Dd
QY      61 RERMELLEBAKCKEMAKFRYILPVYGI CEEPVGLVMEYMETGSLLEKLASEPLPMDLRR 120
:|:|:|
Dd      62 RERMELLEBAKCKEMAKFRYILPVYGI COEPVGLVMEYMETGSLLEKLASEPLPMDLRR 121
QY      121 IITHETAVGNMFLHOMAPLILHLDLKANTILLDHAYHV -KISDGLKACNGLSHSHLSMD 179
:|:|:|
Dd      122 IYHETAVGNMFLHOMASPPLHLHDLKANTILLDHAYOMSERLDPGLKACNGMSHSHLSMD 181
QY      180 GLFGTIAVLPERRIRREKSLPDTKHDVYSFAIYIMVGLTQKKEPADEKNIILHMYEVYKG 239
Dd      182 GLFGTIGVLPERRIRREKSLPDTKHDVYSFAIYIMVGLTONNFEPADEKNIILHMYEVYKG 241
QY      240 HRPHELPRVOCARPRACSHILRLMORQWQODPRRPRFOETSTETEDLCEKPDDEVKETHA 259
Dd      242 HRPHELPRICRPRRACASLIGLMORCMWADPOVRPRFOETSTETEDLCEKPDDEVKOLAH 301
QY      300 DLDVVSPEPRSEEVVP -ARLKASAPRTEPDNDVLSBELLSQDLSGV -SQAVEBPEELSSRS 356
Dd      302 EBGKSSLSLEKSEARPESSRLKRAASAPRFDNDCSLSBELLSQDLSGIFPRLLKPEELSSRS 361
QY      357 SSESKLPPSSGSKRLSGVSSVDSAPSSRSGLSLSFREPSTSLGTTTRPREBAACGCHV 416
Dd      362 SBECKLPSSSGRRLSGVSSVDSAPSSRSGLSLSFREPASTGDLGPDTIQKKLVDAIIS 421
QY      417 ROTSXLMKLIQPOVDVLALDSCASLIHLAVEAQOECAKWLILNANPNLNNRSGTPLLH 476
Dd      422 GQTSRLMKLIQPOVDVLVDDSSLSLHLAVEAQOECYKWLILNANPNLNNRSGTPLLH 481
QY      477 MAVERVRGVVBILLARKISVNAKEDDONTALHPAANGDE 517
Dd      482 MAVERGRGIVELLARKTSVNAKEDDONTALHPAANGDE 522

```

RESULT 10
US-09-069-023-3
; Sequence 3, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:

```

? APPLICANT: Nunez, Gabriel
? APPLICANT: Inohara, Naohiro
? APPLICANT: Koseki, Takeyoshi
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
? TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
? FILE REFERENCE: UM-0333
? CURRENT APPLICATION NUMBER: US/09/069,023A
? CURRENT FILING DATE: 1998-04-27
? NUMBER OF SEQ ID NOS: 38
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 3
? LENGTH: 530
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-069-023-3

Query Match      13.4%   Score 545;   DB 3;   Length 530;
Best Local Similarity 33.3%   Pred. No. 9.9e-40;
Matches 150; Conservative 59; Mismatches 123; Indels 118; Gaps 177.

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Query Match	13.4%	Score 545	DB 3	Length 530
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Best Local Similarity 33.3%; Pred. No. 9.9e-40;
Matches 150; Conservative 59; Mismatches 123; Indels 118; Gaps 17;

```

QY      8 PAA|A|L|T|T|P|D|A|G|E|F|T|G|K|V|G|G|V|Q|V|V|V|H|V|H|V|H|V|H|T|V|A|L|C|S|P|S|L|H|V|D|-----|D|R|R 63
Db      5 P|Y|K|A|D|R|-----|Y|S|R|G|A|S|G|I|V|S|A|R|H|A|D|R|V|O|V|A|V|K|-----|M|H|I|H|P|L|D|S|R 50
QY      64 M|E|L|E|A|K|K|O|K|E|A|K|P|R|Y|I|L|P|V|G|I|C|R|E|P|-----|V|G|V|H|V|E|N|E|T|S|L|E|K|L|A|S|-----|P|L|P|W|L 117
Db      51 K|O|V|R|E|H|E|L|H|R|K|R|F|S|Y|I|P|I|G|I|C|N|E|P|E|P|G|I|V|E|T|W|P|N|G|S|L|N|E|L|H|R|K|E|Y|P|D|V|A|W|L 110
QY      118 R|F|R|I|H|E|T|A|V|G|A|N|F|L|H|C|A|P|R|H|L|H|D|L|K|R|A|N|I|L|D|A|H|H|V|K|I|S|P|F|L|A|K|N|G|S|H|S|H|D|S 177
Db      111 R|F|R|I|H|E|I|M|A|G|V|U|Y|I|N|N|M|P|R|L|H|H|D|L|T|O|N|I|L|D|N|E|R|H|V|K|I|A|F|G|S|K|R|H|H|S|S|R|S 170
QY      178 M|-----|O|G|L|F|C|T|A|Y|L|P|R|E|R|I|-----|E|K|S|R|L|F|D|T|G|H|D|V|S|F|A|I|Y|I|W|O|V|L|T|O|K|K|F|A|D|E|K|I|L|H 231
Db      171 S|K|A|P|E|S|-----|G|T|I|T|W|P|E|N|Y|E|P|G|Q|S|R|A|-----|S|I|K|H|D|Y|S|A|V|I|T|W|E|V|L|S|R|K|Q|P|E|D|V|N|P|L|Q 227
QY      232 I|W|K|V|V|K|G|R|P|-----|E|L|P|V|C|R|A|P|R|A|C|S|H|I|I|R|M|O|R|C|W|O|G|D|R|P|R|V|R|P|T|O|E|I|T|S|E|T|L 286
Db      228 I|W|S|V|S|Q|H|R|P|V|N|E|S|L|P|Y|D|I|R|H|R|A|-----|M|I|S|I|E|B|G|M|A|Q|N|D|E|R|P|S|F|K|L|E|I|E|P|V 283
QY      287 C|E|R|P|D|E|V|E|T|A|H|D|L|V|K|S|P|R|P|R|E|B|V|P|R|A|L|K|R|A|S|A|T|P|F|N|D|V|S|L|S|E|L|I|S|O|L|D|S|G|V|S|A 346
Db      284 L|R|-----|T|E|E|T|L|E|A|V|Q|L|-----|T|E|E|T|L|E|A|V|Q|L|-----|T|E|E|T|L|E|A|V|Q|L|-----|T|E|E|T|L|E|A|V|Q|L 299
QY      347 V|E|G|B|E|L|S|R|S|S|E|S|K|L|P|S|S|G|S|G|R|L|S|G|V|S|Y|D|A|F|S|R|G|S|L|S|P|R|E|R|P|S|T|D|L|G|T|R|R|P 406
Db      300 -----|K|T|K|Q|S|V|S|A|H|I|H|C|D|K|K|H|E|-----|L|S|L|-----|N|I|P|V|H|G|P 3311
QY      407 E|E|R|A|C|G|C|H|R|V|D|T|S|-----|K|L|K|I|L|O|P|O|V|D 432
Db      332 Q|E|R|C|G|S|S|O|L|H|E|N|S|G|P|E|T|R|S|E|L|P|A|P|O|N|D 361

```

RESULT 11
US-09-069-023-1

```

: Sequence 1 Application US/09069023A
: Patent No. 6348573
:
: GENERAL INFORMATION:
: APPLICANT: Nunez, Gabriel
: APPLICANT: Inohara, Naohiro
: APPLICANT: Koseki, Takeyoshi
:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
:
: TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
:
: FILE REFERENCE: UM-03333
:
: CURRENT APPLICATION NUMBER: US/09/069,023A
:
: CURRENT FILING DATE: 1998-04-27
:
: NUMBER OF SEQ ID NOS: 38
:
: SOFTWARE: PatentIn Ver. 2.0

```

```

; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-1

```

Query Match 13.3%; Score 541.5; DB 3; Length 531;
Best Local Similarity 34.0%; Pred. No. 26-39;
Matches 145; Conservative 57; Mismatches 118; Indels 107; Gaps 16;

```
QY 31 GGFQGVYKVRHVMKWTWAIKCSPLHYD---DREKMLLEBAKMEAKFRYLLPYVG 86
DB 18 GASGVSSARRHADMRVQAVK---HLHHTPLDSEKQDVLEAEILHKARFSYLLPIIG 74
QY 87 ICRBP--VGLVMEYMETGSLSEKLASE---PLPMDLRFRIIHTAVGMFLHCAAPLL 140
DB 75 ICNBEPLGIVTEYVPMNSLNEILHRKTEYPDVAMPLEFRILHEIALGVNYLHNTPTPL 134
QY 141 HLDLKPANILLDAHNYKISDGLAKCNGLSHSHDLMS---DGLFGTAVLPPERIR-- 194
DB 135 HHDLKTQNTILLDNEFVKIADFGLSKWRMMSLSQSRSSKAPDG--GTLIYMPENYBERG 192
QY 195 EKSRLPDTKHDVYSFAIYWGVLTKCKPFADEKNILHIMVYVKGHRP-----ELPPYCR 249
DB 193 QKSRRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVQGRFVINEESLPYDIP 251
QY 250 APPRACSHLIRIMORCMQDPRVRPTFOEITSETEDLCEKPDDEVKETAHDLVDVSPREP 309
DB 252 HHRAR---MISLIESGMQNPDPERPSFLKCLIELEPVLR----- 286
QY 310 RSEVVPARLKASAPTFEDNDYLSLELSQLDSGVSAQVGEPELRSSESSESLPSSGSGK 369
DB 287 -----TFE-EITFLEAVIQL-----KTKLQSVSSAI 312
QY 370 RLSGVSVDSAFSSRSGSLSFEREPTSDLGTTTREPBEACGCHRVDTG---KLMTI 425
DB 313 HLCDDKKQME-----LSL-----NIPVNHGPQEBSSGSQLHENSGETSRSL 355
QY 426 LQPODVD 432
DB 356 PAPQDND 362
```

RESULT 12

US-09-019-942-1
Sequence 1, Application US/09019942

Patent No. 6033855
GENERAL INFORMATION:
APPLICANT: Berlin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-019-942-1

Query Match 13.3%; Score 541.5; DB 3; Length 540;
Best Local Similarity 34.0%; Pred. No. 2,1e-39;
Matches 145; Conservative 57; Mismatches 118; Indels 107; Gaps 16;

```
QY 31 GGFQGVYKVRHVMKWTWAIKCSPLHYD---DREKMLLEBAKMEAKFRYLLPYVG 86
DB 27 GASGVSSARRHADMRVQAVK---HLHHTPLDSEKQDVLEAEILHKARFSYLLPIIG 83
QY 87 ICRBP--VGLVMEYMETGSLSEKLASE---PLPMDLRFRIIHTAVGMFLHCAAPLL 140
DB 84 ICNBEPLGIVTEYVPMNSLNEILHRKTEYPDVAMPLEFRILHEIALGVNYLHNTPTPL 143
QY 141 HLDLKPANILLDAHNYKISDGLAKCNGLSHSHDLMS---DGLFGTAVLPPERIR-- 194
DB 144 HHDLKTQNTILLDNEFVKIADFGLSKWRMMSLSQSRSSKAPDG--GTLIYMPENYBERG 201
QY 195 EKSRLPDTKHDVYSFAIYWGVLTKCKPFADEKNILHIMVYVKGHRP-----ELPPYCR 249
DB 202 QKSRRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVQGRFVINEESLPYDIP 260
QY 250 APPRACSHLIRIMORCMQDPRVRPTFOEITSETEDLCEKPDDEVKETAHDLVDVSPREP 309
DB 261 HHRAR---MISLIESGMQNPDPERPSFLKCLIELEPVLR----- 295
QY 310 RSEVVPARLKASAPTFEDNDYLSLELSQLDSGVSAQVGEPELRSSESSESLPSSGSGK 369
DB 296 -----TFE-EITFLEAVIQL-----KTKLQSVSSAI 321
QY 370 RLSGVSVDSAFSSRSGSLSFEREPTSDLGTTTREPBEACGCHRVDTG---KLMTI 425
DB 322 HLCDDKKQME-----LSL-----NIPVNHGPQEBSSGSQLHENSGETSRSL 364
QY 426 LQPODVD 432
DB 365 PAPQDND 371
```

RESULT 13

US-09-099-041A-2
Sequence 2, Application US/09099041A

Patent No. 6340576
GENERAL INFORMATION:
APPLICANT: Berlin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-099-041A-2

Query Match 13.3%; Score 541.5; DB 3; Length 540;
Best Local Similarity 34.0%; Pred. No. 2,1e-39;
Matches 145; Conservative 57; Mismatches 118; Indels 107; Gaps 16;

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QY 31 GGFQGVYKVRHVMKWTWAIKCSPLHYD---DREKMLLEBAKMEAKFRYLLPYVG 86
DB 27 GASGVSSARRHADMRVQAVK---HLHHTPLDSEKQDVLEAEILHKARFSYLLPIIG 83
```

QY ICRBP--VGLVMEYMETGSEKLEKLASE-----PLPMDLRFRIIHTAVGMNFIHGMAPPRL 140
DB ICNEPEFGLIVTEYMPNGSLNELHRTKTEYDPVAMPFLRIHIEALGVNLIHNTPL 143
QY 141 HLDLKPANILIDAHYHVKISDFGLAKCNGLSHSHDLSM-----DGLFTIAYLPPERIR-- 194
DB 144 HHDLTQNIILIDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEG--GTIIYMPENYEPG 201
QY 195 EKSLRFTKHDVYSFAIYIWGVLTOKKPPADEKNILHIMVKKVKGHRP-----ELPPYCR 249
DB 202 QKSRRA-SIKHDIYSVAIYIWEVLSKQPFEDVTNPLQIMYSVSGHREVINEESSLPYDIP 260
QY 250 ARPACSHLIRLMRCMQGDPFRVPTFOBITSETEDLCEKPDDEVKETAHDLVDVKSPPRP 309
DB 261 HRAR-----MISLIESGMAQNDEPERSFLKCLIELEPVLR----- 295
QY 310 RSEVVPARLKRASAPTFDNDYLSLSLSQLDSGVSAQAVEGEBELSRSSSESKLPSSGSGK 369
DB 296 -----TFE-BITFLEAVIQL-----KTKIKQSVSSAI 321
QY 370 RLSGVSSVDSAFSSRGSLSTSFEREPTSDLGTTTREPBEACGCHRYDTS---KLMKI 425
DB 322 HLCCKKKME-----LSL-----NIPVNHGPQEBSCSSQLHENSGBPETSRL 364
QY 426 LQPDVD 432
DB 365 PAPQDND 371

RESULT 14

US-09-069-023-27
; Sequence 27, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: US-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 27
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-27

Query Match 13.3%; Score 541.5; DB 3; Length 540;
Best Local Similarity 34.0%; Pred. No. 2.1e-39;
Matches 145; Conservative 57; Mismatches 118; Indels 107; Gaps 16;

QY 31 GSGFGVYKVRHVHMKTWLAIKCPSLHYD---DERMELLEBAKMEMAKRYILPYVG 86
DB 27 GASGTSSARADNRGVAVK--HLHIHTPLDSEKQVLRKAEILHKARFSTYILPLG 83
QY 87 ICRBP--VGLVMEYMETGSEKLEKLASE-----PLPMDLRFRIIHTAVGMNFIHGMAPPRL 140
DB 84 ICNEPEFGLIVTEYMPNGSLNELHRTKTEYDPVAMPFLRIHIEALGVNLIHNTPL 143
QY 141 HLDLKPANILIDAHYHVKISDFGLAKCNGLSHSHDLSM-----DGLFTIAYLPPERIR-- 194
DB 144 HHDLTQNIILIDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEG--GTIIYMPENYEPG 201
QY 195 EKSLRFTKHDVYSFAIYIWGVLTOKKPPADEKNILHIMVKKVKGHRP-----ELPPYCR 249
DB 202 QKSRRA-SIKHDIYSVAIYIWEVLSKQPFEDVTNPLQIMYSVSGHREVINEESSLPYDIP 260
QY 250 ARPACSHLIRLMRCMQGDPFRVPTFOBITSETEDLCEKPDDEVKETAHDLVDVKSPPRP 309

DB 261 HRAR-----MISLIESGMAQNDEPERSFLKCLIELEPVLR----- 295
QY 310 RSEVVPARLKRASAPTFDNDYLSLSLSQLDSGVSAQAVEGEBELSRSSSESKLPSSGSGK 369
DB 296 -----TFE-BITFLEAVIQL-----KTKIKQSVSSAI 321
QY 370 RLSGVSSVDSAFSSRGSLSTSFEREPTSDLGTTTREPBEACGCHRYDTS---KLMKI 425
DB 322 HLCCKKKME-----LSL-----NIPVNHGPQEBSCSSQLHENSGBPETSRL 364
QY 426 LQPDVD 432
DB 365 PAPQDND 371

RESULT 15

US-09-245-281-2
; Sequence 2, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; EARLIER FILING DATE: 1999-02-05
; EARLIER FILING DATE: 1998-12-08
; EARLIER FILING DATE: 1998-06-17
; EARLIER FILING DATE: 1998-06-17
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-2

Query Match 13.3%; Score 541.5; DB 3; Length 540;
Best Local Similarity 34.0%; Pred. No. 2.1e-39;
Matches 145; Conservative 57; Mismatches 118; Indels 107; Gaps 16;

QY 31 GSGFGVYKVRHVHMKTWLAIKCPSLHYD---DERMELLEBAKMEMAKRYILPYVG 86
DB 27 GASGTSSARADNRGVAVK--HLHIHTPLDSEKQVLRKAEILHKARFSTYILPLG 83
QY 87 ICRBP--VGLVMEYMETGSEKLEKLASE-----PLPMDLRFRIIHTAVGMNFIHGMAPPRL 140
DB 84 ICNEPEFGLIVTEYMPNGSLNELHRTKTEYDPVAMPFLRIHIEALGVNLIHNTPL 143
QY 141 HLDLKPANILIDAHYHVKISDFGLAKCNGLSHSHDLSM-----DGLFTIAYLPPERIR-- 194
DB 144 HHDLTQNIILIDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEG--GTIIYMPENYEPG 201
QY 195 EKSLRFTKHDVYSFAIYIWGVLTOKKPPADEKNILHIMVKKVKGHRP-----ELPPYCR 249
DB 202 QKSRRA-SIKHDIYSVAIYIWEVLSKQPFEDVTNPLQIMYSVSGHREVINEESSLPYDIP 260
QY 250 ARPACSHLIRLMRCMQGDPFRVPTFOBITSETEDLCEKPDDEVKETAHDLVDVKSPPRP 309
DB 261 HRAR-----MISLIESGMAQNDEPERSFLKCLIELEPVLR----- 295
QY 310 RSEVVPARLKRASAPTFDNDYLSLSLSQLDSGVSAQAVEGEBELSRSSSESKLPSSGSGK 369
DB 296 -----TFE-BITFLEAVIQL-----KTKIKQSVSSAI 321
QY 370 RLSGVSSVDSAFSSRGSLSTSFEREPTSDLGTTTREPBEACGCHRYDTS---KLMKI 425
DB 322 HLCCKKKME-----LSL-----NIPVNHGPQEBSCSSQLHENSGBPETSRL 364
QY 426 LQPDVD 432

|||
Db 365 PAPQDND 371

Search completed: September 17, 2005, 06:44:08
Job time : 1216.92 secs

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OM protein - protein search, using sw model

Run on: September 16, 2005, 07:27:24; Search time 208.039 Seconds
(without alignments)
1929.780 Million cell updates/sec

Title: US-10-658-904-2

Perfect score: 4078
Sequence: 1 MEGDGGTPTWALALRTFPDAG.....SLKFGGHCAPATILRRSKT 784

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_spprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3976	97.5	784	2	Q9H4D1	Q9h4d1 homo sapien
2	3959	97.1	784	2	Q96FT1	Q96ft1 homo sapien
3	3943	96.7	832	1	R1K4_HUMAN	P57078 homo sapien
4	3628	89.0	786	2	Q9ERK0	Q9erko mus musculu
5	2541	62.3	720	2	Q7ZYM2	Q7zym2 xenopus lae
6	2514.5	61.7	719	2	Q6GPN2	Q6gpn2 xenopus lae
7	2389.5	58.6	820	2	Q8UH03	Q8juh3 brachydanto
8	1881	46.1	387	2	Q9NTA1	Q9nta1 homo sapien
9	1215.5	29.8	755	2	Q8NFD2	Q8nfd2 homo sapien
10	1196.5	29.3	352	2	Q8NFD2	Q8nfd2 homo sapien
11	1141.5	28.0	745	2	Q8BZ25	Q8bz25 m mus muscu
12	566	14.0	594	2	Q8JHU4	Q8jhu4 brachydanto
13	545.5	13.4	539	1	R1K2_MOUSE	P58801 mus musculu
14	541.5	13.3	540	1	R1K2_HUMAN	Q43353 h receptor-
15	541	13.3	1549	2	Q9VAB1	Q9vab1 drosophila
16	540	13.2	1549	2	Q24241	Q24241 drosophila
17	515	12.6	1136	2	Q9N180	Q9n180 bos taurus
18	514	12.6	1159	2	Q9NCP8	Q9ncp8 drosophila
19	514	12.6	1571	2	Q7KVS2	Q7kvs2 drosophila
20	513.5	12.6	1726	2	Q8VC68	Q8vc68 mus musculu
21	513.5	12.6	1943	2	Q61307	Q61307 rat mus muscu
22	512.5	12.6	2622	2	Q70511	Q70511 rattus norv
23	509.5	12.5	1887	2	Q7Z3G4	Q7z3g4 homo sapien
24	509.5	12.5	4377	1	ANK3_HUMAN	Q12955 homo sapien
25	505	12.4	1004	2	Q7JUNZ0	Q7jun0 caenorhabdi
26	505	12.4	1786	2	Q17344	Q17344 caenorhabdi
27	505	12.4	1809	2	Q17487	Q17487 caenorhabdi
28	505	12.4	1815	2	Q17488	Q17488 caenorhabdi
29	505	12.4	1841	2	Q8MGO0	Q8mg00 caenorhabdi
30	505	12.4	1867	2	Q17486	Q17486 caenorhabdi
31	505	12.4	2039	2	Q17489	Q17489 caenorhabdi

32	505	12.4	6994	2	Q17343	Q17343 caenorhabdi
33	505	12.4	6994	2	Q17490	Q17490 caenorhabdi
34	502	12.3	1145	2	Q7PE28	Q7pez8 anopheles g
35	502	12.3	1501	2	Q7OKD3	Q7okd3 anopheles g
36	500.5	12.3	792	2	Q7Q172	Q7q172 anopheles g
37	500	12.3	1719	2	Q13768	Q13768 homo sapien
38	500	12.3	1856	2	Q99407	Q99407 homo sapien
39	500	12.3	1880	1	ANK1_HUMAN	P16157 homo sapien
40	499.5	12.2	1848	2	Q61302	Q61302 mus musculu
41	499.5	12.2	1862	2	ANK1_MOUSE	Q02357 mus musculu
42	485.5	11.9	1762	2	Q88521	Q88521 rattus norv
43	484.5	11.9	3924	1	ANK2_HUMAN	Q01484 homo sapien
44	483.5	11.9	1088	2	Q13484	Q13484 homo sapien
45	483	11.8	1427	2	Q6DDZ1	Q6ddz1 xenopus lae

ALIGNMENTS

RESULT 1	ID	PRELIMINARY	PRT	784 AA.
AC Q9H4D1				
DT 01-MAR-2001 (TREMBlrel. 16, Created)				
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)				
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)				
GN Protein Kinase.				
DE Name=dk;				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX NCBI_Taxid=9606;				
RN [1]				
RP SEQUENCE FROM N.A. Pubmed=10948194; DOI=10.1074/jbc.M004771200;				
RX MEDLINE=20549657; Pubmed=10948194; DOI=10.1074/jbc.M004771200;				
RA Baehr C., Rohrer A., Stempke L., Rincke G., Marks F., Gschwendt M.;				
RT "Dik, a novel protein kinase that interacts with protein kinase				
RT Cdelta. Cloning, characterization, and gene analysis."				
RT J. Biol. Chem. 275:36350-36357(2000).				
CC -1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.				
DR EMBL; AJ278016; CAC04247.1; -				
DR HSSP; Q60778; 10Y3.				
DR GO; GO:0005524; F:ATP binding; NAs.				
DR GO; GO:0005515; F:protein binding; IPI.				
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.				
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.				
DR InterPro; IPR002110; ANK.				
DR InterPro; IPR011009; Kinase like.				
DR InterPro; IPR001969; Pept_Asp_AS.				
DR InterPro; IPR000719; Prot_Kinase.				
DR InterPro; IPR008271; Ser_Thr_kin_AS.				
DR InterPro; IPR001245; Tyr_kinase.				
DR Pfam; PF00023; Ank; 10.				
DR Pfam; PF00069; Pkinase; 1.				
DR PRINTS; PR01415; ANKYRIN.				
DR PRINTS; PR01109; TYRKINASE.				
DR ProDom; PD000001; Prot_Kinase; 1.				
DR SMART; SM00248; ANK; 10.				
DR PROSITE; PS50088; ANK_REPEAT; 9.				
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.				
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.				
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.				
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.				
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.				
KW ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;				
KW Transference.				
SO SEQUENCE 784 AA; 86407 MW; F3C7D5D52A35AF91 CRC64;				
Query Match	97.5%	Score 3976;	DB 2;	Length 784;
Best Local Similarity	98.1%	Pred. No. 2e-202;		
Matches 769;	Conservative 4;	Mismatches 11;	Indels 0;	Gaps 0;
QY 1	MEGDGGTPTWALALRTFPDAGFTGWEKVGSGFGGVYKRVHVMKTLAIKCSPLHYDD	60		

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Db      1 MEGDGGTTPWALALRTDPAGETGEMKVGSGGFGQVYKVRHVHAKTWLAIKCSPLHADD 60
Qy      61 RERMELLEBAKKEMAKFRYYILPYVGI CREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
Db      61 RERMELLEBAKKEMAKFRYYILPYVGI CREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
Qy      121 IIFHTAVGMNPLHCAAPPLHLDLKPANILLDAHVHVKISDFGLAKCNGLSHSDLSMDG 180
Db      121 IIFHTAVGMNPLHCAAPPLHLDLKPANILLDAHVHVKISDFGLAKCNGLSHSDLSMDG 180
Qy      181 LFGTAYLPERPERIRKRSLEFDTKHVDVSFAIYIMGVLTQCKEFADEKRIILHIMVXVGH 240
Db      181 LFGTAYLPERPERIRKRSLEFDTKHVDVSFAIYIMGVLTQCKEFADEKRIILHIMVXVGH 240
Qy      241 RPELPVCRARBRACSHLIRLMQRCWQDPRVRPTFOBITSETEDLCCKPDDEVETAMD 300
Db      241 RPELPVCRARBRACSHLIRLMQRCWQDPRVRPTFOBITSETEDLCCKPDDEVETAMD 300
Qy      301 LDVKSPPPRSRVAVARLKRAAPFPNDYSLSELSSQDGSVGVQAVGPEELSSSSSS 360
Db      301 LDVKSPPPRSRVAVARLKRAAPFPNDYSLSELSSQDGSVGVQAVGPEELSSSSSS 360
Qy      361 KLPSSGSGKRLSGVSVDSAFSSRGSLSLSPFEREPSTDLGTTTAPPEEACGCHRVDP 420
Db      361 KLPSSGSGKRLSGVSVDSAFSSRGSLSLSPFEREPSTDLGTTTAPPEEACGCHRVDP 420
Qy      421 KLMKTLQPOVDLALDSGASLIHLAVEAQECACWLLNNANPNLSNRSGSTPLHMAVE 480
Db      421 KLMKTLQPOVDLALDSGASLIHLAVEAQECACWLLNNANPNLSNRSGSTPLHMAVE 480
Qy      481 BRVRGVVELLARKI SVNAKDEQMTALHFAQNDDESTRLLLEKNASVNEVDEEGTP 540
Db      481 BRVRGVVELLARKI SVNAKDEQMTALHFAQNDDESTRLLLEKNASVNEVDEEGTP 540
Qy      541 RRVKRVVELLARKI SVNAKDEQMTALHFAQNDDESTRLLLEKNASVNEVDEEGTP 540
Db      541 RRVKRVVELLARKI SVNAKDEQMTALHFAQNDDESTRLLLEKNASVNEVDEEGTP 540
Qy      541 MNAVCOHOGENIVRILIRGVDSVLSQKQDAMLPLHYAAMOGHLPIVKLLAKOPGVVNAQ 600
Db      541 MNAVCOHOGENIVRILIRGVDSVLSQKQDAMLPLHYAAMOGHLPIVKLLAKOPGVVNAQ 600
Qy      601 TLDGRTPLHLAQRGHYVARILIDLCSDVNVCSLLAQPLHVAEAGTHTTARLLHKG 660
Db      601 TLDGRTPLHLAQRGHYVARILIDLCSDVNVCSLLAQPLHVAEAGTHTTARLLHKG 660
Qy      661 AKKEAVTSDGTALHLAARNGHLATVKILVEEKADVLARGPILNORALHAAHGHSEVYE 720
Db      661 AKKEAVTSDGTALHLAARNGHLATVKILVEEKADVLARGPILNORALHAAHGHSEVYE 720
Qy      721 ELVSADVIDLFDGQGLSALHLAQRHAQTVETTLRHGHINLQSLKFGQGHGPAATLLR 780
Db      721 ELVSADVIDLFDGQGLSALHLAQRHAQTVETTLRHGHINLQSLKFGQGHGPAATLLR 780
Qy      781 RSKT 784
Db      781 RSKT 784

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RESULT 2

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ID      Q96T11 PRELIMINARY; PRT; 784 AA.
AC      Q96T11;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Hypothetical protein FLJ14518.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID:9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      PubMed:14702039; DOI=10.1038/ng1285;
RA      Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA      Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

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RA      Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA      Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA      Murakami K., Yaenda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA      Sudo H., Hosoiri T., Kaku Y., Kodaira H., Komoto H., Sugawara M.,
RA      Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA      Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA      Niimiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA      Tanai H., Kimata M., Watanabe M., Hiraka S., Chiba Y., Ishida S.,
RA      Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hovuta T., Kusano J.,
RA      Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA      Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA      Muesashi K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA      Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA      Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA      Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA      Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA      Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA      Fujimori Y., Komiyama M., Taehiro H., Tanigami A., Fujiwara T.,
RA      Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,
RA      Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA      Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA      Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA      Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA      Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA      Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA      Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT      "Complete sequencing and characterization of 21,243 full-length human
RT      cDNAs."
RT      Nat. Genet. 36:40-45(2004).
CC      -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR      HMBP; AK027424; BAB5102.1; -.
DR      EMBL; AK027424; BAB5102.1; -.
DR      GO; GO:0005524; P:ATP binding; IEA.
DR      GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR      GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR      GO; GO:0016740; F:protein-tyrosine kinase activity; IEA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR      InterPro; IPR002110; ANK.
DR      InterPro; IPR011009; Kinase_like.
DR      InterPro; IPR001969; Pept_Asp_AS.
DR      InterPro; IPR000719; Prot_kinase.
DR      InterPro; IPR008271; Ser_thr_pkin_AS.
DR      InterPro; IPR001245; Tyr_kinase.
DR      Pfam; PF00023; Ank; 10.
DR      Pfam; PF00063; Kinase; 1.
DR      PRINTS; PR01415; ANKTYRN.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00248; ANK; 10.
DR      PROSITE; PS00086; ANK_REPEAT; 9.
DR      PROSITE; PS0297; ANK_REPEAT; 1.
DR      PROSITE; PS00141; ASP_PROTEASE; UNKNOWN; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;
KW      Transferase
SQ      SEQUENCE 784 AA; 86348 MW; 05B193B4EB9B5F5F CRC64;

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Query Match 97.1%; Score 3959; DB 2; Length 784;
 Best Local Similarity 97.8%; Pred. No. 1.6e-201;
 Matches 767; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

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Qy      1 MEGDGGTTPWALALRTDPAGETGEMKVGSGGFGQVYKVRHVHAKTWLAIKCSPLHADD 60
Db      1 MEGDGGTTPWALALRTDPAGETGEMKVGSGGFGQVYKVRHVHAKTWLAIKCSPLHADD 60
Qy      61 RERMELLEBAKKEMAKFRYYILPYVGI CREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
Db      61 RERMELLEBAKKEMAKFRYYILPYVGI CREPVGLVMEYMETGSLKLLASEPLPMDLRF 120
Qy      121 IIFHTAVGMNPLHCAAPPLHLDLKPANILLDAHVHVKISDFGLAKCNGLSHSDLSMDG 180
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Db 121 ITHETAVGNMPLHCAAPRLHLDKRPANILLDAHYHVKISDFGLAKNGLSHSHSLMDG 180
 QY 181 LFGTAYLPERPERIREKSLFTDKHDVYSFAIYIWGLTQKPPADKNTLIHMYKVGKH 240
 Db 181 LFGTAYLPERPERIREKSLFTDKHDVYSFAIYIWGLTQKPPADKNTLIHMYKVGKH 240
 QY 241 RBLPLPVCAARRACRASHLRLMORCMQSPRRPPTFOETSTTEPLCEPDDEVETAMD 300
 Db 241 RBLPLPVCAARRACRASHLRLMORCMQSPRRPPTFOETSTTEPLCEPDDEVETAMD 300
 QY 301 LVPKSPERPERSEVPARLKRASAPFPDNYSLSELLSQDGSVQAVEGPELSSSSSS 360
 Db 301 LVPKSPERPERSEVPARLKRASAPFPDNYSLSELLSQDGSVQAVEGPELSSSSSS 360
 QY 361 KLPSGSGKRLSGVSVDSAFSSRGLSLSPERPEPSTDLGTTTRPEERACGCHVRDTS 420
 Db 361 KLPSGSGKRLSGVSVDSAFSSRGLSLSPERPEPSTDLGTTTRPEERACGCHVRDTS 420
 QY 421 KLMTLIQPDVDLALDGSALHLAVAQECACAKLLNNANPNLSNRSGSTPLHMAVE 480
 Db 421 KLMTLIQPDVDLALDGSALHLAVAQECACAKLLNNANPNLSNRSGSTPLHMAVE 480
 QY 481 RRVAGVVELLARKISVNAKDEDOPTALHFAAONGDESTRLLEKNAVNEVEEGATP 540
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 Db 541 MHVACQHQGENTVRLLRGVDSLQKDAWLPVHYAANQGLPIYKLLAKPGVSVNAQ 600
 QY 601 TLDRPTPLHAAORGHYRVARILIDCSVNVCSLLAQPLHVAATGTSRARIILHNG 660
 Db 601 TLDRPTPLHAAORGHYRVARILIDCSVNVCSLLAQPLHVAATGTSRARIILHNG 660
 QY 661 AGKEAVTSQGYTALHFAARNGHATVKLLVEEKADVLARGPLNQTALHAAAGHSEVYE 720
 Db 661 AGKEAVTSQGYTALHFAARNGHATVKLLVEEKADVLARGPLNQTALHAAAGHSEVYE 720
 QY 721 ELVSADVIDLFDROGLSALHLAAQGHAAQTVELLRHGAHINQSLKFGQGHGPAATLIR 780
 Db 721 ELVSADVIDLFDROGLSALHLAAQGHAAQTVELLRHGAHINQSLKFGQGHGPAATLIR 780
 QY 781 RSKT 784
 Db 781 RSKT 784
 RESULT 3
 ID RIK4 HUMAN STANDARD; PRT; 832 AA.
 AC P57078; Q96RH0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Serine/threonine-protein kinase RIK4 (EC 2.7.1.37) (Receptor-
 interacting serine-threonine kinase 4) (Ankyrin repeat domain protein
 3) (PKC-delta-interacting protein kinase).
 GN Name=RIK4; Synonyms=ANKRD3, DIR;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fetal kidney, and Fetal lung;
 RA Shimizu N., Kudoh J., Shibuya K.;
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Tokoki Y., Choi D.-K., Soeda E.,
 RA Onki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,

RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald K., Rump A., Schilhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Saeki T., Nagamine K., Mitsuyma S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,
 RA Schaefer M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
 RA Ramer J., Beck A., Klages S., Hemmig S., Rieseemann L., Dagand E.,
 RA Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehnach H., Reinhardt R., Yaspo M.-L.,
 RT "The DNA sequence of human chromosome 21."
 RL Nature 405:311-319(2000).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P57078-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P57078-2; Sequence=VSP_004862;
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -1- SIMILARITY: Contains 10 ANK repeats.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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 CC or send an email to license@iesb-stb.ch).
 CC -----
 CC EMBL, AB047783; BAB56136.1; -
 CC EMBL, AP001743; BAA35526.1; -
 CC HSSP; Q60778; 10Y3.
 CC GeneW; HGNC:496; RIK4.
 DR MIM; 605706; -
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr Pkin_AS.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00023; Ank; 10.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00248; ANK; 10.
 DR PROSITE; PS50088; ANK_REPEAT; 9.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Alternative splicing; ANK repeat; ATP-binding; Repeat;
 KW Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 22 286
 FT REPEAT 485 514 ANK 1.
 FT REPEAT 518 547 ANK 2.
 FT REPEAT 551 580 ANK 3.
 FT REPEAT 584 613 ANK 4.
 FT REPEAT 617 647 ANK 5.
 FT REPEAT 651 680 ANK 6.
 FT REPEAT 684 713 ANK 7.
 FT REPEAT 717 746 ANK 8.
 FT REPEAT 750 780 ANK 9.
 FT REPEAT 782 811 ANK 10.
 FT NP_BIND 28 36 ATP (By similarity).
 FT BINDING 51 51 ATP (By similarity).
 FT ACT_SITE 143 143 Proton acceptor (By similarity).
 FT VARSELIC 278 325 Missing (in isoform 2).
 FT FTId=VSP_004862.
 FT M -> V (in Ref. 1).
 SQ SEQUENCE 832 AA; 91610 MW; 5DBFPD5F04F7ECB CRC64;
 Query Match 96.7%; Score 3943; DB 1; Length 832;
 Best local Similarity 92.4%; Pred. No. 1.2e-200;

Matches	769; Conservative	4; Mismatches	11; Indels	48; Gaps	1;
Qy	1	MEGGGTWALALATPTDAGEFTGKXVGGGFGVYRVHVMKTWLAICSPSLAYDD	60		
Db	1	MEGGGTWALALATPTDAGEFTGKXVGGGFGVYRVHVMKTWLAICSPSLAYDD	60		
Qy	61	RERMLLEAKKEMAKFRYILPVYIGREPGVIMWEMSGLEKILASRPLMDLFR	120		
Db	61	RERMLLEAKKEMAKFRYILPVYIGREPGVIMWEMSGLEKILASRPLMDLFR	120		
Qy	121	IIHETAVGNPLHCAAPPLHLDLKPANILLDAHVKISDFGLAKCNGLSHSHDLSMDG	180		
Db	121	IIHETAVGNPLHCAAPPLHLDLKPANILLDAHVKISDFGLAKCNGLSHSHDLSMDG	180		
Qy	181	LFGTAYIPPERIRKRSKLPFTKADYVSPALYIKVLTQKKPFADEKNIILIMKVKVGH	240		
Db	181	LFGTAYIPPERIRKRSKLPFTKADYVSPALYIKVLTQKKPFADEKNIILIMKVKVGH	240		
Qy	241	RPELPVCRARPRACSHILRLMORCMQDPRVRPTF-----	276		
Db	241	RPELPVCRARPRACSHILRLMORCMQDPRVRPTF-----	276		
Qy	277	-----OETSETEDLCCKPDDEVKETAHDLVKSPPERPSE	312		
Db	301	RSPGGRFLSEVILRYTCPLSSPOEITSFTEDLCEKPDDEVKETAHDLVKSPPERPSE	360		
Qy	313	VVPARLKASAPFTPNVYSLSELISQDLSGVQAVEGPELSRSSSEKLPSSGSGKRLS	372		
Db	361	VVPARLKASAPFTPNVYSLSELISQDLSGVQAVEGPELSRSSSEKLPSSGSGKRLS	420		
Qy	373	GVSSVDSAPSSRGSLSLSPEREPTSDGTRRPREEACGCRVADTKIMKTILOPOVD	432		
Db	421	GVSSVDSAPSSRGSLSLSPEREPTSDGTRRPREEACGCRVADTKIMKTILOPOVD	480		
Qy	433	LALDSGASLHLAVEAGEBCAKWILLNNANPNLSNRGSPPLHNAVERRYGVVELLA	492		
Db	461	LALDSGASLHLAVEAGEBCAKWILLNNANPNLSNRGSPPLHNAVERRYGVVELLA	540		
Qy	493	RKISVNADEDMWTLHPAONGDSSSTRLLLEKASVNEVDPERTPMVAACQHGQENI	552		
Db	541	RKISVNADEDMWTLHPAONGDSSSTRLLLEKASVNEVDPERTPMVAACQHGQENI	600		
Qy	553	VRIILRGVDSLOGKDMWLPVHYAMOGHLPVTLAKOPGVSNAAOTLDGRTPLHAA	612		
Db	601	VRIILRGVDSLOGKDMWLPVHYAMOGHLPVTLAKOPGVSNAAOTLDGRTPLHAA	660		
Qy	613	QRGHYRVARILLDCSDVNVCSLLAQTPPLHVAETGHTSTARLLHKGAKRAVTSQYT	672		
Db	661	QRGHYRVARILLDCSDVNVCSLLAQTPPLHVAETGHTSTARLLHKGAKRAVTSQYT	720		
Qy	673	ALHLLAARGHLATVQLVBEKADVLRGPINOTALHLLAARGHSEVVELYSADVIDLFD	732		
Db	721	ALHLLAARGHLATVQLVBEKADVLRGPINOTALHLLAARGHSEVVELYSADVIDLFD	780		
Qy	733	EOGSLALHLAAGRAHQAQVETLLRHGAHINLOSLKFOGSGHPAATLLRSKT	784		
Db	761	EOGSLALHLAAGRAHQAQVETLLRHGAHINLOSLKFOGSGHPAATLLRSKT	832		

RESULT 4

ID	QSERK0	PRELIMINARY;	PRT;	786 AA.
AC	QSERK0;			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)			
DE	PKC-regulated kinase PKC (Receptor-interacting serine-threonine kinase 4).			
DE	Name=Ripk4; Synonym=Ankrd3;			
GN	Mus musculus (Mouse).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			

RN	[1]	SEQUENCE FROM N.A.
RP	STRAIN=BALB/c;	
RC	MEBLINE=21293027; PubMed=11278382;	
RX	Chen L., Halder K., Ponda M., Cariappa A., Rowitch D., Pillai S.;	
RA	"Protein kinase C-associated kinase (PKC), a novel membrane-	
RT	associated, ankyrin repeat-containing protein kinase.";	
RL	J. Biol. Chem. 276:21737-21744(2001).	
RN	[2]	SEQUENCE FROM N.A.
RP	STRAIN=BALB/c;	
RC	Chen L., Halder K., Cariappa A., Pillai S.;	
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	
RN	[3]	SEQUENCE FROM N.A.
RP	STRAIN=NMRI; TISSUE=Mammary tumor;	
RC	MEBLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Hopkins R.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,	
RA	Altschul S.F., Moore T., Max S.T., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,	
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Boesk S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Pailey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,	
RA	Walling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywniński M.I., Skalska U., Smalins D.B., Schmech A., Schein J.E.,	
RA	Jones S.U., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=NMRI; TISSUE=Mammary tumor;	
RA	Strausberg R.;	
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.	
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.	
DR	EMBL; AF302137; AAC30871.2; -	
DR	EMBL; BC057871; AA57871.1; -	
DR	HSSP; Q60778; 1073.	
DR	MGD; MGI:191638; Ripk4.	
DR	GO; GO:0005524; F:ATP binding; IEA.	
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.	
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	GO; GO:0016740; F:transferase activity; IEA.	
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.	
DR	InterPro; IPR002110; ANK.	
DR	InterPro; IPR011009; Kinase like.	
DR	InterPro; IPR000719; Prot kinase.	
DR	InterPro; IPR008271; Ser_Thr_kinase.	
DR	InterPro; IPR012451; Tyr_kinase.	
DR	Pfam; PF00023; Ank; 10.	
DR	PRINTS; PRO1415; ANKYRIN.	
DR	PRINTS; PRO0109; TYRKINASE.	
DR	PRODOM; PD000001; Prot kinase; 1.	
DR	PROSITE; PS50088; ANK_REPEAT; 9.	
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.	
DR	PROSITE; PS01017; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE; PS01018; PROTEIN_KINASE_ST; 1.	
KW	ANK repeat; ATP-binding; Kinase; Receptor;	
KW	Serine/threonine-protein kinase; Transferase.	
SQ	SEQUENCE 786 AA; 86612 MW; 66CE2C25EB9A40C CRC64;	

Query Match 89.0%; Score 3628; DB 2; Length 786;
 Best Local Similarity 88.9%; Pred. No. 5.5e-184;

Matches	699;	Conservative	34;	Mismatches	51;	Indels	2;	Gaps	1;
QY	1	MEGDGTPWALALRTFDAGEFTGKVGSGGFGGVYRVHVMKWTWAIKCSPLAHVD							60
DB	1	MEGEGRGWALGLRTFDAGFPAKMEKVGSGGFGGVYRVHVMKWTWAIKCSPLAHVD							60
QY	61	RRRMELIBAKKMEAKRRYIIPVYGIQCEPGLVMEWEGSLAKLASPLPMDLFR							120
DB	61	RRRMELIBAKKMEAKRRYIIPVYGIQCEPGLVMEWEGSLAKLASPLPMDLFR							120
QY	121	IIHERAVGNFLHCAAPPLIHLDPANILDAHVKISDGLACKNGLSHSHDLSMDG							180
DB	121	IYHERAVGNFLHCAAPPLIHLDPANILDAHVKISDGLACKNGLSHSHDLSMDG							180
QY	181	LEGTIAYLPERIRERKSLFDTRKDVYSFAIYVIGVLTQKPEPADEKNIHIMVKVKGH							240
DB	181	LEGTIAYLPERIRERKSLFDTRKDVYSFAIYVIGVLTQKPEPADEKNIHIMVKVKGH							240
QY	241	REBELPVPCARPARASHILRMQRCQGDPRVRPTFOETSTSEDLCEKPDDEVKETAHD							300
DB	241	REBELPVPCARPARASHILRMQRCQGDPRVRPTFOETSTSEDLCEKPDDEVKETAHD							300
QY	301	LDVKSPPPEPRSEVP--ATLKASAPTPNDYSLSELSQLDSGVQAVGEPELSRSSS							358
DB	301	LDVKSPPPEPRSEVP--ATLKASAPTPNDYSLSELSQLDSGVQAVGEPELSRSSS							358
QY	359	BSKLPSSSGSKRLSGVSVDSAFSSRSGSLSLSPEREPSTSDLGTRRPEEAACGCHRYVD							418
DB	359	BSKLPSSSGSKRLSGVSVDSAFSSRSGSLSLSPEREPSTSDLGTRRPEEAACGCHRYVD							418
QY	419	TSKLMKILOPOVDLALDSGASLHLAVAGOEBCAKMLNNANPNLSNRGSTRPLHMA							478
DB	419	TSKLMKILOPOVDLALDSGASLHLAVAGOEBCAKMLNNANPNLSNRGSTRPLHMA							478
QY	479	VERBRVGVVELLARKISVNAKDEQWTLHFAQNGDESTRLLLEKVASVNEVDFEGR							538
DB	479	VERBRVGVVELLARKISVNAKDEQWTLHFAQNGDESTRLLLEKVASVNEVDFEGR							538
QY	539	TEWVAACQHQENIVEILLRQGVSLQKQDAMLPLHYAAMQHLPIYVLAKQPGSVN							598
DB	539	TEWVAACQHQENIVEILLRQGVSLQKQDAMLPLHYAAMQHLPIYVLAKQPGSVN							598
QY	599	AOTLDGRTPLHAAQGRHVRVARIILDCSDVNVCSLQOTPLHYAAEFGHSTARIILH							658
DB	599	AOTLDGRTPLHAAQGRHVRVARIILDCSDVNVCSLQOTPLHYAAEFGHSTARIILH							658
QY	601	AOTLDGRTPLHAAQGRHVRVARIILDCSDVNI CSLQOTPLHYAAEFGHSTARIILH							660
DB	601	AOTLDGRTPLHAAQGRHVRVARIILDCSDVNI CSLQOTPLHYAAEFGHSTARIILH							660
QY	659	RAGAGAAVSDGVTALHLAABNGHLATVTLVEEKADYVARGPLNOTALHLAAAGHSEV							718
DB	659	RAGAGAAVSDGVTALHLAABNGHLATVTLVEEKADYVARGPLNOTALHLAAAGHSEV							718
QY	719	VEELVSADYIDLFEQGLSALHLAAQGRHVAQVETLLRHGAHINIQLKFGGCHGPAATL							778
DB	719	VEELVSADYIDLFEQGLSALHLAAQGRHVAQVETLLRHGAHINIQLKFGGCHGPAATL							778
QY	779	LRRSKT 784							
DB	781	LRRSKT 786							

RP	SEQUENCE FROM N.A.
RC	TISU=Embryo;
RX	MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh P.,
RA	Ditchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Ueda T.B., Toshitoki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Falley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA	Krzywinski M.I., Skalski U., Smallos D.E., Scherch A., Schein J.E.,
RA	Jones S.J., Marra M.A.,
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISU=Embryo;
RX	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA	Richardson P.,
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT	initiative."
RT	Dev. Dyn. 225:384-391 (2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISU=Embryo;
RA	Klein S., Strausberg R.,
RA	Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
CC	-1. Similarity: Belongs to the Ser/Thr protein kinase family.
DR	EMBL; BC043634; AAA43634.1; -.
DR	HSP; P42773; IBU9.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR	GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR	InterPro; IPR002110; ANK.
DR	InterPro; IPR011009; Kinase_1like.
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR	InterPro; IPR001245; Tyr_kinase.
DR	Pfam; PF00023; Ank; 8.
DR	Pfam; PF00069; Kinase; 1.
DR	PRINTS; PR01415; ANKYRIN.
DR	PRINTS; PR01019; TYRKINASE.
DR	ProDom; PD000001; Prot_kinase; 1.
DR	SMART; SM00248; ANK_8.
DR	PROSITE; PS50086; ANK_REPEAT; 7.
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR	PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW	ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;
KW	transferase.
SC	SEQUENCE 720 AA; 79853 MW; FOBB851A0B380ADB CRC64;
QY	Query Match 62.3%; Score 2541; DB 2; Length 720;
QY	Best Local Similarity 70.1%; Pred. No. 1.8e-126;
DB	Matches 491; Conservative 86; Mismatches 117; Indels 6; Gaps 3;
DB	1 MEGDGTWALALRTFDAGEFTGKVGSGGFGGVYRVHVMKWTWAIKCSPLAHVD 60
DB	2 VDKGASPWDMDGLRTFDGSRFCGMEKVGSGGFGGVYRVHVMKWTWAIKCSPLAHVD 61

```
OY 61 RERMBLEBAKKEMAKFRYLIPYVIGCREPVGIVMEYMGTSLEKTLASEPLPMDLFR 120
DB 62 KERVELLEBAKKEMAKFRCLIPYVIGISDPVGLVMEYMGTSLEKTLASECLPMDLFR 121
OY 121 IIHETAVGNFLLHOMAPPLHLDLKPANILLDAHYHVKISDFGLAKCNGLSHSHDLSMDG 180
DB 122 IIHETAVGNFLLHOMAPPLHLDLKPANILLDGHYHVKISDFGLAKCNGLSHSHDLSMDG 181
OY 181 LFGTAYLPPERIREKSRFLPDKHIVSFAIVYMGVLTQKKPRADENKIILHIMKVYKGH 240
DB 182 ICGTIAYLPPERIFKRNCFDTPKHIVSFAIVYMGVLTQKKPRADENKIILHIMKVYKGH 241
OY 241 RPFLPPVCRARPRASHLIRLMQRCMGSDPRVPRPFQETSTEDLCKEPPDEV--KETA 298
DB 242 RPDIQOVRRVPRQOQGMILQMKCEKMDKPRPFQETSTEDLCKEPPDEV--KETA 301
OY 299 HDLD--VKSPPRESEVVPARLKRASAPTFDNDYSLSELSQLDGSVQAVEGPELSRS 356
DB 302 QELQKVGKEAPQWMTSQABGKRSPTPAFDKDYSLSELSQLDGSISQTMGPGCLSHS 361
OY 357 SSESLLPSSSGSKRLSGVSVDSAFSSSGSLSTFERPSTSDLTTRPREBAAGCHRV 416
DB 362 VSEPLAS--SDKRLSGVSVDSAFSSSGSLSTFERPSTSDLTTRPREBAAGCHRV 419
OY 417 RDTSLKMLIOPQVDLALDGSASLHLAVEAGCECAKMLLNANPNLSNRSGSTPLH 476
DB 420 GDTALMLIOPQVDLALDGSASLHLAVEAGCECAKMLLNANPNLSNRSGSTPLH 479
OY 477 MAVERRVGVVLLIARKISVNAKDEDMQWALHPAONGDESSSTYLLIEKNAVNDPE 536
DB 480 IASDKKRLKIVELLIGKKIHVNAKDEDMQWALHPAONGDESSSTYLLIEKNAVNDPE 539
OY 537 GRTPMHVAQCGQENIVLILRGDVSLOQKDALPLHYAMQCHLPIVYLLAKQPGVS 596
DB 540 GRTPLHVAQCGQENIVLILRGDVSLOQKDALPLHYAMQCHLPIVYLLAKQPGVS 599
OY 597 VNAQTLDRTPPLHLAAGRGHYVARILLIDLCSDVAVCSLLAQTPPLHVAETGHTSTAIL 656
DB 600 INAQTSIDRTPLHLAAGRGHYVARILLIDLCSDVAVCSLLAQTPPLHVAETGHTSTAIL 659
OY 657 LHRGAGKEAVTSDGYTALHLAARNGHLATVKILVEKADV 696
DB 660 LSRGASINAVTTEGTALDLASNLGHSYAVKILMDQSDV 699
RESULT 6
OQ6PN2 PRELIMINARY; PRT; 719 AA.
AC OQ6PN2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, last annotation update)
DE MGCB2765 protein.
GN Name=MGCB2765;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_taxid=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
MEDLINE=22389557; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schelefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Hasle F.,
RA Diachenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullane S.J.,
RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
RA Krzywnicki M.I., Skaleja U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DB EMBL: BC073081; AAF73081.1; -.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO: GO:0016740; P:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR001009; Kinase like.
DR InterPro: IPR000719; Prot. kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR008271; Ser_Thr_kin AS.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00023; Ank; 8.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR01415; ANKTRIN.
DR PRODOM: PD000001; TYRKINASE.
DR SMART: SM00248; ANK; 8.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS50088; ANK_REPEAT; 7.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 719 AA; 80027 MW; CB23FE8A5CA14B77 CRC64;
Query Match 61.7%; Score 2514.5; DB 2; Length 719;
Best Local Similarity 69.7%; Pred. No. 4.7e-125;
Matches 487; Conservative 83; Mismatches 124; Indels 5; Gaps 2;
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QY 241 REPPEVCRARPRACSHLIRLMQRCMGDPVRVPTFGQITSTEDLCEKPDDEVKETAHD 300
 DB 242 RDDLSQLIPRVRPOQCGMIQIMKECMNDKPRRPFQETSTETVLCTHDEDTSCVQOTQ 301
 QY 301 L---DVKSPPERSEVVPARLRASAPFPDNDYSISELLSQDGSQVAQVEPELSRSS 357
 DB 302 LQGVKTOGALEKRTSQABGKRSSTPAKGDYISSELLSQDSDGISQMEPRLCSHSV 361
 QY 358 SSSKLPSSSGKRLSGVSSVDSAFSSRGLSISFERBPSDGLGTRRPEERACCHVR 417
 DB 362 SSSPOLAS--SDKRLSGVSSVDSAFSSRGLSISFERKDSVLDLSASDQKKLVAVIYCG 419
 QY 418 DTSKMLKTIQPOVDVLLDGSGLHLAVBAQSECAKWLNNANPNLSNRGSTPLM 477
 DB 420 DTTKMLKTIQPOVDVLLIEGRSSLSHLAVENQEECAKLLYNASPNMTNKKSGTPLHI 479
 QY 478 AVEERRVGVVELLARKISVNAKDEDOQTALPPAQNQDESSTRLLLEKNAVSEVDFEG 537
 DB 480 ASDKCLKNIVELLVKKLVNNTDEDFALHFSAQNGDECTTRMLLEKNAISLTVVDIKG 539
 QY 538 RTRPVACQGGQENTVIRILRRGVDSLQGXAMPPLHYAAMQGHLPYKLLAKQGVSV 597
 DB 540 RRPPLHVAQGGQENTVIRVIRRGADLTFKGDQNNMLAHYAAMQGHNLIVKLLAKQGANI 599
 QY 598 NQOTLDGRTPLHLAQRGHYRVARILIDCSVNVCSLLAQTPHYAAATGHTSTRALL 657
 DB 600 NQOTSDGRSPLHLAQRGHYRVARILVDRCVNIIPSNMKRPLHYAAATGHTSTRALL 659
 QY 658 HRGAGKEAVTSDGYTALHLAARNGHATVYKLLVEEKADY 696
 DB 660 SRGASINALTTRGFTALDLASNLGHSAYKLLMDEQSNV 698

RESULT 7

ID 08JH03 PRELIMINARY; PRT; 820 AA.
 AC 08JH03;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
 DE Protein kinase PKK.
 GN Name=PKK; ORFNames=zgc:55705; (Danio rerio).
 OS Brachydanio rerio (Zebrafish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RX MEDLINE=22191376; PubMed=12091384; DOI=10.1074/jbc.M202222200;
 RA Muto A., Rutland J., McAllister-Lucas L.M., Lucas P.C., Yamaoka S.,
 Chen F.F., Lin A.J., Mak T.W., Nunez G., Inohara N.,
 "Protein kinase C-associated kinase (PKK) mediates Bcl10-independent
 NF-kappa B activation induced by phorbol ester.",
 J. Biol. Chem. 277:31871-31876(2002).
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Schaller G.D.,
 Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.P., Bhat N.K.,
 Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
 Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
 Brownstein M.J., Ustin T.B., Toehyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Pahey J., Helton B., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krywninski M.I., Skalek U., Smalley D.E., Scherch A., Schein J.E.,
 RA Jones S.U., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RA Strausberg R.,
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AF487541; AAM76921.1; -
 DR EMBL: BC045432; AAH45432.1; -
 DR HSSP: P16157; IN11.
 DR ZFIN: ZDB-GENE-040426-2042; zgc:55705.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; P:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR Pfam: PF00023; Ank; 10.
 DR PRINTS: PR01415; ANKRN.
 DR Prodom: PD000001; Prot_kinase; 1.
 DR SMART: SM00248; ANK; 10.
 DR PROSITE: PS50088; ANK_REPEAT; 9.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
 DR ANK repeat; ATP-binding; Kinase; Serine/threonine-protein kinase;
 KW Transferase.
 SQ SEQUENCE 820 AA; 89985 MW; 4A53D6A99B3E8B90 CRC64;

Query Match 58.6%; Score 2389.5; DB 2; Length 820;
 Best Local Similarity 61.3%; Pred. No. 2.3e-118;
 Matches 471; Conservative 110; Mismatches 169; Indels 19; Gaps 8;
 QY 1 MEGDGTPLMALATRTPAGEFTGKEKVGSGFGQVYVVRHVHMTWLAKCPSPLHYVD 60
 DB 1 MDVPSNSGIMGLKTPFASFGSWKIGSGGFGQVYVVRHVHMTWLAKCPSPLHYDD 60
 QY 61 RERMLLEBAKKMKMAKFRYILPYVGICRBEFVGLVMEYMETGSLBKLIASEPLPVDLRR 120
 DB 61 KERALLLEBAKKMKMAKFRYILPYVGICRBEFVGLVMEYMETGSLBKLIASEPLPVDLRR 120
 QY 121 ITHETAVGMNPLHCAAPPLHLHLDPANITLDAHNVKISDRLAKCKGSLSHSDLSMDG 180
 DB 121 ITHETAVGMNPLHCAAPPLHLHLDPANITLDAHNVKISDRLAKCKGSLSHSDLSMDG 180
 QY 181 LFTGTAIVLPPERIRKESRLPTKHDVYSFAIVMGVLTQKKRPFADKKIILHIMVYVKGH 240
 DB 181 FCGITAIYVPPERIRKESRLPTKHDVYSFAIVMGVLTQKKRPFADKKIILHIMVYVKGH 240
 QY 241 REPPEVCRARPRACSHLIRLMQRCMGDPVRVPTFGQITSTEDLCEKPDDEVKETAHD 300
 DB 241 RDDLSQLIPRVRPOQCGMIQIMKECMNDKPRRPFQETSTETVLCTHDEDTSCVQOTQ 300
 QY 301 LDVKSPPERSEVVPARLRASAPFPDNDYSISELLSQDGSQVAQVEPELSRSS 354
 DB 301 BPECSPCAPPASSEGTNDQKQVPRPSANLP--EKQYISSELLTQDSDGSRSLSNVQ-- 356
 QY 355 RSSSKLPSSSGKRLSGVSSVDSAFSSRGLSISFERBPSDGLGTRRPEERACCHVR 414
 DB 357 -ESLESK--DNTSRGLSGVSSVDSAFSSRGLSISFERKDSVLDLSASDQKKLVAVIYCG 410
 QY 415 RVDTSKMLKTIQPOVDVLLDGSGLHLAVBAQSECAKWLNNANPNLSNRGSTPLM 474
 DB 411 RTEDIKMLKTIQPOVDVLLDGSGLHLAVBAQSECAKWLNNANPNLSNRGSTPLM 470

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RA the PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs."; Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RX MEDLINE=204993374; Pubmed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugihara Y., Shibata K., Itoh M.,
 RA Komoto H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RA Kono H., Akiyama J., Nishi K., Kitzunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,
 RA Fujiwake S., Inoue K., Togawa T., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
 RL [6]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Vagina;
 RC STRAIN=C57BL/6J; TISSUE=Vagina;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hoti F., Imocani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Komoto H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahita S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi F., Yashima S., Yashima S., Yashima S.,
 RL submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC EMBL, AK036872; BAC29613.1; --
 DR HSP, Q60786; 10Y3.
 DR MED, MG1:3045301; 9930020N01R1k.
 DR GO, GO:0005524; F:ATP binding; IEA.
 DR GO, GO:0003677; F:DNA binding; IEA.
 DR GO, GO:0016740; F:protein serine/threonine kinase activity; IEA.
 DR GO, GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR008271; Ser_Thr_pkin_AS.
 DR Pfam, PF00023; Ank; 11.
 DR Pfam, PF00069; Kinase; 1.
 DR PRINTS, PRO1415; ANKYRIN.
 DR PRODOM, PD000001; Prot kinase; 1.
 DR SMART, SMO0248; ANK; 11.
 DR PROSITE, PS50088; ANK_REPEAT; 11.
 DR PROSITE, PS50297; ANK_REPEAT; 1.
 DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE, PS00108; PROTEIN_KINASE_SF; 1.
 KW ANK repeat; ATP-binding; DNA-binding; Hypothetical protein; Kinase;
 KW Serine/threonine-protein kinase; Transferrase.
 SO SEQUENCE 745 AA; 82479 MW; DD3919EDD19EBB4D CR664;

Matches	272: Conservative	115: Mismatches	280: Indels	91: Gaps	12,
Qy	11	LALLRTFDAGEP--TGWEKVGSGGFGQYKVRVHNMKTMALIKCPSLHVD--DRRMELL	67		
Db	22	LGSLTVFTRPDDFEEMHLVASGGFSKVFARHHRKMRTOYAIKSPCLQKETTSSEVCLF	81		
Qy	68	EEAKKEMAAFRYILTPRYGICREVEGLVMEVMETGSLKLLASBPLPMDLRFRIRHETAV	127		
Db	82	EEAVYMERKIFOHIVSTIVGCKOPLGIVMEFMSGSLEKLPHTSLCPWLKLRIRHETSL	141		
Qy	128	GMNFIHCAAPRLHLDLCKPANILLDAHYHKISDPGLAK--CNGLSHSHDLSMDGLFETIA	186		
Db	142	AMNFIHSTKPPRLHLDLCKPANILLDNMRYKISDPGLSKMMEGSTQYQYERSALRSTLS	201		
Qy	187	YLPPERIRKSRRLFTDTHGVSPFAIVIGVLTKKPPADAKENILHIMVKVKGHPFLP	246		
Db	202	YIPPEMFLNNKAAQPEYDVSFAIVIMEILTKKPYAG--LNMWTIIRVAAGKRPSELQD	260		
Qy	247	VCRAPPAACSLILTMORCMQGPDRVPTQOITSEFEDLCERPDDEVKSTADHLDVKS	306		
Db	261	VSDMEPEEVHQMVMIMKRCWDQDCKKPCFLMAVETMLLST-----FQSP	307		
Qy	307	-PEERSEVPAARLKRASAPTFDNDYSLESLLSQDSSGVAQVAGEPEELSRSSSEKLPSS	365		
Db	308	MTDVGCEALYOKV--SCKPSLSQPHKYSKVENQ-----EIASVSSDSL---	349		
Qy	366	GSGKRSLGSSVSDSAFSSRGSLSLSEFEREPSTSDLTGTRRPEBEACGCHRVDTSKLMT	425		
Db	350	-----KMILQSDSKSLVAVSDVENR-----	370		
Qy	426	LQPDVDLADSGSLHLAVEAGQESCAKMLLNANPNLSNRGSTPLHMAVERVYG	485		
Db	371	-----ATPLHFTVAGSLSLQVRLSLSHDVVQCQTASGVTPLLIADQDQPD	417		
Qy	486	VVELLARKISVNAKDDEQWTFALFFAONGDESTRLLLEKNASVNEVEDEGRTPMHVAAC	545		
Db	418	LCALLIHAAGDTNLADEGMAPLHPAONGDDHTRAKLLIDHGLVNAAREHGWTPLHIAA	477		
Qy	546	QHGEENTVRIILRRGVDSLSQKQDAPLPHYAAWQGHPLVKKLIAPQGVSVNAQTLDGR	605		
Db	478	QNNFENVARILLVSRQADLSPHBAEGKTPPLHVAAYFHIGIKLLSQ--GAELDAQGNLR	536		
Qy	606	TPHLHAAORGHYVARILLIDLCSPVAVNCSLAQTPPLVAATEGTTSTARLLIRHGAKEA	665		
Db	537	TPHLHAAVERGKVRPAIOHLKCGALPDLIDHSGVSPHIAAARGDOLI.FKMLIRYGALEL	596		
Qy	666	VTSDGYTALHIAANGHILATYKILVERKADVLNAGPNOTALHIAAAGHSEVVEELVSA	725		
Db	597	RTQGSWTPPLHATYKGHLEIITHQAKSHVDLDALSGSWTPPLHIAAQEGEVMALLQOC	656		
Qy	726	DV-IDLFDEQGLSALHIAAQGRHAQYETLLRHGANIN	762		
Db	657	GANNPAAQSGSWTPPLHIAVHKGTPLGTTLHLEYADLH	694		
RESULT 12					
Q8JHU4 PRELIMINARY; PRT; 584 AA.					
AC	01-OCT-2002 (Tremblrel. 22, Created)				
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)				
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)				
DE	Protein kinase RICK.				
GN	Name=ripk2; Synonyms=rick;				
OS	Brachydanio rerio (zebrafish) (Danio rerio).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Danio.				
NCBI	Taxid=7955;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	Medline=96241596; Pubmed=9575181; DOI=10.1074/jbc.273.20.12296;				
RA	Medline=N.2., del Peso L., Koseki T., Chen S., Nunez G.;				

RT "RICK, a novel protein kinase containing a caspase recruitment domain,
RT interacts with CLARP and regulates CD95-mediated apoptosis.",
RL J. Biol. Chem. 273:12296-12300(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2291376; PubMed=12091384; DOI=10.1074/jbc.M20222200;
RA Muto A., Ruland J., McAllister-Lucas L.M., Lucas P.C., Yamacka S.,
RA Chen F.F., Lin A., Mak T.W., Nunez G., Inohara N.,
RT "Protein kinase C-associated kinase (PKC) mediates Bcl10-independent
RT NF-kappa B activation induced by phorbol ester.",
RL J. Biol. Chem. 277:31871-31876(2002).
DR EMBL, AF487540; AAM76920.1; -.
DR ZFIN, ZDB-GENE-030902-3; rtpk2.
DR GO, GO:0005622; C:intracellular; IEA.
DR GO, GO:0005524; F:ATP binding; IEA.
DR GO, GO:0005515; F:protein binding; IEA.
DR GO, GO:0004468; F:protein-tyrosine kinase activity; IEA.
DR GO, GO:0042981; F:regulation of apoptosis; IEA.
DR InterPro, IPR001315; CARD.
DR InterPro, IPR011029; DEATH_like.
DR InterPro, IPR011009; Kinase_like.
DR InterPro, IPR008271; Ser_Thr_pkin_AS.
DR InterPro, IPR001245; Tyr_kinase.
DR Pfam, PF00619; CARD; 1.
DR Pfam, PF00069; PKINASE; 1.
DR PRINTS, PR00109; TYRKINASE.
DR ProDom, PD000001; Prot_kinase; 1.
DR PROSITE, PS50209; CARD; 1.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
DR KINASE.
SQ SEQUENCE 584 AA; 66124 MW; 7AAEFCB65DEB9C0 CRC64;

Query Match 14.0%; Score 563; DB 2; Length 584;
Best Local Similarity 29.5%; Pred. No. 3.9e-22;
Matches 177; Conservative 97; Mismatches 197; Indels 128; Gaps 25;

QY 21 EFTGMEKVGSGFGQYKRVHMKTWLAIKC-----SPSLAVYDREHREMLSEAKKMEVA 76
DB 27 KATDLHYIKSGFGVYFRAQHSMDKRTVAIKCIKLDSF---VGERRNCLLEAEVLAHKA 83
QY 77 KERYLLPVYVICRNP--VGLVMEYMETGSLSEKLASEPI---PMDLRRIIHTETAVGMN 130
DB 84 RFNHIIQIFGVNCEPEFCITETVMNGSLDELHKKDIPYAVAMPRLRIIYEIALGVN 143
QY 131 FLHCAPRLIHLDDLKPANILLDAHTVAKISDGLAC-NGLSHS-DSMDGLFTIATL 188
DB 144 FLHNSPRLIHLDDLKQNTIMQGEYHVKIADPGLSKPSPALDHQRLRLPAEMGGTVIYM 203
QY 189 PPERLR-ESKRLPDTGVDYSPFAIVMGVLTOKKPPADEKNILHIVKVGKRRPE---- 243
DB 204 PPEYEPSTKRTDVKIMYSTAIIMWYLSKRIPEEATNPQIMFSLRGARPTGID 263
QY 244 -LPVYCRAPRACSHLIRLMQRCWQDPRVPTPOBITSETBDLCEKPPD-EVKETAHDL 301
DB 264 SLPPVDLPSR---ETLIMTSGWTANPDERPFLCLLEBPMLRRPDEIDVLEAV--L 317
QY 302 DYK-----SPPEPRSSVVPARLKRASAPFPDN-DYLSLSLLQOLDSGVQAYE 348
DB 318 EVKRIKRRPSSCCSSTOSNGKIKBEKCVKELNVPMFDMNSTSGSGSCSQEAEISQ--- 374
QY 349 GPBELSRSSSESLTPSSGSGKRLSGVSS-----VSAFSSRGSLSLSFEREP 395
DB 375 -PEPLTIST-----PSQGA---YAGLPSSLSMLPDPKPKLMDNC--SPNNLSPEYQTA 423
QY 396 STSDLGTTTRRPEEACGCHRVDPISKLMLIQ-----POVDLALDSGASLHLAVEA 448
DB 424 VVSDLNIIPK-----AAHPQSESELALAIQPLTLHPHQDVTAFDD----- 465
QY 449 GQEECAKMLLNNANPRLSRRGSTPLHMAVERRVAGVLELLARKISVNAKDEDDQWTAL 508

DB 466 -QGPAAWIA-----ARREVVROMTEACIANSGLDALSRELLMR---EDYELV 511
QY 509 HPAQNGDESTRLLLEKMSVNVDPFGRTPMHVAOQGENIVRLIRGVDPVSLQG 567
DB 512 N---QTRTAAKVRLLD-----TCRHSEEFRCVVVVRGLQDKQMG 549

RESULT 13
ID RIK2_MOUSE STANDARD; PRT; 539 AA.
AC P58801;
DT 28-FEB-2003 (Rel. 41, Created)
DR 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Receptor-interacting serine/threonine-protein kinase 2 (EC 2.7.1.37).
GN Name=RipK2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21891093; PubMed=11894097; DOI=10.1038/416190a;
RA Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;
RT "Involvement of receptor-interacting protein 2 in innate and adaptive
RT immune responses.",
RL Nature 416:190-194(2002).
CC -1- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappa-B (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated.
CC -1- SUBUNIT: Binds to CLARP/CLARP and CASP1 via their CARD domains.
CC Binds to BIRC3/C-IAP1 and BIRC2/C-IAP2. TRAF2, TRAF5 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- PTM: Autophosphorylated (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AF461040; AAL96436.1; -.
DR MGD, MGI:1891456; RipK2.
DR InterPro, IPR001315; CARD.
DR InterPro, IPR011029; DEATH_like.
DR InterPro, IPR011009; Kinase_like.
DR InterPro, IPR000719; Prot_kinase.
DR InterPro, IPR008271; Ser_Thr_pkin_AS.
DR Pfam, PF00619; CARD; 1.
DR Pfam, PF00069; PKINASE; 1.
DR ProDom, PD000001; Prot_kinase; 1.
DR SMART, SM00114; CARD; 1.
DR PROSITE, PS50209; CARD; 1.
DR PROSITE, PS50107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS50018; PROTEIN_KINASE_ST; 1.
KW Apoptosis; ATP-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 18 294
FT DOMAIN 431 523
FT NP_BIND 24 32
FT BINDING 47 47
FT ACT_SITE 146 146
FT PROTON_ACCEPTOR 146 146
SQ SEQUENCE 539 AA; 60400 MW; 42951BP97CA15DFA CRC64;
Query Match 13.4%; Score 545.5; DB 1; Length 539;

Best Local Similarity 34.6%, Pred. No. 6.2e-21;
Matches 151; Conservative 60; Mismatches 134; Indels 91; Gaps 17;

QY 31 GGFQGVYKVRHVKMTALIKCSPSLHVD---DREMLLEAKKEMAKERYILPYVG 86
DQ 27 GASGVTSARADWRVRVAVK---HLHITPLDSESRDILREABILHAKAFSYILPLIG 83
QY 87 ICRRP--VGLVMEYTWGSLLEKLASE---PLWMDLRFRIHETAVGMNHLHCAPPL 140
DQ 84 ICNPEPFGIVTEYMPGSLNELLHRTKTEYDIPAMPLFRILHETALGVNLYHNNPPL 143
QY 141 HLDKPPANILLDAHVKISDFGLAKCNGL---SHSHDLSMDGLFTIAYLPPERIR- 194
DQ 144 HHDKTQNIILLDNHVKYKADPGLSKMTMMSLSQSRYSKSAPEG--GTLIMPEENTYEG 201
QY 195 EKSLRPTDHDVSPALVYVGLTQKRPADKNTLIMVKYVKGHPRLPPVCRAPRA 254
DQ 202 OKSRA-SVKHDIYSYAVIMMEVLKSRQPFEEVTPLOIMYSVSGHRDPTSE--ENLPFD 258
QY 255 CSH--LIRLMQRCQSDPRVRP-----TFQKIT-----S 281
DQ 259 IPRHGLMISLIQSGAQNDRPSPFLKCLILEPVLRTFEDITLEAVITQKKAKIOSS 318
QY 282 ETEBDCEKPDDEVKETAHDLVKSPPEDRSEVVPARLKRASAPTEPDNDYSLSELLSOL- 339
DQ 319 STIHLCDKMD---LSINIPANHPQRES-----CGSSILSRNTG 355
QY 340 DSGVSGAVEGPEELSRSSSEKLPSSGSKRLSGVSYD-----SAPSRGSLISF 391
DQ 356 SPGRSRSLSAPQDKFLSGAPQDCSLKAKHCPGNHSDGIVSVPPGAALFCDRRASCSL 415
QY 392 E-REBSTDIGTTRP 406
DQ 416 AVISPFLEVKGSERP 431

RESULT 14

RICK2 HUMAN STANDARD; PRT; 540 AA.
AC 043533;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Receptor-interacting serine/threonine-protein kinase 2 (BC 2.7.1.37)
DE (RIP-2) (CARD-containing interleukin-1 beta converting enzyme
DE associated kinase) (CARD-containing IL-1 beta ICE-kinase)
DE (UNQ277/PRO314).
GN Name=RIPK2; Synonyms=CARDIAK, RICK, RIP2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RX MEDLINE=98241596; PubMed=9575181; DOI=10.1074/jbc.273.20.12296;
RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.,
RT "RICK, a novel protein kinase containing a caspase recruitment domain,
RT interacts with CLARP and regulates CD95-mediated apoptosis.",
RL J. Biol. Chem. 273:12296-12300(1998).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RX TISUS=endothelial cell;
RA MEDLINE=98307936; PubMed=9642260; DOI=10.1074/jbc.273.27.16968;
RA McCarthy J.V., Ni J., Dixit V.M.,
RT "RIP2 is a novel NF-kappaB-activating and cell death-inducing
RT kinase.",
RL J. Biol. Chem. 273:16968-16975(1998).
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.
RX MEDLINE=98381580; PubMed=9705938; DOI=10.1016/S0960-9822(07)00352-1;
RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
RA Matmann C., Tschopp J.,

RT "identification of CARDIAK, a RIP-like kinase that associates with
RT caspase-1.",
RL Curr. Biol. 8:885-888(1998).
RN [4]
RP SEQUENCE FROM N.A.
RA Ozersky P., Holmes A., Broly M.,
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Platzner M., Varon R.,
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chu C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Bacon D., Foster J., Grimaldi C., Gu Q., Hase P.E., Helens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehgali S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.,
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.",
RL Genome Res. 13:2265-2270(2003).
RN [7]
RP SEQUENCE FROM N.A.
RC TISUS=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedon T.B., Toshitsuki S., Carinci P., Prange C.,
RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltón E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherich A., Schein J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappa-B.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Binds to CFLAR/CLARP and Casp1 via their CARD domains.
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF3 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,
CC peripheral blood leukocytes, spleen, kidney, testis, prostate,
CC pancreas and lymph node.
CC -1- PTM: Autophosphorylated.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC [3]
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CC -----
 DR EMBL; AF027706; AAC34970.1; -
 DR EMBL; AF078530; AAC27722.1; -
 DR EMBL; AF064824; AAC25668.1; -
 DR EMBL; AC004003; AAC24561.1; -
 DR EMBL; AF117829; -; NOT_ANNOTATED_CDS.
 DR EMBL; AY358814; AA089173.1; -
 DR EMBL; BC004553; AA04553.1; -
 DR Genew; HGNC:10020; RIPK2.
 DR H-invDB; HIX0007636; -
 DR MIM; 603455; -
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
 DR GO; GO:0004871; F:signal transducer activity; IBP.
 DR GO; GO:0006915; P:apoptosis; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IBP.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR007719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00114; CARD; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS50107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR Apoptosis; ATP-binding; Phosphorylation;
 KW Serine/threonine-protein kinase; transferase.
 FT DOMAIN 18 294
 FT NP_BIND 432 524 CARD.
 FT BINDING 47 47 ATP (By similarity).
 FT ACT_SITE 146 146 Proton acceptor.
 FT MUTAGEN 47 47 K->A: Abolishes kinase activity.
 FT MUTAGEN 146 146 K->M: Reduces FAS-mediated apoptosis.
 FT MUTAGEN 146 146 D->N: Abolishes kinase activity.
 SQ SEQUENCE 540 AA; 61194 MW; 575A69239505792 CRC64;
 Query Match 13.3%; Score 541.5; DB 1; Length 540;
 Best Local Similarity 34.0%; Pred. No. 1e-20;
 Matches 145; Conservative 57; Mismatches 118; Indels 107; Gaps 16;
 31 GGGGYYKRVHMKTKLAKSPSLHVD---DRERMELBEAKKEMAKRYTILPVYG 86
 27 GASGVSSARHADMVQVAVK---HLHHTPLDSEKQVLEAELIKARSTILPILIG 83
 87 ICRP--VGLAMEYMETGSLKILASE---PLPMDLRRIIHTAVGNPLHCAPPL 140
 84 ICNEPFGIVTEYMNSLNLRLKRTYPPVAVPLRRIILHEIALGVNVLHNTPL 143
 141 HLDLKPANILLDAHYVKISDGLACKGSLSHSDM---DGLFGLTAIYPPERIR-- 194
 144 HHDLTKQNLILNDFEFTKIDFGLSKRMKMSLSQSSKXABEG--GTLIYMPPEYBEG 201
 195 EKSRLPDTGHDVYSFAIIVGVLTKCKPPADEKNILHIMVKVKGHRP-----ELPPVCR 249
 202 QKSRRA-SIKHDIYSTAVITWEVLSRKQPEEDVTNPLQIWTYSQGRFPYNESLPYDLP 260
 250 AAPRACSHLIRLMQRCOCQDPRVPTFOBITSETEDLCRKPDEVKETAHDLVKSPPRP 309
 261 HBAR---MISLESQAQNPDRPSPFLKCLIELEVLRL----- 295
 310 RSEVVPARLKRASAPTFNDYISLSLLQDSCVSAVAGPERLSSSESLTPSSGSGK 369
 296 -----TFE-EITFLAVIQL-----KTKTKQVSSAI 321
 370 RLISGVSVDSAPSSRSLISFPERBSTSLGTTTRPEEBACGCHVRDTS-----KLMTI 425
 322 HLCDDKKKME-----LSL-----NIPVNHGPQEBSSCGSSQLHNSGSPETSRSL 364

QY 426 LQPDVD 432
 Db 365 PAPQDND 371
 RESULT 15
 Q9VAB1 PRELIMINARY; PRT; 1549 AA.
 ID Q9VAB1
 AC Q9VAB1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE CG1651-PA (CG1651-pb)
 GN Name=Ank; ORFNames=CG1651,
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabot G.L.,
 RA Abiri J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butts J.K., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dubin K.J., Evangelista C.C., Ferraz C., Ferrier S., Glasner K.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jajael M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laevo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relier K., Remington K., Saunders R.D., Scheefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Splitter B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Myers E.W., Rubin G.M., Venter J.C., Zhu X., Smith H.O.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kromiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber F.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence."
 RL Science Biol. 3:RSEBARCH0079-RSEBARCH0079 (2002).

RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svitskas R.,
 RA Patel S., Friese B., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RL a genomic perspective.";
 RN Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RP [4]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hildebeck P., Huang Y., Kaminler J.S., Milburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.D., Whitfield E.J., Bayraktaroglu B., Bernan B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter C., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RL systematic review.";
 RN Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RP [5]
 RN SEQUENCE FROM N.A.
 RP FLYBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FLYBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003845; AAF59369.2; -
 DR HSSP; P16157; IN11.
 DR FLYBase; FBgn0011747; Ank.
 DR GO; GO:0045169; C:fusome; NAS.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR GO; GO:0045170; C:spectrosome; IDA.
 DR GO; GO:0007016; P:cytoskeletal anchoring; IDA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR00488; Death.
 DR InterPro; IPR000906; ZUS.
 DR Pfam; PF00023; Ank; 23.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00791; ZUS; 1.
 DR PRINTS; PR01415; ANKCRIN.
 DR SMART; SM00246; ANK; 23.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00218; ZUS; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 21.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KM ANK repeat.
 SQ SEQUENCE 1549 AA; 170167 MW; 3ECEC852B1484DFF CRC64;
 Query Match 13.3%; Score 541; DB 2; Length 1549;
 Best Local Similarity 34.7%; Pred. No. 4.2e-20;
 Matches 128; Conservative 76; Mismatches 155; Indels 10; Gaps 6;
 QY 396 STSDIGTRRPEEACGCHRVADTSKIMKILQPO-DVDLADSGASLHLAVEAGQECA 454
 DB 427 ATTESGLTPLHVASFMGCINI-----VYLLQHEASADLPTRIGETPLHLAARAOADI 481
 QY 455 KMLLNANPNISNRGSTPLHMAVERVRGVVELLARKISVNAKDQWTALHFAON 514
 DB 482 R-ILIRSAKVDAIAEGQTPLHVASRLNININIMILLQHGABINAOXNDKXSALHIAKE 540
 QY 515 GDESSTRLLEKNAVNEVDPEGRTPMHVACOHQENTVIRILRRGVDSIQKDAWPL 574
 DB 541 GQENTVQVLELNGAENNAVTKGFTPLHACKYKQNVQIILONGASIDFGKNDVTP 600
 QY 575 HYAANQHLPIVKLLAKQPGVSVNAQTLDGRTPLHLAAQRGHYRVARILIDLCSQDVNCS 634
 DB 601 HVATHYNNPSIYELLKKN-GSSPNLCARNGQCAHIAICKKQVLEITAMQLQHGADVNIIS 659

QY 635 LLAOTPLHVAEFGHTSTARLLHRGAKREAVTSDGYTALHLAARNGHLATVXLVEKA 694
 DB 660 KSGFSPHLAAQGNVDMVQLLEYGV-ISAANKGLTPLHVAQBGHVLSQITLEHGA 718
 QY 695 DVLARGLNQTALHLAAHGHSEVEBELVSADV-IDLFDEQGLSALHLAAQGRHAQTVER 753
 DB 719 NISERTNGTTPHMAAHYGHLDLVKFFIENDADIEMSNIGYTPHLQMAQGHIMINL 778
 QY 754 LLRHGAHIN 762
 DB 779 LLRHKANPN 787

Search completed: September 17, 2005, 02:43:22
 Job time : 251.039 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 13:13:47; Search time 63.5676 Seconds
(without alignment)
1186.673 Million cell updates/sec

Title: US-10-658-904-2

Sequence: 1 MEGDGGTFWALALALRTFDAG.....SLKFGGHHGPAATLLRSKT 784

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1885.5	46.2	397	2	T46445	hypothetical prote
2	540	13.2	1549	2	T13940	ankyrin - fruit fl
3	513.5	12.6	1765	2	T42714	ankyrin 3, splice
4	513.5	12.6	1943	2	T42715	ankyrin 3, splice
5	513.5	12.6	1943	2	T42713	ankyrin 3, splice
6	513.5	12.6	1961	2	T42716	ankyrin 3, splice
7	509.5	12.5	4377	2	A55575	ankyrin 3, long sp
8	505	12.4	2039	2	T15347	ankyrin-related un
9	500	12.3	1856	2	B35049	ankyrin 1, erythro
10	500	12.3	1880	2	A35049	ankyrin 1, erythro
11	500	12.3	1881	1	SJHUK	ankyrin 1, erythro
12	499.5	12.2	1848	2	S37771	ankyrin - mouse
13	499.5	12.2	1862	2	I49502	ankyrin 2, neuroma
14	484.5	11.9	3924	2	S37431	death-associated p
15	422.5	10.4	1423	1	I37275	hypothetical prote
16	406.5	10.0	426	2	AE2149	hypothetical prote
17	405	9.9	791	2	T42691	hypothetical prote
18	397.5	9.7	1062	2	T14151	inv protein - mous
19	396.5	9.7	1062	2	T30255	inversin - mouse
20	389.5	9.6	1401	2	S11527	alpha-latrotoxin p
21	385	9.4	671	2	T09479	serine/threonine p
22	382	9.4	1411	2	S30355	alpha-latrotoxin p
23	380	9.3	579	2	UCS955	transforming growt
24	373.5	9.2	606	2	UCS956	transforming growt
25	370	9.1	567	2	UCS957	transforming growt
26	353.5	8.7	656	2	I49299	receptor interacti
27	350.5	8.6	2584	2	T24158	hypothetical prote
28	350.5	8.6	2606	2	T24157	hypothetical prote
29	350	8.6	1435	2	T32930	hypothetical prote

30	349.5	8.6	1031	2	T43458	hypothetical prote
31	347.5	8.4	368	2	T18184	ankyrin repeat pro
32	347.5	8.4	736	2	T05137	protein kinase hom
33	338.5	8.3	1184	2	T00253	gene Ankhzn protei
34	333.5	8.2	557	2	T46507	hypothetical prote
35	326.5	8.0	991	2	T25412	hypothetical prote
36	325.5	8.0	1188	2	T19552	hypothetical prote
37	324.5	8.0	855	2	T10655	hypothetical prote
38	323	7.9	606	2	AC2508	hypothetical prote
39	320	7.8	1166	2	B96598	protein F20N2.4 li
40	318.5	7.8	443	2	T01182	hypothetical prote
41	318	7.8	394	2	JU0229	mixed-lineage prot
42	317	7.8	934	1	H71274	probable ankyrin -
43	314	7.7	656	2	T10664	serine/threonine-s
44	314	7.7	801	2	T01289	probable protein k
45	313	7.7	1196	2	T09356	brassinosteroid-in

ALIGNMENTS

RESULT 1	
T46445	hypothetical protein DKFZP434B2328.1 - human (fragment)
C.Species: Homo sapiens (man)	
C.Date: 04-Feb-2000	#sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C.Accession: T46445	
R.BioCcker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.	
submitted to the Protein Sequence Database, January 2000	
A.Reference number: Z23032	
A.Accession: T46445	
A>Status: preliminary	
A.Molecule type: mRNA	
A.Residues: 1-397 <AAA>	
A.Cross-references: UNIPROT:Q9NTA1; EMBL:AL137448	
A.Experimental source: adult testis; clone DKFZP434B2328	
C.Genetics:	
A.Note: DKFZP434B2328.1	
Query Match	46.2%; Score 1885.5; DB 2; Length 397;
Best Local Similarity	94.5%; Pred. No. 5.3e-89;
Matches 375; Conservative 6; Mismatches 15; Indels 1; Gaps 1;	
QY	368 SLSFERESTSDIGTRRPEREACGCHRVDRPSKLMKTILOPOVDVLDLDSGASLHLAVE 447
DB	2 ALTF-ASFLPADLGTDDVQKKLVDAIVSGTISKMLIQDQVDLALDSGASLHLAVE 60
QY	448 AGQEECAKMLLNANPNLSNRGSLPLHMAVERRVRGVVELLARKISVANXDEQWTA 507
DB	61 AGQEECAKMLLNANPNLSNRGSLPLHMAVERRVRGVVELLARKISVANXDEQWTA 120
QY	508 LHPAANGDESSSTRLLLEKNASVNEVDEGRTPMHVAQCHQGENIVRILLRGVDSVLOG 567
DB	121 LHPAANGDESSSTRLLLEKNASVNEVDEGRTPMHVAQCHQGENIVRILLRGVDSVLOG 180
QY	568 KDAMPLHYAAMQGHLPVKKLAKQPGVSVNAQTLDGTPHLHAAQGHYRVARILIDLC 627
DB	191 KDAMPLHYAAMQGHLPVKKLAKQPGVSVNAQTLDGTPHLHAAQGHYRVARILIDLC 240
QY	628 SDVNCSSILAOPTPLVAALGHTSTARLLLRGAKGKAVTSQGYTALHAAANGHLATVK 687
DB	241 SDVNCSSILAOPTPLVAALGHTSTARLLLRGAKGKAVTSQGYTALHAAANGHLATVK 300
QY	688 LLVEEKADVLARGLPQNTALHLLAAAGHSEVVEEIVSADVIDLFPBOGLSALHLLAAQGRH 747
DB	301 LLVEEKADVLARGLPQNTALHLLAAAGHSEVVEEIVSADVIDLFPBOGLSALHLLAAQGRH 360
QY	748 AQTVEITLRHGAHITLQSLKFGGHHGPAATLLRSKT 784
DB	361 AQTVEITLRHGAHITLQSLKFGGHHGPAATLLRSKT 397
RESULT 2	

T13940
ankyrin - fruit fly (*Drosophila melanogaster*)
C|Species: *Drosophila melanogaster*
C|date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C|accession: T13940
R|Dubreuil, R.R.; Yu, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
A|Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in *Drosophila*
A|Reference number: Z17820; MUID:95024098; PMID:7937942
A|Accession: T13940
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-1549 <DUB>
A|Cross-references: UNIPROT:Q2441; EMBL:L35601; NID:g557083; PID:g557084; PIRN:AA032008
C|Genetic8:
A|Cross-references: FLYBase:FBgn0011747

	Query Match	13.2%;	Score 540;	DB 2;	Length 1549;
	Best Local Similarity	34.7%;	Pred. No. 7.5e-20;		
	Matches 128;	Conservative 76;	Mismatches 155;	Indels 10;	Gaps 6;
Qy	STSDLGTRRPEEBCGCHRVDRTSKLMKIIPQ-DVLAIDSGASLHLAVEAGECECA	454			
Dd	ATTEBGLTPLVAASMGCIIN-----VYLLQHESADLPPIRGETPLHAAARNQDDII	481			
Qy	KWLLINNANPNLSNRGSTPLHMAVERRRVGVEILLARKISVNAKEDONTALHPAQN	514			
Dd	R-IILRSRAKVAVIAREGOTPLVASRLGNINIIMLLQHGAIEINAOSDKXSALHIAKE	540			
Qy	GDESSITLLEKNASVNEVFEGARTPMHVAOHOGENIVRIILIRGVDSVOGGDAMLPL	574			
Dd	GOENIVQVLLENAGENNNAVTKKGFTPLHACKYGRKNVVQLLONGASIDPQGNDVTPL	600			
Qy	HYAAMQGHLPYVKLLAKOPGVSVNAQTLDGRTPLHAAQRHYVARILLIDLCSDVNC	634			
Dd	HVATHYNPSIYEILLIKN-GSSPNLCARNGOCALHIACKNNYLEIAMQLLHGADVNIIS	659			
Qy	LIAQTPLPVAAETGHTSTARLLIRHGAGKEAVTDSGYTALLHAARNGHLAVKLVYEKA	694			
Dd	KSGFSPPLHLAAOGGVDNVQILLBYGV-ISAANKGLPLPHVAOEGHVIVSQILLBERGA	718			
Qy	DVLAQPLNQTLHLTHAAAGHSEVEELVSADV-IDLFDEOGLSALHLAAQGRALQVET	753			
Dd	NISESTRNGYTPPLHAAHYGHLDLYKFETENDADIEMSNIGYTPPLHQAAGGHMINTL	778			
Qy	LIRHGAHIN 762				
Dd	LIRHRKANPN 787				

RESULT 3
 T42714
 ankryrin 3, splice form 2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 #sequence _revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42714
 R:Peeters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ank3 (epithelial ankryrin), a widely distributed new member of the ankryrin gene
 the repeat domain
 A:Reference number: Z22237, MUID:95340633, PMID:7615634
 A:Accession: T42714
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1765 <PER>
 A:Cross-references: UNIPROT:O61307; EMBL:I40632; NID:G710548; PID:G710551; PIDN:AAB01605
 A:Experimental source: strain C57BL/6J; kidney
 C:Genetics:
 A:Gene: Ank3
 A:Map position: 10
 A:Introns: 1587/1
 C:Superfamily: ankryrin; ankryrin repeat homology
 C:Keywords: alternative splicing

Query Match	12.6%;	Score 513.5;	DB 2;	Length 1765;
Best Local Similarity	35.8%;	Pred. No. 2e-18;		
Matches 132;	Conservative 51;	Mismatches 151;	Indels 35;	Gaps 4;
QY	VDLALDSGSLHLTAAVEAGQECACKWLLNNANPNLSNRGSTPLHMAVERRVGVVELL	490		
DB	343 VDDVTNDVLTALHVAAHCGHYKAKYKVLDDKKSFPNAKALNGFPLHIACKKRRIRVVELL	402		
QY	491 LARKISVNAKDEDQWTALHPAAQNGDESSSTRILLEKNASVNEVDPEGRTPMHWACQHQOE	550		
DB	403 LKHGASIAVATESGSLTPIHVAAFMGHVNIVSQLMHGHASPNITNVREGTALHMAARSGQA	462		
QY	551 NIVRTLLRGVVDVLSQGDAMTLPIHYAAMQGHPIYKGLAKPGQSVNAOQLDRTPLHL	610		
DB	463 EVKRLTVQDGAQVEAKADQDTPHLHSARLKGADIVQQLDQ--GASPNAAITTSGLTPLHL	521		
QY	611 AARGGHYRVARLLIILCSPDVN-----VCSLLAQ-----	638		
DB	522 AAREHEDVAAARLLDHLGASLSITTKGPTPIHVAAKYKGLVASILLQKSAPDAAGKSG	581		
QY	639 -TPLHVAAFETGTTSTRALLLRGAGKEAVTSDGYTALHLAARNGHLATVKLLVEKKDVL	697		
DB	582 LPLHVAAYDYQKVALLLDQASPHAAAKNRYTPHLHIAKKNQMDIATSLSEYGADAN	641		
QY	698 ARGPNQTLHLTAAAHGSEVVEELVSADY-IDLPDEQGLSALHLAQRRAHQFVETLLR	756		
DB	642 AVTRGIGASVHLAAQEGHVDWVSLLSRRNANVLSNKSGLTPLHLAAQEDRVVNAEVLVN	701		
QY	757 HGAHINLQGS 765			
DB	702 QGAHYDAQRT 710			

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RESULT 4
T42715
ankyrin 3, splice form 3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42715
R:Peterson, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L
J. Cell Biol. 130, 313-330, 1995
A>Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: Z22237; MID:95340633; PMID:7615634
A:Accession: T42715
A>Status: preliminary; translated from GB/EMBL/DD8J
A:Molecule type: mRNA
A:Residues: 1-1940 <PEP>
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:introns: 834/1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match      12.6%; Score 513.5; DB 2; Length 1940;
Best Local Similarity 35.8%; Pred. No. 2.2e-18;
Matches 132; Conservative 51; Mismatches 151; Indels 35; Gaps 4;

Dy 431 VDLALDSGSLHLAAVEAGECECAKMLLNANPNLSNRSGSTPLHMAVERVRGVLEL 490
|||:::||::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 343 VDDVTNDYITALLVNAHCCHYKAIVLLDKASBPNAALNGFTLHLACKNRIRVMELL 402

491 IARKISVNAKDEDPWTALHPFAONGDESSTRLLLEKNASVNEVDPEGETPMVAQCQOE 550
|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 403 LHGGASTQAVTSSGLPRHVAAFMGHVNIYSQLMHHGASPTTVRGFTALHMAARSGOA 462

551 NIVRIILRRGVDSLQGDAMLPHTAAMOGHLPIYVLAKAQPGVSVAAGTLDRGTPLHL 610
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
463 EVRYRVYVGAGVGAENAKADQDTDFIHSARLGKADIYOOLLQQ--GASPVAATTSGYTPHL 521

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QY 611 AAQRGHYVARILLDLCSDVN-----VCSLLAQ----- 638
DB 522 AAREGHEVDVAAFLDHDGASLITTKKGFPLHVAAKYGLKLEVASILLQKSASPDAAKSG 581
QY 639 -TPLHVAETGHTSTARLLHHRGAGKEAVTSDGYTALHAAANGHLATVKLLVEEKADVL 697
DB 582 LTPHVAAHYDNOKVALLLDQASPHAAKNGITPLHIAAKKQMDATSLIEYGADAN 641
QY 698 ARGPLNQTALHAAAHGSEVVEELVSADV-IDLPDEQGLSALHIAAQGRHAQVETTLR 756
DB 642 AVTRGSIASVHLAAQEGHVDVWSLLSRANVNLNKSGLTPLHIAAQEDRVNVAEVLVN 701
QY 757 HGAHINLOS 765
DB 702 QGAHVDAQT 710

RESULT 5
T42713
ankyrin 3, splice form 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42713
R:Peterson, L.L.; John, K.M.; Lu, P.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A>Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: 222237; PMID:95340633; PMID:7615634
A:Accession: T42713
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1943 <P>
A:Cross-references: UNIPROT:Q61307; EMBL:LA0632; NID:G710548; PID:G710550; PIDN:AA01606
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 855/1
C:Function:
A:Description: supposed to play an important role in the polarized distribution of many
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 12.6%; Score 513.5; DB 2; Length 1943;
Best Local Similarity 35.8%; Pred. No. 2.2e-18;
Matches 132; Conservative 51; Mismatches 151; Indels 35; Gaps 4;

QY 431 VDLALDSGASLLHVAEGOECAKWLNNANPNLSNRGSTPLHMAVERVAGVETL 490
DB 343 VDDVTNDVLTALHVAACGHYKAVKVLDDKASPNKALNGFTPLHIAKKRIRVETL 402
QY 491 LARKISVNAKDDQMTALHFAANGDESTRLLLEKNAVNEVDPEGRTPMVAOCHGOE 550
DB 403 LKHGASIQAVTESGLTPHVAAPMGHVNIVSQMHGASPTTNVREGTALHMAASGQA 462
QY 551 NIVRILLRGGVDSIQGDAMLPLHYAANQGHLPYKLLAKOPGVSVNAQTLDGRTPLH 610
DB 463 EVRYLVQDGAQVBAKADQTPHISARLGKADIVQGLIQ-QASPNAAATSGTTPHL 521
QY 611 AAQRGHYVARILLDLCSDVN-----VCSLLAQ----- 638
DB 522 AAREGHEVDVAAFLDHDGASLITTKKGFPLHVAAKYGLKLEVASILLQKSASPDAAKSG 581
QY 639 -TPLHVAETGHTSTARLLHHRGAGKEAVTSDGYTALHAAANGHLATVKLLVEEKADVL 697
DB 582 LTPHVAAHYDNOKVALLLDQASPHAAKNGITPLHIAAKKQMDATSLIEYGADAN 641
QY 698 ARGPLNQTALHAAAHGSEVVEELVSADV-IDLPDEQGLSALHIAAQGRHAQVETTLR 756
DB 642 AVTRGSIASVHLAAQEGHVDVWSLLSRANVNLNKSGLTPLHIAAQEDRVNVAEVLVN 701

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QY 757 HGAHINLOS 765
DB 702 QGAHVDAQT 710

RESULT 6
T42716
ankyrin 3, splice form 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42716
R:Peterson, L.L.; John, K.M.; Lu, P.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A>Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: 222237; PMID:95340633; PMID:7615634
A:Accession: T42716
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1961 <P>
A:Cross-references: UNIPROT:Q61307; EMBL:LA0632; NID:G710548; PID:G710552; PIDN:AA01607
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 12.6%; Score 513.5; DB 2; Length 1961;
Best Local Similarity 35.8%; Pred. No. 2.2e-18;
Matches 132; Conservative 51; Mismatches 151; Indels 35; Gaps 4;

QY 431 VDLALDSGASLLHVAEGOECAKWLNNANPNLSNRGSTPLHMAVERVAGVETL 490
DB 343 VDDVTNDVLTALHVAACGHYKAVKVLDDKASPNKALNGFTPLHIAKKRIRVETL 402
QY 491 LARKISVNAKDDQMTALHFAANGDESTRLLLEKNAVNEVDPEGRTPMVAOCHGOE 550
DB 403 LKHGASIQAVTESGLTPHVAAPMGHVNIVSQMHGASPTTNVREGTALHMAASGQA 462
QY 551 NIVRILLRGGVDSIQGDAMLPLHYAANQGHLPYKLLAKOPGVSVNAQTLDGRTPLH 610
DB 463 EVRYLVQDGAQVBAKADQTPHISARLGKADIVQGLIQ-QASPNAAATSGTTPHL 521
QY 611 AAQRGHYVARILLDLCSDVN-----VCSLLAQ----- 638
DB 522 AAREGHEVDVAAFLDHDGASLITTKKGFPLHVAAKYGLKLEVASILLQKSASPDAAKSG 581
QY 639 -TPLHVAETGHTSTARLLHHRGAGKEAVTSDGYTALHAAANGHLATVKLLVEEKADVL 697
DB 582 LTPHVAAHYDNOKVALLLDQASPHAAKNGITPLHIAAKKQMDATSLIEYGADAN 641
QY 698 ARGPLNQTALHAAAHGSEVVEELVSADV-IDLPDEQGLSALHIAAQGRHAQVETTLR 756
DB 642 AVTRGSIASVHLAAQEGHVDVWSLLSRANVNLNKSGLTPLHIAAQEDRVNVAEVLVN 701
QY 757 HGAHINLOS 765
DB 702 QGAHVDAQT 710

RESULT 7
A55575
ankyrin 3, long splice form - human
N:Alternate names: ankyrin G
C:Species: Homo sapiens (man)
C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55575
R:Kordeli, E.; Lambert, S.; Bennett, V.
J. Biol. Chem. 270, 2352-2359, 1995
A>Title: Ankyrin-G, A new ankyrin gene with neural-specific isoforms localized at the ax
A:Reference number: A55575; PMID:95138209; PMID:7836469
A:Accession: A55575

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A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-4377 <KOR>
A:Cross-references: UNIPROT:Q12955; GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025
C:Genetics:
A:Gene: GDB:ANK3
A:Cross-references: GDB:424503; OMIM:600465
A:Map position: 10q21-10q21
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C:Keywords: alternative splicing; peripheral membrane protein
F:73-105/Domain: ankyrin repeat homology <AN01>
F:106-138/Domain: ankyrin repeat homology <AN02>
F:139-171/Domain: ankyrin repeat homology <AN03>
F:172-200/Domain: ankyrin repeat homology <AN04>
F:201-223/Domain: ankyrin repeat homology <AN05>
F:234-266/Domain: ankyrin repeat homology <AN06>
F:267-299/Domain: ankyrin repeat homology <AN07>
F:300-332/Domain: ankyrin repeat homology <AN08>
F:333-365/Domain: ankyrin repeat homology <AN09>
F:366-398/Domain: ankyrin repeat homology <AN10>
F:399-431/Domain: ankyrin repeat homology <AN11>
F:432-464/Domain: ankyrin repeat homology <AN12>
F:465-497/Domain: ankyrin repeat homology <AN13>
F:498-530/Domain: ankyrin repeat homology <AN14>
F:531-563/Domain: ankyrin repeat homology <AN15>
F:564-596/Domain: ankyrin repeat homology <AN16>
F:597-629/Domain: ankyrin repeat homology <AN17>
F:630-662/Domain: ankyrin repeat homology <AN18>
F:663-695/Domain: ankyrin repeat homology <AN19>
F:696-728/Domain: ankyrin repeat homology <AN20>
F:729-761/Domain: ankyrin repeat homology <AN21>
F:762-794/Domain: ankyrin repeat homology <AN22>
F:795-827/Domain: ankyrin repeat homology <AN23>

Query Match 12.5%; Score 509.5; DB 2; Length 4377;
Best Local Similarity 35.2%; Pred. No. 9,46-18;
Matches 130; Conservative 52; Mismatches 152; Indels 35; Gaps 4;

Qy 431 VDLALDSASLHLAVEAGQECATKLLNANPMLSNRSGSTPLHMAVERKGVZEL 490
Db 360 VDDVTNDYLTALHVAHCGHKYKAVLVLLDKCKNPAKALNGFTPLHACKNRKIKWELL 419
Qy 491 LARKTSVNAKQEDQDTALHFAAQNQDESSTRLLEKSNVNEVDEGRTPMHVACQHQE 550
Db 420 LKHGASIGAVTBSGTPRHVAAPFKGHVNVISQLMHGNSPMTVNRGSETALHMAARSQA 479
Qy 551 NIVRLILRRGVNLSQGDAMLPRLHYAAMQGHLPYVKLLAQPGVSVNAQTLDEGTPHL 610
Db 480 EVVRVLYVDGAQVEAKADDDQTPRLHISARLGRADIVQDLQO-GASPVAAATTSGYTPHL 538
Qy 611 AAGRGHYVARLILDLGSDVN-----VCSLLAQ----- 638
Db 539 SARBEHEVVAFLDLHGASLSTTTKKGFTPLHVAAKYGLKLEVANLLDKKSASPDAAKSG 598
Qy 639 -TPHVAATGHTSTAPRLILHRGAGKEAVTSDGTALHAAARNGHILATVKLLVEEKADVL 697
Db 599 LTPHVAHYNDQKATALLLDGASPHAAAKNGYTPRLHAAKQMDATATLLTBEGGADAN 658
Qy 698 ARGPLNQALHAAAGHSEVEELVSADV-IDLFEQGLSALHAAQGRHAQVETTLR 756
Db 659 AVTRGIGASVHLAAQEGHVDWVSLILGRANVNLINSGSLTPHLAAQEDRVNVAEVLVN 718
Qy 757 HGAHNTLOS 765
Db 719 QGAHVDAQT 727

RESULT 8
T15347
ankyrin-related unc-44 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text change 09-Jul-2004
C:Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282

R:Gatung, S.
Submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid B0350.
A:Reference number: Z18332
A:Accession: T15347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2039 <GAT>
A:Cross-references: UNIPROT:Q17489; EMBL:U50071; NID:g1208871; PID:g1208873; PIDN:AAA9344
A:Accession: T15346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1000, 'SKQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVBE'
32, 'S', 2034-2035, 'GSPTRSVPEERHSHQHDHSGST' <GA2>
A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1
A:Accession: T15344
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'ORSTIVAESTSEQVPE', 1934-1935, 'EC'
<GA3>
A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208874; PIDN:AAA93444.1
A:Accession: T15345
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVBE'
PTRRSVEPERHSHQHDHSGST' <GA4>
A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208876; PIDN:AAA93446.1
R:Otsuka, A.J.; Franco, R.; Yang, B.; Shih, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontrakulpoor
U. Cell Biol. 129, 1081-1092, 1995
A:Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Caer
A:Reference number: A57282; MUID:95263663; PMID:77494957
A:Accession: A57282
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-852, 'GGG', 856-1000, 'SKQHRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEI
'SHED', 2007-2008, 'TT', 2011, 2017, 'TT', 2020-2022, 'SHIS' <OTS>
A:Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608
A:Accession: B57282
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E'
V', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPTRRSVEPERHSH', 1984-1985, 'EDHGS', 19
A:Accession: C57282
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 194, 'P', 196, 'T', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, 824, 'S', 826, 'ER', 829, 'E'
4, 'TV', 1828, 'ESTS', 1833, 'QV', 1836, 'E', 1934-1935, 'EQS', 1939, 'ESBS', 1944, 'REDGSTVTT', 194
A:Cross-references: GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:g790604
C:Genetics:
A:Gene: CESP:unc-44
A:Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979/
C:Superfamily: ankyrin; ankyrin repeat homology
F:164-192/Domain: ankyrin repeat homology <AN04>
F:358-390/Domain: ankyrin repeat homology <AN11>
F:391-423/Domain: ankyrin repeat homology <AN11>

Query Match 12.4%; Score 505; DB 2; Length 2039;
Best Local Similarity 26.0%; Pred. No. 6,36-18;
Matches 189; Conservative 97; Mismatches 277; Indels 160; Gaps 20;

Qy 160 SDFGLAKNGLSHSDSMGLFETIAYL--PPERIEKSRLEPTKIDVYSFA--IWIWG 215
Db 57 TDINTSNANGLSHLSKSGHSVVAEELIKRQAVDVAARKNGTALHISLNGOSLIYV 116
Qy 216 VLTQKKPFADEKNIILHIMVYVVGKRPDLPPVCARPACSHLIR----- 260
Db 117 ILVE-----NCANVNVQSVNGFTPLVMAAGENHEVVKYLLKGGANQALSTEDGFTP 168
Qy 261 LMGRCNQGDRVRRTPPEIISFTE-----DLCEKPDDEVKET-----AADDLVKSPPEP 309
Db 169 LAVALQGHDRVVAVVLLENDKGRVRLPALHIAAKQDDTPAATLILONEHNPVTS---- 224

RESULT 9

B35049
ankyrin 1, erythrocyte splice form 3 - human
N.Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
M.Contains: ankyrin 2.2, erythrocyte
C.Species: Homo sapiens (man)
C.Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
C.Accession: B35049
R.Lambert, S.; Yu, H.; Pichal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; F.
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A.Title: cDNA sequence for human erythrocyte ankyrin.
A.Reference number: A35049; MUID:90175370; PMID:1689849
A.Accession: B35049
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-1856 <LAM>
C.Genetics:
A.Gene: GDB:ANK1; ANK
A.Cross-references: GDB:118737; OMTW:182900
A.Map position: 8p11.2-8p11.2
C.Superfamily: ankyrin; ankyrin repeat homology
C.Keywords: alternative splicing
F.2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MA>
F.2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte form 3 #status predicted <MA>
F.44-76/Domain: ankyrin repeat homology <AN01>
F.77-109/Domain: ankyrin repeat homology <AN02>
F.110-142/Domain: ankyrin repeat homology <AN03>
F.143-171/Domain: ankyrin repeat homology <AN04>
F.172-204/Domain: ankyrin repeat homology <AN05>
F.205-237/Domain: ankyrin repeat homology <AN06>
F.238-270/Domain: ankyrin repeat homology <AN07>
F.271-303/Domain: ankyrin repeat homology <AN08>

Dy 310 RSEVVPARLRKAAPPTPNDSYSELISQDLSGVSQAIVEGEELSRSSSESKELPSSSGK 369
Db 225 KSGETPLHI-----AAHGHK-NVGQL--LEKGANVNYQAHHNISPLHVATKM----- 270
Oy 370 RLGSVSDVASFSRRGLSLSPFEREPSTSDIGTTRRPPEEACGGHYVDYSKLMILOPQ 429
Db 271 ---GRTNAMNLISRGAII-----DSRTKDLITPLH---CAARSHGD-----Q 307
Oy 430 DVDIALDSAGSL-----LHLAV 446
Db 308 VVDLLVVGADPISAKTNGGLAPLHMAAQGDHVDAARTLLYHRAPVDVTVDYLTPLVAA 367
Oy 447 EAGGECECKXMTLLNNANNLNRRGSTPLHNAVERRVGVTEILLAKISYNADDEQWT 506
Db 368 HCGHVRVAKKLLIDBSADNSPRALNGFTPLHACKKNRIKVLELLIKYRALAEATESGLT 427
Oy 507 ALHPAAQGDSESTRLELKNAVNVEVFEEERTPMHVAQHCHQENIYAILRRGVDSLQ 566
Db 428 PLHVAAPFGAIINITYILYLLQGANGPDVETVRBETPLHIAARANQTDVYKVLIRNGAKDAQ 487
Oy 567 GKDAMLPLHVAAMOQHRLPYVKLLAKQPESVSNAAQTLDGRTPLHIAAQGHYVARILIDL 626
Db 488 ARELOTPLHIASRLGNITDIYLLL-QAGANSNAATTBDMSYPLHIAAKGQEBAVGIILDH 546
Oy 627 CSD-----VVCSLIAQ-----TPLHVAAEHGHSYA 653
Db 547 NADTKTLTKKGFPLHLASKYGNLEVVALLERGTDPVIDIEKNQOTPLHVAAHNNDKVA 606
Oy 654 RLILHRCGKRAVNSDGYTALHIAABNGHLATVKKLYBEKADYLAARGEPLNTALHLAAH 713
Db 607 MLILENGSASAAAKNGTTPHLIAKKKQMEIASTILOPKADPNPAKSAGTPLHLSAOE 666
Oy 714 GHSEVVEELV-SADVITDFDEQGLSALHIAAQGRHAQTVEITLRRGAHINLSLKFOGKH 772
Db 667 GHKEISGLIENGSDVGAKANNGLTAMLCAQEDHVPAPAQLLYNNGAELN---SKTVAGY 723
Oy 773 GP 774
Db 724 TP 725

[illegible]

QY 481 RRAGVVELLLARKISVNAKDEDOFTALHPAAQNGDESSSTLLLEKNASVNEVDEEGTTP 540
DB 315 GDHLDCVRLLOQYDAEIDDTLLDHLTPPLHVAACGHRVAVKLLDKGAKPNSRLNGFTTP 374
QY 541 MVAACQHQENIVRLIRRGVDSLOQKQAMPLHYAAMOGHLPYKLLAAQPGVSVAQ 600
DB 315 LHIACKKHVRVMEILLTKGASIDAVTESGLTPPLHVASFMGHPPLVKNLL-QRGASPVVS 433
QY 601 TLDEGTPLHAAQGRHVRARILLIDLCSDVNVCSLLAQTPLHVAAEFTGHTSTARLLHRG 660
DB 434 NVKVEPTLHMAABAGHTEVAKYLLQNKAKVNAKAKDDQTPHICARIGHTMNVKLLLENN 493
QY 661 AGKAVTSDGTALHAAQNGHATVYKLLVEKADVLARGPLNQALHAAAHGSEVVE 720
DB 494 ANPMLATJATGHTPLHIAAREGHVETVLLALEKBAQACMTKKKFTPLHVAAYKGVVAE 553
QY 721 ELV-----SADVIDLP----- 731
DB 554 LLLERDHPNAAGKNGLTPLHVAVHHNNIDIVKLLLRGSGPHSPANNGTTPHIAAKON 613
QY 732 -----DEQSLALHAAQGRHAAQTVEYETLLRHGAHINLOS----- 765
DB 614 QVEVARSLLOQGSANASVQGTTPHIAAAGEHAEVALLSKQANGNLAKSGLTPLH 673
QY 766 LKFGGCHGPATLL 779
DB 674 LVAQEGHVPVADVLL 687

RESULT 12

S37771

ankyrin, erythrocyte - mouse

C:Species: Mus musculus (house mouse)

C:Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C:Accession: S37771

R:Bitkemeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.

J. Biol. Chem. 268, 9533-9540, 1993

A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found am

A:Reference number: S37771; MUID:93252825; PMID:8486643

A:Accession: S37771

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1848 <BIR>

A:Cross-references: UNIPROT:Q61302; EMBL:X69063; NID:g311816; PIDD:CAA48601.1; PID:g3118

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

F:48-80/Domain: ankyrin repeat homology <AN01>
F:81-113/Domain: ankyrin repeat homology <AN02>
F:114-146/Domain: ankyrin repeat homology <AN03>
F:147-175/Domain: ankyrin repeat homology <AN04>
F:176-208/Domain: ankyrin repeat homology <AN05>
F:209-241/Domain: ankyrin repeat homology <AN06>
F:242-274/Domain: ankyrin repeat homology <AN07>
F:275-307/Domain: ankyrin repeat homology <AN08>
F:308-340/Domain: ankyrin repeat homology <AN09>
F:341-373/Domain: ankyrin repeat homology <AN10>
F:374-406/Domain: ankyrin repeat homology <AN11>
F:407-439/Domain: ankyrin repeat homology <AN12>
F:440-472/Domain: ankyrin repeat homology <AN13>
F:473-505/Domain: ankyrin repeat homology <AN14>
F:506-538/Domain: ankyrin repeat homology <AN15>
F:539-571/Domain: ankyrin repeat homology <AN16>
F:572-604/Domain: ankyrin repeat homology <AN17>
F:605-637/Domain: ankyrin repeat homology <AN18>
F:638-670/Domain: ankyrin repeat homology <AN19>
F:671-703/Domain: ankyrin repeat homology <AN20>
F:704-736/Domain: ankyrin repeat homology <AN21>
F:737-769/Domain: ankyrin repeat homology <AN22>
F:770-802/Domain: ankyrin repeat homology <AN23>

Query Match 12.2%; Score 499.5; DB 2; Length 1848;
Best Local Similarity 37.1%; Pred. No. 1.1e-17;
Matches 127; Conservative 52; Mismatches 154; Indels 9; Gaps 4;

QY 442 LHLAVEAGQESCAKMLNNANPULSRRGSTPLHMAVERVGVVELLLARKISVNAKD 501
DB 181 LHLARRDDRTAAVLLQNDPNPVLSTKFTPLHIAAHENINVAQLLNRGASVAFTP 240
QY 502 EDQWTALHPAAQNGDESSSTLLLEKNASVNEVDEEGTTPHVAACQHQENIVRLIRGV 561
DB 241 QNGITPLHIASRRGNVIMVRLIDRGAAQIEFTQDELTPLHICARNGHVRISEILLHGA 300
QY 562 DVSLQGDAMPLHYAAMOGHLPYKLLAAQPGVSVAQTLDSGTPLHAAQGRHVRAR 621
DB 301 PIQAKTRNGLSPIHMAAQGHLDVRLLL-QYNABIDITLLDTPPLHVAACGHRVAK 359
QY 622 ILIDLCSDVNVCSLLAQTPLHVAAEFTGHTSTARLLHRGAKGKAVTSDGTALHAAARNG 681
DB 360 VLLDKGAPNSRLNGFTPLHIACKKHVRVMEILLTKGASIDAVTESGLTPPLHVASFMG 419
QY 682 HLAATVLLVEEKADVLARGPLNQALHAAAHGSEVVEBLVSDV--IDLPEQGLISA 738
DB 420 HLPVIVQULLQGSAPNSVNVVETPLHMAABAGHTEVAKYLLQNKAKANAKAKDDQ--TP 477
QY 739 LHLAAQGRHAAQTVEYETLLRHGAHINLOSUKFGGCHGPATLLR 780
DB 478 LHCARIGHTGMVKLLLENGASPNLAT---TAGHTPLHTAR 516

RESULT 13

I49502

ankyrin - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49502

R:White, R.A.; Bitkemeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.

Mamm. Genome 3, 281-285, 1992

A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory dom

A:Reference number: I49502; MUID:92345117; PMID:1386265

A:Accession: I49502

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1862 <RBS>

A:Cross-references: UNIPROT:Q02357; GB:M84756; NID:g191939; PIDD:AAA37236.1; PID:g191940

C:Genetics:

A:Gene: Ank-1

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

F:40-72/Domain: ankyrin repeat homology <AN02>
F:73-105/Domain: ankyrin repeat homology <AN03>
F:106-138/Domain: ankyrin repeat homology <AN04>
F:139-167/Domain: ankyrin repeat homology <AN05>
F:168-200/Domain: ankyrin repeat homology <AN06>
F:201-233/Domain: ankyrin repeat homology <AN07>
F:234-266/Domain: ankyrin repeat homology <AN08>
F:267-299/Domain: ankyrin repeat homology <AN09>
F:300-332/Domain: ankyrin repeat homology <AN10>
F:333-365/Domain: ankyrin repeat homology <AN11>
F:366-398/Domain: ankyrin repeat homology <AN12>
F:399-431/Domain: ankyrin repeat homology <AN13>
F:432-464/Domain: ankyrin repeat homology <AN14>
F:465-497/Domain: ankyrin repeat homology <AN15>
F:498-530/Domain: ankyrin repeat homology <AN16>
F:531-563/Domain: ankyrin repeat homology <AN17>
F:564-596/Domain: ankyrin repeat homology <AN18>
F:597-629/Domain: ankyrin repeat homology <AN19>
F:630-662/Domain: ankyrin repeat homology <AN20>
F:663-695/Domain: ankyrin repeat homology <AN21>
F:696-728/Domain: ankyrin repeat homology <AN22>
F:729-761/Domain: ankyrin repeat homology <AN23>
F:762-794/Domain: ankyrin repeat homology <AN23>

Query Match 12.2%; Score 499.5; DB 2; Length 1862;
Best Local Similarity 37.1%; Pred. No. 1.1e-17;
Matches 127; Conservative 52; Mismatches 154; Indels 9; Gaps 4;

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